```
398077
Seq. No.
                  LIB3431-010-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  502
E value
                  8.0e-51
Match length
                  142
% identity
NCBI Description
                  (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                  398078
Seq. ID
                  LIB3431-010-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q548603
BLAST score
                  210
                  8.0e-17
E value
Match length
                  82
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >qi 478404 pir JQ2247 photosystem I chain D precursor -
                  barley >qi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
                  398079
Seq. No.
                  LIB3431-010-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501190
BLAST score
                  214
E value
                  5.0e-17
Match length
                  63
% identity
NCBI Description
                  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
                  >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
                  - maize >gi 596080 (U17351) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  398080
                  LIB3431-010-P1-K1-G6
Seq. ID
Method
                  BLASTX
                  g548605
NCBI GI
BLAST score
                  306
E value
                  1.0e-51
Match length
                  132
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
                  398081
Seq. No.
                  LIB3431-010-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  567
                  2.0e-58
E value
```

Match length 122 % identity 87 NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >qi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf ~1508256A ribulose bisphosphate carboxylase S [Oryza sativa] 398082 Seq. No. Seq. ID LIB3431-010-P1-K1-G8 Method BLASTX NCBI GI q115796 BLAST score 737 E value 2.0e-78 Match length 148 96 % identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 218174 dbj BAA00537 (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza sativa] 398083 Seq. No. Seq. ID LIB3431-010-P1-K1-G9 Method BLASTX NCBI GI g2737973 BLAST score 742 E value 5.0e-79 Match length 145 96 % identity NCBI Description (U83625) protein kinase ZmMEK1 [Zea mays] 398084 Seq. No. LIB3431-010-P1-K1-H10 Seq. ID . Method BLASTX NCBI GI g3551523 BLAST score 247 E value 6.0e-21 156 Match length -37 % identity NCBI Description (AB017026) oxysterol-binding protein [Mus musculus] 398085 Seq. No. Seq. ID LIB3431-010-P1-K1-H11 Method BLASTX NCBI GI q231610 BLAST score 257 E value 4.0e-22 Match length 74 76 % identity ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR NCBI Description >gi_67880 pir_PWNTG H+-transporting ATP synthase (EC

3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi 19785 emb CAA45152 (X63606) ATP synthase

NCBI Description

398086 Seq. No. Seq. ID LIB3431-010-P1-K1-H5 Method BLASTX NCBI GI q4206112 BLAST score 639 E value 5.0e-67 127 Match length % identity 94 (AF097662) alpha tubulin [Mesembryanthemum crystallinum] NCBI Description 398087 Seq. No. LIB3431-010-P1-K1-H9 Seq. ID Method BLASTX NCBI GI g3876874 BLAST score 211 9.0e-17 E value Match length 88 % identity 43 (Z81535) Similarity to Human signal recognition particle NCBI Description receptor alpha subunit (SW:P08240) [Caenorhabditis elegans] 398088 Seq. No. LIB3431-010-P1-N1-A10 Seq. ID Method BLASTX NCBI GI g2911886 BLAST score 154 6.0e-12 E value 56 Match length % identity 70 NCBI Description (AF047663) Contains similarity to Pfam domain: PF00448 (SRP54), Score=14.7, E-value=2.7e-12, N=1 [Caenorhabditis elegans) 398089 Seq. No. Seq. ID LIB3431-010-P1-N1-A11 Method BLASTN NCBI GI g218207 BLAST score 187 1.0e-101 E value 323 Match length 89 % identity Oryza sativa mRNA for the small subunit of NCBI Description ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS1139 398090 Seq. No. Seq. ID LIB3431-010-P1-N1-A3 Method BLASTN NCBI GI g218209 BLAST score 124 E value 3.0e-63 Match length 248 % identity 98

(gamma subunit) [Nicotiana tabacum]

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

Oryza sativa mRNA for the small subunit of

pOSSS2106 Seq. No. 398091 Seq. ID LIB3431-010-P1-N1-A5 Method BLASTX NCBI GI q3367536 BLAST score 233 E value 2.0e-19

Match length 48 % identity 92

(AC004392) Contains similarity to symbiosis-related like NCBI Description

protein F1N20.80 gi 2961343 from A. thaliana BAC gb AL022140. EST gb T04695 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 398092

LIB3431-010-P1-N1-A9 Seq. ID

Method BLASTX NCBI GI q417544 BLAST score 206 2.0e-16 E value Match length 43 % identity

PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR NCBI Description

(PHOTOSYSTEM I 20 KD PROTEIN) (PSI-D) (PS I SUBUNIT 5) >gi 320209 pir A60695 photosystem I chain II precursor cucumber >gi_625966_pir__JQ2132 photosystem I complex 20K protein precursor - cucumber >gi_227772_prf__1710320A

photosystem I 20kD protein [Cucumis sativus]

Seq. No. 398093

LIB3431-010-P1-N1-B1 Seq. ID

Method BLASTN q2072554 NCBI GI BLAST score 185 E value 1.0e-100 Match length 185

% identity

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

Seq. No. 398094

Seq. ID LIB3431-010-P1-N1-B11

Method BLASTX NCBI GI q6093830 BLAST score 157 E value 1.0e-10 Match length 50 % identity

PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) NCBI Description

[CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi 3337435 (AF060198) PsbY precursor;

putative photosytem II peptide [Spinacia oleracea]

Seq. No. 398095

LIB3431-010-P1-N1-B4 Seq. ID

BLASTN Method

Match length

```
NCBI GI
                     g20262
  BLAST score
                     315
  E value
                     1.0e-177
  Match length
                     327
  % identity
                     99
  NCBI Description O.sativa light-induced mRNA
                     398096
  Seq. No.
  Seq. ID .
                     LIB3431-010-P1-N1-B5
  Method
                     BLASTN
                                   35
  NCBI GI
                     q1835730
  BLAST score
                     65
  E value
                     3.0e-28
  Match length
                     109
   % identity
  NCBI Description
                     Oryza sativa photosystem II 10 kDa polypeptide mRNA,
                     complete cds
  Seq. No.
                     398097
                     LIB3431-010-P1-N1-B6
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g115813
  BLAST score
                     152
  E value
                     6.0e-10
  Match length
                     33
                     85
  % identity
                     CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
  NCBI Description
                     CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                     chlorophyll a/b-binding protein [Lycopersicon esculentum]
  Seq. No.
                     398098
                     LIB3431-010-P1-N1-C10
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g2244734
  BLAST score
                     275
                     2.0e-24
  E value
Match length
                     60
  % identity
                     88
  NCBI Description (D88414) actin [Gossypium hirsutum]
                     398099
  Seq. No.
  Seq. ID
                     LIB3431-010-P1-N1-C11
  Method
                     BLASTN
  NCBI GI
                     g6006355
  BLAST score
                     307
  E value
                     1.0e-172
  Match length
                     331
                     98
  % identity
  NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
  Seq. No.
                     398100
                     LIB3431-010-P1-N1-C12
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     g2072726
  BLAST score
                     283
  E value
                     1.0e-158
```

```
% identity
NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2
                   398101
Seq. No.
Seq. ID
                   LIB3431-010-P1-N1-C2
Method
                   BLASTN
NCBI GI
                   q3885887
                   359
BLAST score
E value
                   0.0e + 00
Match length
                   366
% identity
                   100
                   Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                   complete cds
                   398102
Seq. No.
Seq. ID
                   LIB3431-010-P1-N1-C4
Method
                   BLASTN
NCBI GI
                   g20181
BLAST score
                   45
E value
                   3.0e-16
                   92
Match length
                   89
% identity
                   Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                   a/b-binding protein
                   398103
Seq. No.
Seq. ID
                   LIB3431-010-P1-N1-C7
Method
                   BLASTX
NCBI GI
                   g115813
BLAST score
                   210
E value
                   1.0e-16
Match length
                   48
                   83
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                   CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                   398104
Seq. ID
                   LIB3431-010-P1-N1-D12
                   BLASTN
Method
NCBI GI
                   g218134
BLAST score
                   349
E value
                   0.0e+00
Match length
                   403
% identity
                   97
NCBI Description Rice mRNA for Histone H3
                   398105
Seq. No.
                   LIB3431-010-P1-N1-D2
Seq. ID
                   BLASTX
Method
                   g5923670
NCBI GI
BLAST score
                   179
E value
                   4.0e-13
                   72
Match length
% identity
```

NCBI Description (AC009326) unknown protein [Arabidopsis thaliana]

- 4.

```
Seq. No.
                  398106
                  LIB3431-010-P1-N1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20262
BLAST score
                  337
E value
                  0.0e + 00
Match length
                  345
% identity
                  99
NCBI Description
                  O.sativa light-induced mRNA
                  398107
Seq. No.
Seq. ID
                  LIB3431-010-P1-N1-D7
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  225
                  1.0e-18
E value
Match length
                  42
                  100
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  398108
Seq. No.
                  LIB3431-010-P1-N1-D8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  152
                  5.0e-80
E value
Match length
                  168
% identity
                  98
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS1139
Seq. No.
                  398109
Seq. ID
                  LIB3431-010-P1-N1-E2
Method
                  BLASTX
NCBI GI
                  g120661
BLAST score
                  154
E value
                  3.0e-10
Match length
                  29
                  93
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
NCBI Description
                  PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
                  dehydrogenase A-subunit precursor [Nicotiana tabacum]
Seq. No.
                  398110
Seq. ID
                  LIB3431-010-P1-N1-E4
Method
                  BLASTX
NCBI GI
                  g231610
BLAST score
                  346
E value
                  6.0e-33
                  87
Match length
% identity
NCBI Description
                  ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
                  >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, chloroplast - common
                  tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase
```

(gamma subunit) [Nicotiana tabacum] 398111 Seq. No. Seq. ID LIB3431-010-P1-N1-E5 Method BLASTN NCBI GI g11957 BLAST score 133 1.0e-68 E value 169 Match length 47 % identity NCBI Description Rice complete chloroplast genome Seq. No. 398112 LIB3431-010-P1-N1-E9 Seq. ID Method BLASTN NCBI GI g20181 BLAST score 160 E value 1.0e-84 Match length 179 98 % identity Rice cab2R gene for light harvesting chlorophyll NCBI Description a/b-binding protein 398113 Seq. No. Seq. ID LIB3431-010-P1-N1-F1 Method BLASTN NCBI GI g218207 BLAST score 217 E value 1.0e-119 221 Match length 100 % identity NCBI Description Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone p0SSS1139 Seq. No. 398114 Seq. ID LIB3431-010-P1-N1-F11 Method BLASTN NCBI GI g6016845 BLAST score 204 E value 1.0e-111 240 Match length % identity 96 NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10 Seq. No. 398115 Seq. ID LIB3431-010-P1-N1-F12 Method BLASTX NCBI GI g266893 BLAST score 637 E value 8.0e-67 Match length 123 % identity 98 RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, NCBI Description

>gi_322416_pir__S28172 ribulose-bisphosphate carboxylase
activase - cucumber >gi_18284_emb_CAA47906_ (X67674)

CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)

398121

rubisco activase [Cucumis sativus]

```
398116
Seq. No.
                  LIB3431-010-P1-N1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g288058
BLAST score
                  53
E value
                   6.0e-21
Match length
                  73
                  93
% identity
                  Z.mays S13 mRNA for cytoplasmic ribosomal protein S13
NCBI Description
                   398117
Seq. No.
                  LIB3431-010-P1-N1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2661765
BLAST score
                  50
                   4.0e-19
E value
                                                                       . . .
Match length
                  82
                                           - (2000)
                   90
% identity
                  Zea mays mRNA for putative porphobilinogen deaminase
NCBI Description
                   398118
Seq. No.
Seq. ID
                  LIB3431-010-P1-N1-G11
Method
                  BLASTN
NCBI GI
                  g218154
                  80
BLAST score
                   6.0e-37
E value
Match length
                  145
                   100
% identity
                  Oryza sativa gene for cytoplasmic aldolase, complete cds,
NCBI Description
                  clone:Aldp
                   398119
Seq. No.
Seq. ID
                  LIB3431-010-P1-N1-G12
                  BLASTN
Method
NCBI GI
                  g2662340
                  269
BLAST score
E value
                   1.0e-150
Match length
                  316
                  96
% identity
                  Oryza sativa mRNA for EF-1 alpha, complete cds
NCBI Description
                   398120
Seq. No.
Seq. ID
                  LIB3431-010-P1-N1-G2
                  BLASTX
Method
NCBI GI
                  g125606
                  250
BLAST score
E value
                   2.0e-21
                  59
Match length
% identity
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248
NCBI Description
                  pyruvate kinase (EC 2.7.1.40) - potato
                  >gi 22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum
                  tuberosum]
```

```
LIB3431-010-P1-N1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548603
BLAST score
                  225
E value
                  2.0e-18
Match length
                  56
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >qi 478404 pir JQ2247 photosystem I chain D precursor -
                  barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
                  398122
Seq. No.
                  LIB3431-010-P1-N1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  297
E value
                  5.0e-27
Match length
                  67
% identity
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                  398123
                  LIB3431-010-P1-N1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132096
BLAST score
                  154
E value
                  3.0e-10
Match length
                  29
% identity
                  100
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR
                   (RUBISCO SMALL SUBUNIT A) >gi_68095_pir__RKRZS6
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS2106) - rice >gi_218210_dbj_BAA00539_
                   (D00644) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa]
                  398124
Seq. No.
Seq. ID
                  LIB3431-010-P1-N1-G9
Method
                  BLASTX
NCBI GI
                  g3126854 ·
BLAST score
                  300
E value
                  2.0e-27
Match length
                  57
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  398125
Seq. No.
Seq. ID
                  LIB3431-010-P1-N1-H1
Method
                  BLASTX
NCBI GI
                  g606817
BLAST score
                  154
E value
                  4.0e-10
Match length
                  28
% identity
                  100
NCBI Description
                  (U08404) carbonic anhydrase [Oryza sativa]
                  >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic
```

. ::

anhydrase 3 [Oryza sativa]

```
398126
Seq. No.
Seq. ID
                  LIB3431-010-P1-N1-H2
Method
                  BLASTN
NCBI GI
                  g19086
BLAST score
                  44
                  2.0e-15
E value
Match length
                  48
                                  TA 2.
% identity
NCBI Description
                  Hordeum vulgare pot. psaE mRNA
                  398127
Seq. No.
                  LIB3431-010-P1-N1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  239
E value
                  1.0e-28
Match length.
                  80
% identity
                  89
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
                  398128
Seq. No.
Seq. ID
                  LIB3431-010-P1-N1-H6
Method
                  BLASTN
NCBI GI
                  g1136121
BLAST score
                  321
E value
                  0.0e + 00
                  324
Match length
% identity
                  100
                  O.sativa mRNA for alpha-tubulin (clone OSTA-136)
NCBI Description
                  398129
Seq. No.
Seq. ID
                  LIB3431-010-P1-N1-H7
Method
                  BLASTN
NCBI GI
                  g2737972
BLAST score
                  38
                  6.0e-12
E value
                  74
Match length
% identity
NCBI Description
                  Zea mays protein kinase ZmMEK1 mRNA, complete cds
                  398130
Seq. No.
Seq. ID
                  LIB3431-011-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g1742187
BLAST score
                  170
E value
                  6.0e-12
Match length
                  121
% identity
NCBI Description
                  (D90771) ORF ID:o260#14; similar to [SwissProt Accession
                  Number P11666 [Escherichia coli] >gi 1742198 dbj BAA14933
                  (D90772) ORF ID:o260#14; similar to [SwissProt Accession
```

Match length

101

```
orf, hypothetical protein [Escherichia coli]
Seq. No.
                   398131
Seq. ID
                  LIB3431-011-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q129233
BLAST score
                   461
E value
                   4.0e-46 ·
Match length
                   120
% identity
                   79
NCBI Description
                  ORYZAIN GAMMA CHAIN PRECURSOR >gi 67646 pir KHRZOG oryzain
                   (EC 3.4.22.-) gamma precursor - rice
                   >gi_218185_dbj_BAA14404_ (D90408) oryzain gamma precursor
                   [Oryza sativa]
Seq. No.
                   398132
Seq. ID
                  LIB3431-011-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q416869
BLAST score
                   320
E value
                   1.0e-29
                  113
Match length
% identity
                   58
                  CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYLSERINE
NCBI Description
                  SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                  >gi 303902 dbj_BAA03542_ (D14722) cysteine synthase
                   [Spinacia oleracea]
Seq. No.
                  398133
Seq. ID
                  LIB3431-011-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g3582333
                  209
BLAST score
E value
                  1.0e-16
Match length
                  88
% identity
NCBI Description
                   (AC005496) hypothetical protein [Arabidopsis thaliana]
                  398134
Seq. No.
                  LIB3431-011-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2708331
BLAST score
                  376
E value
                  3.0e - 36
Match length
                  119
% identity
                   (AF038557) ligand gated channel-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  398135
                  LIB3431-011-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4755193
BLAST score
                  445
E value
                  3.0e-44
```

Number P11666] [Escherichia coli] >gi 1787591 (AE000231)

```
% identity
NCBI Description
                   (AC007018) putative ribosomal protein S17 [Arabidopsis
                  thaliana]
Seq. No.
                  398136
Seq. ID
                  LIB3431-011-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  301
E value
                  3.0e-27
Match length
                  93
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  398137
Seq. No.
Seq. ID
                  LIB3431-011-P1-K1-B2
                                                                            . . .
Method
                  BLASTX
NCBI GI
                  g1621477
BLAST score
                  378
E value
                  2.0e-36
Match length
                  81
% identity
                  85
NCBI Description (D85868) reverse transcriptase [Oryza sativa]
                  398138
Seq. No.
Seq. ID
                  LIB3431-011-P1-K1-B4
                  BLASTX
Method
                  g5880709
NCBI GI
BLAST score
                  205
                  3.0e-16
E value
Match length
                  43
% identity
                  (AF137379) CFO subunit III of ATP synthase [Nephroselmis
NCBI Description
                  olivacea]
Seq. No.
                  398139
                  LIB3431-011-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3850566
BLAST score
                  263
E value
                  7.0e-23
Match length
                  134
% identity
                  43
NCBI Description (AC005278) F15K9.3 [Arabidopsis thaliana]
                  398140
Seq. No.
                  LIB3431-011-P1-K1-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  294
                  1.0e-164
E value
Match length
                  298
% identity
                  100
```

NCBI Description Oryza sativa mRNA for the small subunit of

```
p0SSS1139
Seq. No.
                  398141
                  LIB3431-011-P1-K1-B9
Seq. ID
Method
                  BLASTX
                  q5734779
NCBI GI
BLAST score
                  156
                  8.0e-11
E value
Match length
                   48
% identity
                   (AC007980) 78688 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  398142
Seq. ID
                  LIB3431-011-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g1843440
BLAST score
                  231
E value
                   5.0e-19
Match length
                  125
% identity
NCBI Description
                   (Z70521) unknown [Cucumis melo]
                  398143
Seq. No.
Seq. ID
                  LIB3431-011-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g3868756
BLAST score
                   469
E value
                   3.0e-47
Match length
                   94
% identity
NCBI Description
                   (D86611) catalase [Oryza sativa]
                  398144
Seq. No.
Seq. ID
                  LIB3431-011-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q320618
BLAST score
                   485
E value
                   5.0e-49
Match length
                  101
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                  398145
Seq. No.
Seq. ID
                  LIB3431-011-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  418
E value
                  1.0e-58
Match length
                  131
% identity
                  82
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
```

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

```
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi 226375 prf 1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]
```

```
398146
Seq. No.
Seq. ID
                   LIB3431-011-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   q133999
BLAST score
                   493
                   7.0e-50
E value
                   100
Match length
% identity
                   100
NCBI Description
                   CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi 70904 pir R3RZ7
                   ribosomal protein S7 - rice chloroplast >gi_12037_emb_CAA33942 (X15901) ribosomal protein S7
                   [Oryza sativa] >gi 12065 emb CAA33919 (X15901) ribosomal
                   protein S7 [Oryza sativa] >gi_226657_prf__1603356CH
                   ribosomal protein S7 [Oryza sativa]
                   398147
Seq. No.
Seq. ID
                   LIB3431-011-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g2625084
BLAST score
                   550
                   1.0e-56
E value
                   129
Match length
% identity
                   85
                   (AF030382) ADP-glucose pyrophosphorylase small subunit
NCBI Description
                   [Cucumis melo var. markuwa Markino]
                   398148
Seq. No.
Seq. ID
                   LIB3431-011-P1-K1-C9
Method
                   BLASTN -
NCBI GI
                   g4574134
BLAST score
                   123
                   6.0e-63
E value
                   146
Match length
                   97
% identity
NCBI Description Oryza sativa cysteine synthase (rcs1) mRNA, complete cds
Seq. No.
                   398149
Seq. ID
                   LIB3431-011-P1-K1-D1
                   BLASTN
Method
NCBI GI
                   g6015437
BLAST score
                   36
E value
                   1.0e-10
                   49
Match length
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                   398150
```

Seq. ID LIB3431-011-P1-K1-D11

BLASTX Method

Seq. No.

Match length

102

```
g2570505
NCBI GI
BLAST score
                   242
E value
                   4.0e-27
Match length
                   87
% identity
NCBI Description
                   (AF022735) proteasome component [Oryza sativa]
                   398151
Seq. No.
Seq. ID
                   LIB3431-011-P1-K1-D3
Method
                   BLASTN
NCBI GI -
                   q3885891
BLAST score
                   110
E value
                   5.0e-55
                   181
Match length
                   97
% identity
NCBI Description
                   Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                   mRNA, complete cds
Seq. No.
                   398152
                   LIB3431-011-P1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5902394
BLAST score
                   440
E value
                   1.0e-43
Match length
                   114
                   76
% identity
                   (AC008148) Putative phosphoglucomutase [Arabidopsis
NCBI Description
                   thaliana]
                   398153
Seq. No.
Seq. ID
                   LIB3431-011-P1-K1-D7
Method
                   BLASTN
NCBI GI
                   g3810868
BLAST score
                   35
E value
                   8.0e-11
Match length
                   35
                   100
% identity
NCBI Description Homo sapiens ST15 mRNA, complete cds
                   398154
Seq. No.
Seq. ID
                   LIB3431-011-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g2407281
BLAST score
                   543
E value
                   8.0e-56
                   105
Match length
                   95
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
                   398155
Seq. No.
Seq. ID
                   LIB3431-011-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g4929595
BLAST score
                   239
E value
                   4.0e-20
```

·...

E value

Match length

1.0e-128

```
% identity
                  46
NCBI Description
                  (AF151821) CGI-63 protein [Homo sapiens]
Seq. No.
                  398156
Seq. ID
                  LIB3431-011-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  181
E value
                  1.0e-13
Match length
                  38
% identity
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  398157
Seq. ID
                  LIB3431-011-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q4056427
BLAST score
                  289
E value
                  6.0e-26
Match length
                  105
% identity
                  53
NCBI Description
                  (AC005322) Contains similarity to gb AJ006354 zinc finger
                  protein (ZAC) from Homo sapiens. [Arabidopsis thaliana]
                  398158
Seq. No.
Seq. ID
                  LIB3431-011-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g115802
BLAST score
                  149
E value
                  2.0e-11
Match length
                  38
% identity
                  100
                  CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll
                  a/b-binding protein (cab-36) - common tobacco
                  >gi 19827 emb CAA41188 (X58230) chlorophyll a/b binding
                  protein [Nicotiana tabacum]
                  398159
Seq. No.
Seq. ID
                  LIB3431-011-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  g4959460
BLAST score
                  35
E value
                  1.0e-10
Match length
                  35
                  100
% identity
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
Seq. No.
                  398160
Seq. ID
                  LIB3431-011-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  g20262
BLAST score
                  233
```

```
% identity
NCBI Description
                  O.sativa light-induced mRNA
Seq. No.
                   398161
Seq. ID
                  LIB3431-011-P1-K1-E4
Method
                  BLASTX
NCBI GI
                   q3047109
BLAST score
                   206
E value
                   3.0e-16
Match length
                   90
% identity
NCBI Description
                   (AF058919) No definition line found [Arabidopsis thaliana]
                   398162
Seq. No.
                  LIB3431-011-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3941480
BLAST score
                   288
                   1.0e-25
E value
                   129
Match length
% identity
                   49
NCBI Description
                   (AF062894) putative transcription factor [Arabidopsis
                  thaliana]
Seq. No.
                  398163
Seq. ID
                  LIB3431-011-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g5679336
                  253
BLAST score
E value
                   9.0e-22
Match length
                   94
% identity
NCBI Description
                   (AF171223) putative zinc finger protein [Oryza sativa]
                  398164
Seq. No.
Seg. ID
                  LIB3431-011-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                   4.0e-20
Match length
                  44
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  398165
Seq. No.
Seq. ID
                  LIB3431-011-P1-K1-F4
Method
                  BLASTN
                  g3377792
NCBI GI
BLAST score
                  67
                  7.0e-30
E value
                  83
Match length
% identity
NCBI Description
                  Oryza sativa ribulose-1,5-bisphosphate
```

carboxylase/oxygenase activase (rca) mRNA, complete cds

Match length

% identity

103

```
398166
Seq. No.
Seq. ID
                  LIB3431-011-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g115796
BLAST score
                  517
                  1.0e-52
E value
                  119
Match length
% identity
                  83
                  CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB) (LHCP) >gi 218174 dbj BAA00537 (D00642) type II
                  light-harvesting chlorophyll a/b-binding protein [Oryza
                  sativa]
                  398167
Seq. No.
Seq. ID
                  LIB3431-011-P1-K1-F8
Method
                  BLASTN'
NCBI GI
                  g218171
BLAST score
                  43
E value
                  2.0e-15
Match length
                  43
% identity
                  100
NCBI Description
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
                  a/b binding protein of photosystem II (LHCPII), complete
Seq. No.
                  398168
Seq. ID
                  LIB3431-011-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  q70642
BLAST score
                  662
E value
                  1.0e-69
Match length
                  136
% identity
                  22
NCBI Description
                  ubiquitin precursor - Arabidopsis thaliana
                  >gi 17678 emb CAA31331 (X12853) polyubiquitin (AA 1 - 382)
                  [Arabidopsis thaliana] >qi 987519 (U33014) polyubiquitin
                  [Arabidopsis thaliana] >gi 226499 prf 1515347A
                  poly-ubiquitin [Arabidopsis thaliana]
Seq. No.
                  398169
Seq. ID
                  LIB3431-011-P1-K1-G11
                                                               × 42
Method
                  BLASTN
NCBI GI
                  q6015437
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description
                  Homo sapiens PEX1 mRNA, complete cds
                  398170
Seq. No.
Seq. ID
                  LIB3431-011-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q3789952
BLAST score
                  516
E value
                  1.0e-52
```

E value

6.0e-30

```
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                   sativa]
Seq. No.
                   398171
Seq. ID
                  LIB3431-011-P1-K1-G2
Method
                  BLASTN
NCBI GI
                  q167086
BLAST score
                   43
E value
                   3.0e-15
                                               45
Match length
                   74
% identity
                   90
NCBI Description
                  Hordeum vulgare photosystem I protein (PSI-L) mRNA,
                  complete cds
                   398172
Seq. No.
Seq. ID
                  LIB3431-011-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  570
E value
                  8.0e-59
Match length
                  124
% identity
                   91
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                   - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
                  398173
Seq. No.
Seq. ID
                  LIB3431-011-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g2499497
BLAST score
                  334
E value
                  5.0e-33
Match length
                  84
% identity
                   95
                  PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 1161600 emb CAA88841 (Z48977) phosphoglycerate kinase
                   [Nicotiana tabacum]
                  398174
Seq. No.
Seq. ID
                  LIB3431-011-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  513
E value
                  3.0e-52
Match length
                  109
                  90
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  398175
Seq. No.
                  LIB3431-011-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g544437
BLAST score
                  323
```

```
Match length
                    70
 % identity
                    87
                   GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN)
 NCBI Description
                   >gi_296358_emb_CAA47018_ (X66377) CIT-SAP [Citrus sinensis]
 Seq. No.
                   LIB3431-011-P1-K1-H1
 Seq. ID
 Method
                   BLASTX
                   q3386621
 NCBI GI
                    412
 BLAST score
 E value
                    2.0e-40
                    97
 Match length
 % identity
 NCBI Description
                    (AC004665) unknown protein [Arabidopsis thaliana]
                   398177
 Seq. No.
 Seq. ID
                   LIB3431-011-P1-K1-H10
 Method
                   BLASTX
 NCBI GI
                   g2754849
 BLAST score
                   578
 E value
                    9.0e-60
 Match length
                   139
 % identity
                    77
                    (AF039000) putative serine-glyoxylate aminotransferase
 NCBI Description
                    [Fritillaria agrestis]
                    398178
 Seq. No.
                   LIB3431-011-P1-K1-H11
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g3478700
 BLAST score
                    461
 E value
                    5.0e-46
 Match length
                   144
 % identity
                    61
                   (AF034387) AFT protein [Arabidopsis thaliana]
 NCBI Description
                   398179
Seq. No.
 Seq. ID
                   LIB3431-011-P1-K1-H12
 Method
                   BLASTN
                   g3273244
 NCBI GI
 BLAST score
                   58
                   5.0e-24
 E value
                   74
 Match length
                   95
 % identity
 NCBI Description Oryza sativa DNA for NLS receptor, complete cds
                   398180
 Seq. No.
 Seq. ID
                   LIB3431-011-P1-K1-H2
 Method
                   BLASTX
 NCBI GI
                   g4079798
 BLAST score
                   224
 E value
                   1.0e-18
 Match length
                   83
 % identity
                    (AF052203) 23 kDa polypeptide of photosystem II [Oryza
 NCBI Description
```

sativa]

```
398181
Seq. No.
                   LIB3431-011-P1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4886307
BLAST score
                   704
E value
                   1.0e-74
Match length
                   135
% identity
                   (AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   398182
Seq. ID
                   LIB3431-011-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g3345477
BLAST score
                   314
E value
                   6.0e-29
Match length
                   111
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                   398183
Seq. No.
Seq. ID
                   LIB3431-011-P1-K1-H7
Method
                   BLASTX .
NCBI GI
                   g733458
BLAST score
                   484
                   9.0e-49
E value
Match length
                   109
% identity
                   84
NCBI Description
                   (U23190) chlorophyll a/b-binding apoprotein CP24 precursor
                   [Zea mays]
Seq. No.
                   398184
Seq. ID
                   LIB3431-011-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   g320618
                   386
BLAST score
E value
                   1.0e-40
Match length
                   116
% identity
                   78
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   398185
Seq. No.
                   LIB3431-011-P1-N1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g542157
BLAST score
                   528
E value
                   5.0e-54
                   124
Match length
                   85
% identity
                  ribosomal 5S RNA-binding protein - Rice
NCBI Description
```

```
LIB3431-011-P1-N1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q21839
BLAST score
                  209
E value
                  2.0e-16
Match length
                   47
% identity
NCBI Description
                   (X57952) phosphoribulokinase [Triticum aestivum]
Seq. No.
                  398187
                  LIB3431-011-P1-N1-A3
Seq. ID
Method
                  BLASTX
                  g129233
NCBI GI
BLAST score
                  268
E value
                  2.0e-23
Match length
                   47
% identity
                   98
                  ORYZAIN GAMMA CHAIN PRECURSOR >qi 67646 pir KHRZOG oryzain
NCBI Description
                   (EC 3.4.22.-) gamma precursor - rice
                  >gi 218185 dbj BAA14404 (D90408) oryzain gamma precursor
                   [Oryza sativa]
Seq. No.
                  398188
Seq. ID
                  LIB3431-011-P1-N1-A8
Method
                  BLASTX
NCBI GI
                  q2384669
BLAST score
                  163
E value
                   3.0e-11
Match length
                  58
% identity
                  53
NCBI Description
                   (AF012656) putative potassium transporter AtKTlp
                   [Arabidopsis thaliana]
Seq. No.
                  398189~
Seq. ID
                  LIB3431-011-P1-N1-B10
Method
                  BLASTX
NCBI -GI
                  q3873807
BLAST score
                  183
E value
                  2.0e-13
Match length
                  137
% identity
NCBI Description
                  (Z49907) B0491.1 [Caenorhabditis elegans]
Seq. No.
                  398190
Seq. ID
                  LIB3431-011-P1-N1-B12
Method
                  BLASTX
NCBI GI
                  q131225
BLAST score ·
                  178
E value
                  7.0e-15
Match length
                  58
% identity
                  63
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
```

```
LIB3431-011-P1-N1-B2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3377848
BLAST score
                   198
E value
                   3.0e-15
Match length
                   95
% identity
                   (AF076274) contains similarity to reverse transcriptases
NCBI Description
                   (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
                   398192
Seq. No.
                   LIB3431-011-P1-N1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q6093830
BLAST score
                   211
E value
                   1.0e-16
Match length
                   94
% identity
                   PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
NCBI Description
                   [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
                   PROTEIN PSBY-2] >gi 3337435 (AF060198) PsbY precursor;
                   putative photosytem II peptide [Spinacia oleracea]
                   398193
Seq. No.
                   LIB3431-011-P1-N1-B4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q11957
BLAST score
                   341
                   0.0e + 00
E value
Match length
                   362
                   98
% identity
NCBI Description
                  Rice complete chloroplast genome
Seq. No.
                   398194
                   LIB3431-011-P1-N1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3924605
BLAST score
                   251
E value
                   2.0e-21
Match length
                   59
% identity
NCBI Description
                   (AF069442) putative inhibitor of apoptosis [Arabidopsis
                   thaliana]
                   398195
Seq. No.
                   LIB3431-011-P1-N1-B6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g218207
BLAST score
                   298
E value
                   1.0e-167
Match length
                  298
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
```

```
LIB3431-011-P1-N1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g421855
BLAST score
                  151
E value
                  1.0e-09
Match length
                  79
% identity
NCBI Description
                  alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana
                  (fragment)
Seq. No.
                  398197
Seq. ID
                  LIB3431-011-P1-N1-C10
Method
                  BLASTX
NCBI GI
                  g3929924
BLAST score
                  163
E value
                  3.0e-11
Match length
                  36
% identity
                  (AB020502) catalase [Oryza sativa]
NCBI Description
Seq. No.
                  398198
Seq. ID
                  LIB3431-011-P1-N1-C3
Method
                  BLASTX
NCBI GI
                  g1504052
                  270
BLAST score
E value
                  1.0e-23
Match length
                  52
% identity
                  100
NCBI Description (D87042) Calcium-dependent protein kinase [Zea mays]
Seq. No.
                  398199
                  LIB3431-011-P1-N1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  217
                  1,0e-17
E value
Match length
                  42
% identity
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
                  398200
Seq. No.
Seq. ID
                  LIB3431-011-P1-N1-C6
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  289
E value
                  8.0e-26
Match length
                  73
                  78
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
```

sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa] Seq. No. 398201 Seq. ID LIB3431-011-P1-N1-C8 Method BLASTX NCBI GI g633678 BLAST score 145 5.0e-09 E value Match length 32 % identity 91 NCBI Description (X83500) ADP-glucose pyrophosphorylase [Spinacia oleracea] Seq. No. 398202 LIB3431-011-P1-N1-C9 Seq. ID Method BLASTN NCBI GI q4574134 BLAST score 147 E value 3.0e-77 Match length 147 100 % identity ·· NCBI Description Oryza sativa cysteine synthase (rcs1) mRNA, complete cds 398203 Seq. No. LIB3431-011-P1-N1-D11 Seq. ID Method BLASTX NCBI GI g2570505 BLAST score 221 3.0e-35 E value 81 Match length % identity (AF022735) proteasome component [Oryza sativa] NCBI Description Seq. No. 398204 LIB3431-011-P1-N1-D3 Seq. ID Method BLASTX NCBI GI q3885892 BLAST score 426 E value 6.0e-42 83 Match length % identity (AF093634) photosystem-1 F subunit precursor [Oryza sativa] NCBI Description Seq. No. 398205 Seq. ID LIB3431-011-P1-N1-D7 BLASTX Method q6016427 NCBI GI BLAST score 292 3.0e-26 E value

(AF068318) regulatory subunit of protein \overline{k} inase CK2; CK2 beta-subunit [Arabidopsis thaliana]

NCBI Description

Match length

% identity

Seq. No. 398206

Seq. ID LIB3431-011-P1-N1-D9

58

Method BLASTN

50826

CASEIN KINASE II BETA-3 CHAIN (CK II) >gi 3493611

NCBI Description

```
NCBI GI
                   g218209
BLAST score
                   149
E value
                   4.0e-78
Match length
                   299
 % identity
                   97
NCBI Description
                   Oryza sativa mRNA for the small subunit of
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS2106
                             , 'A''
                   398207
Seq. No.
                   LIB3431-011-P1-N1-E12
 Seq. ID
Method
                   BLASTX
NCBI GI
                   q115802
BLAST score
                   217
E value
                   1.0e-17
Match length
                   40
                   100
 % identity
                   CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-36) (LHCP) >gi 100311 pir S21827 chlorophyll
                   a/b-binding protein (cab-36) - common tobacco
                   >qi 19827 emb CAA41188 (X58230) chlorophyll a/b binding
                   protein [Nicotiana tabacum]
 Seq. No.
                   398208
 Seq. ID
                   LIB3431-011-P1-N1-E3
Method
                   BLASTX
NCBI GI
                   q417260
BLAST score
                   326
E value
                   3.0e-30
Match length
                   81
 % identity
                   77
NCBI Description
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
                   lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                   light-regulated gene [Oryza sativa]
 Seq. No.
                   398209
 Seq. ID
                   LIB3431-011-P1-N1-E5
Method
                   BLASTX
NCBI GI
                   q517500
BLAST score
                   234
E value .
                   1.0e-19
Match length
                   79
 % identity
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                   protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                   OE17 protein [Pisum sativum]
 Seq. No.
                   398210
 Seq. ID
                   LIB3431-011-P1-N1-E9
Method
                   BLASTX
NCBI GI
                   q3212877
BLAST score
                   180
E value
                   3.0e-13
Match length
                   40
% identity
```

(AC004005) Lea-like protein [Arabidopsis thaliana]

BLAST score

```
398211
Seq. No.
                  LIB3431-011-P1-N1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4115931
BLAST score
                  225
                  2.0e-18
E value
                  57
Match length
                  75
% identity
NCBI Description
                  (AF118223) contains similarity to Guillardia theta ABC
                  transporter (GB:AF041468) [Arabidopsis thaliana]
                  398212
Seq. No.
                  LIB3431-011-P1-N1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  205
                  5.0e-16
E value
Match length
                  44
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  398213
Seq. ID
                  LIB3431-011-P1-N1-F3
Method
                  BLASTX
NCBI GI
                  g131192
BLAST score
                  205
E value
                  3.0e-16
Match length
                  45
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >qi 100606 pir S20937
                  photosystem I chain V precursor - barley
                  >gi 19091 emb CAA42727_ (X60158) photosystem I polypeptide
                  PSI-G precursor [Hordeum vulgare]
Seq. No.
                  398214
Seq. ID
                  LIB3431-011-P1-N1-F4
Method
                  BLASTX
NCBI GI
                  q132166
BLAST score
                  160
E value
                  6.0e-11
Match length
                  31
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                  >qi 81660 pir S04048 ribulose-bisphosphate carboxylase
                  activase precursor - Arabidopsis thaliana
                  >gi 16471 emb CAA32429 (X14212) rubisco activase (AA 1 -
                  473) [Arabidopsis thaliana]
Seq. No.
                  398215
Seq. ID
                  LIB3431-011-P1-N1-F5
Method
                  BLASTX
NCBI GI
                  q115802
```

```
E value
                  3.0e-09
Match length
                  30
% identity
                  87
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
                  CAB-36) (LHCP) >gi 100311 pir S21827 chlorophyll
                  a/b-binding protein (cab-36) - common tobacco
                  >gi 19827 emb CAA41188 (X58230) chlorophyll a/b binding
                  protein [Nicotiana tabacum]
Seq. No.
                  398216
                  LIB3431-011-P1-N1-F8
Seq. ID
Method
                  BLASTX
                  g3036949
NCBI GI
BLAST score
                  264
E value
                  4.0e-23
Match length
                  50
% identity
                  100
NCBI Description
                  (AB012638) light harvesting chlorophyll a/b-binding protein
                  [Nicotiana sylvestris]
Seq. No.
                  398217
Seq. ID
                  LIB3431-011-P1-N1-F9
Method
                  BLASTX
NCBI GI
                  q1076678
BLAST score
                  243
                  1.0e-20
E value
Match length
                  48
                  100
% identity
                  ubiquitin / ribosomal protein S27a - potato (fragment)
NCBI Description
                  398218
Seq. No.
                  LIB3431-011-P1-N1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131176
BLAST score
                  304
                  1.0e-27
E value
Match length
                  59
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                  >gi 72683 pir F1BH4 photosystem I chain IV precursor -
                  barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
                  -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A
                  10.8kD photosystem I protein [Hordeum vulgare var.
                  distichum]
                  398219
Seq. No.
Seq. ID
                  LIB3431-011-P1-N1-G12
Method
                  BLASTN
NCBI GI
                  g3789951
BLAST score
                  191
E value
                  1.0e-103
Match length
                  414
% identity
                  99
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
```

complete cds

```
398220
Seq. No.
                  LIB3431-011-P1-N1-G2
Seq. ID -
Method
                  BLASTX
                  g6006283 -
NCBI GI
BLAST score
                  151
                  8.0e-10
E value
Match length
                  41
% identity
NCBI Description
                   (AB015861) photosystem I subunit PSI-L [Arabidopsis
                  thaliana]
Seq. No.
                  398221
                  LIB3431-011-P1-N1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  402
E value
                  9.0e-40
Match length
                  105
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
Seq. No.
                  398222
                  LIB3431-011-P1-N1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3738261
BLAST score
                  416
                  9.0e-41
E value
Match length
                  91
% identity
                   (AB018412) chloroplast phosphoglycerate kinase [Populus
NCBI Description
                  nigra]
Seq. No.
                  398223
                  LIB3431-011-P1-N1-G9
Seq. ID
Method
                  BLASTX
                  q485512
NCBI GI
BLAST score
                  326
E value
                  3.0e-30
Match length
                  70
% identity
NCBI Description salt-associated protein csaA - sweet orange
                  398224
Seq. No.
Seq. ID
                  LIB3431-011-P1-N1-H10
Method
                  BLASTX
NCBI GI
                  g2754849
BLAST score
                  186
E value
                  7.0e-14
Match length
                  43
% identity
NCBI Description
                  (AF039000) putative serine-glyoxylate aminotransferase
```

[Fritillaria agrestis]

```
398225
Seq. No.
Seq. ID
                  LIB3431-011-P1-N1-H11
Method
                  BLASTN
NCBI GI
                  g531030
BLAST score
                  60
                  5.0e-25
E value
Match length
                  116
% identity
                  88
NCBI Description
                  Pennisetum ciliare apomixis-associated mRNA
                  >gi 531483 emb Z36546 PCAPOSPA3 P.ciliare (Higgins)
                  apospory associated mRNA, 876bp
                  >qi 549985 qb U13149 PCU13149 Pennisetum ciliare possible
                  apospory-associated mRNA clone pSUB 3-1a, partial cds
Seq. No.
                  398226
                  LIB3431-011-P1-N1-H12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3273244
BLAST · score
                  59
E value
                  1.0e-24
Match length
                  95
                  91
% identity
NCBI Description Oryza sativa DNA for NLS receptor, complete cds
                  398227
Seq. No.
Seq. ID
                  LIB3431-011-P1-N1-H2
Method
                  BLASTX
NCBI GI
                  q4079798
BLAST score
                  277
                  1.0e-24
E value
Match length
                  52
% identity
                  100
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
                  398228
Seq. No.
                  LIB3431-011-P1-N1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4886307
BLAST score
                  294
E value
                  2.0e-26
Match length
                  67
% identity
NCBI Description
                   (AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase
                  [Arabidopsis thaliana]
Seq. No.
                  398229
Seq. ID
                  LIB3431-011-P1-N1-H7
Method
                  BLASTX
NCBI GI
                  g543939
BLAST score
                  208
E value
                  2.0e-16
Match length
                  43
% identity
                  95
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN CP24 PRECURSOR
```

>gi_541819_pir__S40210 chlorophyll a/b-binding protein CP24

```
LIB3431-011-P1-N1-H9
Seq. ID
Method
                  BLASTX
                  q115787
NCBI GI
BLAST score
                  449
                  1.0e-44
E value
Match length
                  96
                  87
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                  398231
Seq. ID
                  LIB3431-012-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q4732091
BLAST score
                  407
E value
                  1.0e-39
Match length
                  99
% identity
NCBI Description
                   (AF126742) bundle sheath defective protein 2 [Zea mays]
Seq. No.
                  398232
Seq. ID
                  LIB3431-012-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  477
E value
                  3.0e-48
Match length
                  90
% identity
NCBI Description
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  398233
Seq. ID
                  LIB3431-012-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q4512684
BLAST score
                  397
E value
                  2.0e-38
Match length
                  96
% identity
NCBI Description
                   (AC006931) unknown protein [Arabidopsis thaliana]
                  >qi 4559324 gb AAD22986.1 AC007087 5 (AC007087) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  398234
Seq. ID
                  LIB3431-012-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  510
E value
                  6.0e-52
Match length
                  102
```

398230

Seq. No.

% identity

94

precursor - spinach >gi_437991_emb_CAA81105.1_ (Z25886) 20 kDa protein of CP24 precursor protein [Spinacia oleracea]

```
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  398235
Seq. No.
                  LIB3431-012-P1-K1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  35
E value
                  2.0e-10
Match length
                  35
                  100
% identity
NCBI Description
                  Homo sapiens PEX1 mRNA, complete cds
                  398236
Seq. No.
                  LIB3431-012-P1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q6015437
BLAST score
                  43
E value
                  4.0e-15
Match length
                  43
% identity
                  100
NCBI Description
                  Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  398237
Seq. ID
                  LIB3431-012-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  221
E value
                  6.0e-18
Match length
                  44
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  398238
Seq. ID
                  LIB3431-012-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g4836934
BLAST score
                  187
E value
                  7.0e-14
Match length
                  86
% identity
NCBI Description
                  (AC006085) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  398239
Seq. ID
                  LIB3431-012-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  253
E value
                  1.0e-140
Match length
                  257
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
```

```
Seq. ID
                  LIB3431-012-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  q3789951
BLAST score
                  62
E value
                  3.0e-26
Match length
                  121
% identity
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein presursor
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  398241
Seq. No.
                  LIB3431-012-P1-K1-B6
Seq. ID
Method
                  BLASTX
                  g3075488
NCBI GI
BLAST score
                  211
E value
                  3.0e-17
Match length
                  59
% identity
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                  398242
Seq. No.
                  LIB3431-012-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548603
BLAST score
                  380
                  1.0e-36
E value
Match length
                  120
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi 478404_pir__JQ2247 photosystem I chain D precursor -
                  barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                  398243
Seq. ID
                  LIB3431-012-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g131225
                  378
BLAST score
                  1.0e-36
E value
Match length
                  85
                  88
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  398244
Seq. No.
Seq. ID
                  LIB3431-012-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g1707018
BLAST score
                  460
                  7.0e-46
E value
                  104
Match length
% identity
                  86
```

NCBI Description (U78721) CutA isolog [Arabidopsis thaliana]

```
Seq. No.
                  398245
                  LIB3431-012-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2244867
BLAST score
                  298
E value
                  6.0e-27
Match length
                  137
% identity
                  44
                  (Z97337) hydroxynitrile lyase like protein [Arabidopsis
NCBI Description
Seq. No.
                  398246
Seq. ID
                  LIB3431-012-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  208
E value
                  3.0e-16
Match length
                  62
                  63
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  398247
Seq. No.
Seq. ID
                  LIB3431-012-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g4079798
BLAST score
                  223
E value
                  2.0e-18
Match length
                  46
% identity
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
                  398248
Seq. No.
                  LIB3431-012-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  304
E value
                  1.0e-27
Match length
                  87
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  398249
Seq. No.
Seq. ID
                  LIB3431-012-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g1353352
BLAST score
                  423
E value
                  2.0e-41
Match length
                  116
% identity
                  72
NCBI Description
                  (U31975) alanine aminotransferase [Chlamydomonas
                  reinhardtii]
```

Method

BLASTX

```
LIB3431-012-P1-K1-C7
Seq. ID
Method
                  BLASTN
                  g1944204
NCBI GI
BLAST score
                  451
                  0.0e + 00
E value
Match length
                  466
                  99
% identity
NCBI Description
                  Oryza sativa mRNA for RicMT, complete cds
Seq. No.
                  398251
                  LIB3431-012-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4585142
BLAST score
                  388
E value
                  2.0e-37
Match length
                  101
% identity
                  (AF088276) NADPH oxidase; gp91; phox homolog [Lycopersicon
NCBI Description
                  esculentum]
Seq. No.
                  398252
Seq. ID
                  LIB3431-012-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q170131
BLAST score
                  176
                  1.0e-12
E value
Match length
                  48
% identity
                  62
NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
                  398253
Seq. No.
                  LIB3431-012-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5091623
BLAST score
                  521
                  5.0e-53
E value
                  125
Match length
% identity
                  (AC007454) Similar to gb U93048 somatic embryogenesis
NCBI Description
                  receptor-like kinase from Daucus carota, contains 4
                  PF_00560 Leucine Rich Repeat domains and a PF_00069
                  Eukaryotic protein kinase domain. [Arabidopsis thaliana]
Seq. No.
                  398254
                  LIB3431-012-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4510363
BLAST score
                  511
E value
                  6.0e-52
Match length
                  123
% identity
NCBI Description
                  (AC007017) putative DNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  398255
                  LIB3431-012-P1-K1-D12
Seq. ID
```

Seq. ID

```
g6056373
NCBI GI
BLAST score
                  218
E value
                  1.0e-19
Match length
                  102
% identity
                  59
NCBI Description
                  (AC009894) elongation factor EF-2 [Arabidopsis thaliana]
Seq. No.
                  398256
Seq. ID
                  LIB3431-012-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q733454
BLAST score
                  575
E value
                  2.0e-59
Match length
                  133
% identity
NCBI Description
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                  [Zea mays]
Seq. No.
                  398257
Seq. ID
                  LIB3431-012-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  q20239
BLAST score
                  119
E value
                  4.0e-60
Match length
                  135
% identity
                  97
NCBI Description
                  O.sativa (rice) shoot-specific GOS5 gene for a putative
                  chloroplast transit peptide
Seq. No.
                  398258
Seq. ID
                  LIB3431-012-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q1055130
BLAST score
                  220
E value
                  8.0e-18
Match length
                  131
% identity
NCBI Description
                  (U39998) coded for by C. elegans cDNA yk92b11.3; coded for
                  by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA
                  yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by
                  C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA
                  yk78c2.3
Seq. No.
                  398259
Seq. ID
                  LIB3431-012-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q3522929
BLAST score
                  589
E value
                  5.0e-61
Match length
                  126
% identity
                  87
NCBI Description
                  (AC002535) putative dTDP-glucose 4-6-dehydratase
                  [Arabidopsis thaliana] >gi 3738279 (AC005309) putative
                  dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
Seq. No.
                  398260
```

LIB3431-012-P1-K1-D9

Match length

```
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  365
E value
                  4.0e-35
Match length
                  94
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  398261
Seq. ID
                  LIB3431-012-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g115794
BLAST score
                  787
                  3.0e-84
E value
Match length
                  156
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
NCBI Description
                  III CAB-13) >gi_72748 pir__CDTO33 chlorophyll a/b-binding
                  protein type III precursor (cab-13) - tomato
                  >gi 19277 emb CAA42818 (X60275) LHCII type III
                  [Lycopersicon esculentum]
Seq. No.
                  398262
Seq. ID
                  LIB3431-012-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g4239891
BLAST score
                  617
                  3.0e-67
E value
Match length
                  151
% identity
                  87
NCBI Description (AB016804) NADP-malic enzyme [Aloe arborescens]
Seq. No.
                  398263
Seq. ID
                  LIB3431-012-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  352
                                                            ٠٠,
                  2.0e-33
E value
Match length
                  90
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  398264
Seq. ID
                  LIB3431-012-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g4531444
BLAST score
                  472
E value
                  3.0e-47
```

Match length

```
% identity
                  (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  398265
Seq. ID
                  LIB3431-012-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  q3075488
BLAST score
                  634
E value
                  3.0e-66
Match length
                  138
% identity
NCBI Description
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                  398266
Seq. No.
                  LIB3431-012-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172874
BLAST score
                  251
E value
                  2.0e-21
                  129
Match length
                  42
% identity
NCBI Description
                  DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
                  >gi_479589_pir__S34823 dehydration-induced protein RD22 -
                  Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
                 [Arabidopsis thaliana] >gi 447134 prf 1913421A rd22 gene
                  [Arabidopsis thaliana]
Seq. No.
                  398267
Seq. ID
                  LIB3431-012-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g100903
BLAST score
                  216
E value
                  2.0e-17
Match length
                  94
                  51
% identity
                  nucleic acid-binding protein - maize >gi 168526 (M74566)
NCBI Description
                 nucleic acid-binding protein [Zea mays]
Seq. No.
                  398268
Seq. ID
                  LIB3431-012-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g3914557
BLAST score
                  671
E value
                  1.0e-70
Match length
                  134
                  94
% identity
                  RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED
NCBI Description
                  PROTEIN) >gi 1155265 (U40219) possible apospory-associated
                  protein [Pennisetum ciliare]
                  398269
Seq. No.
Seq. ID
                  LIB3431-012-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g733456
BLAST score
                  672
E value
                  9.0e-71
```

```
% identity
   NCBI Description
                      (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
                      [Zea mays]
   Seq. No.
                      398270
                     LIB3431-012-P1-K1-F12
   Seq. ID
   Method
                     BLASTX
   NCBI GI
                     g1835731
   BLAST score
                      455
  E value
                     2.0e-45
   Match length
                     93
                      95
   % identity
                     (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
   NCBI Description
   Seq. No.
                     398271
   Seq. ID
                     LIB3431-012-P1-K1-F9
   Method
                     BLASTN
   NCBI GI
                     q3885891
   BLAST score
                     144
   E value
                     3.0e-75
  Match length
                     197
   % identity
                      98
                     Oryza sativa photosystem-1 F subunit precursor (PSI-F)
   NCBI Description
                     mRNA, complete cds
                     398272
   Seq. No.
   Seq. ID
                     LIB3431-012-P1-K1-G1
   Method
                                  . .
                     BLASTN
                     q3885891
   NCBI GI
   BLAST score
                     105
                     3.0e-52
   E value
  Match length
                     125
   % identity
                     96
  NCBI Description
                     Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                     mRNA, complete cds
   Seq. No.
                     398273
   Seq. ID
                     LIB3431-012-P1-K1-G10
  Method
                     BLASTX
  NCBI GI
                     g2754849
  BLAST score
                     278
                                        . . .
👺 E value
                     4.0e-25
  Match length
                     64
   % identity
  NCBI Description
                      (AF039000) putative serine-glyoxylate aminotransferase
                      [Fritillaria agrestis]
                     398274
   Seq. No.
   Seq. ID
                     LIB3431-012-P1-K1-G12
  Method
                     BLASTX
  NCBI GI
                     g1632822
   BLAST score
                     461
   E value
                     3.0e-46
  Match length
                     92
   % identity
                     97
  NCBI Description
                     (Y08962) transmembrane protein [Oryza sativa] >gi_1667594
                      (U77297) transmembrane protein [Oryza sativa]
```

```
398275
Seq. No.
Seq. ID
                  LIB3431-012-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g115525
BLAST score
                  162
E value
                  8.0e-19
Match length
                  78
% identity
NCBI Description
                  CALMODULIN >gi 71685 pir MCSP calmodulin - spinach
                  398276
Seq. No.
Seq. ID
                  LIB3431-012-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1709846
BLAST score
                  226
E value
                  2.0e-18
Match length
                  133
                  38
% identity
                  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >qi 706853 (U04336)
NCBI Description
                  22 kDa component of photosystem II [Lycopersicon
                  esculentum]
                  398277
Seq. No.
                  LIB3431-012-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  626
E value
                  2.0e-65
Match length
                  128
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  398278
Seq. No.
                                                     ÷,
                  LIB3431-012-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1353352
BLAST score
                  342
E value
                  5.0e-32
                  104
Match length
% identity
NCBI Description
                  (U31975) alanine aminotransferase [Chlamydomonas
                  reinhardtii]
                  398279
Seq. No.
                  LIB3431-012-P1-K1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g122106
BLAST score
                  389
                  1.0e-37
E value
                  79
Match length
% identity
NCBI Description
                  HISTONE H4 >gi_70771 pir HSZM4 histone H4 - maize
                  >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana
                  >gi_2119028_pir__S60475 histone H4 - garden pea
                  >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum
```

Seq. No.

Seq. ID

Method

NCBI GI

E value

Seq. No. Seq. ID

Method

NCBI GI BLAST score

E value

Seq. No. Seq. ID

Method

NCBI GI

E value

Seq. No.

Seq. ID Method

NCBI GI

E value Match length

BLAST score

% identity

NCBI Description

thaliana]

BLAST score

Match length

% identity

Match length % identity

BLAST score

Match length % identity

```
aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis
                  thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis
                  thaliana] >gi 168499 (M36659) histone H4 (H4Cl3) [Zea mays]
                  >gi 168501 (M13370) histone H4 [Zea mays] >gi_168503
                  (M13377) histone H4 [Zea mays] >gi 498898 (U10042) histone
                  H4 homolog [Pisum sativum] >gi 1806285 emb CAB01914_
                  (Z79638) histone H4 homologue [Sesbania rostrata]
                  >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
                  >qi 4580385 gb AAD24364.1 AC007184 4 (AC007184) histone H4
                  [Arabidopsis thaliana] >gi 6009915 dbj BAA85120.1_
                  (AB018245) histone H4-like protein [Solanum melongena]
                  >gi 225838 prf 1314298A histone H4 [Arabidopsis thaliana]
                  398280
                  LIB3431-012-P1-K1-G9
                  BLASTX
                  g3075382-
                  212
                  7.0e-17
                  110
NCBI Description
                  (AC002505) putative peroxisome assembly protein PER8
                  [Arabidopsis thaliana] >gi 3075384 (AC004484) putative
                  peroxisome assembly protein PER8 [Arabidopsis thaliana]
                  398281
                  LIB3431-012-P1-K1-H1
                  BLASTX
                  g3355477
                  441
                  1.0e-43
                  105
                  (AC004218) putative P-glycoprotein, pgpl [Arabidopsis
NCBI Description
                  thaliana]
                  398282
                  LIB3431-012-P1-K1-H10
                  BLASTN
                  q6015437
                  36
                  1.0e-11
                  36
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
                  398283
                  LIB3431-012-P1-K1-H2
                  BLASTX
                  g4102703
                  468
                  1.0e-52
                  140
```

(AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis

```
398284
Seq. No.
                 . LIB3431-012-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2653558
BLAST score
                  776
E value
                  6.0e-83
Match length
                  159
% identity
                  91
                  (D50679) ferredoxin-sulfite reductase precursor [Zea mays]
NCBI Description
Seq. No.
                  398285
                  LIB3431-012-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982453
BLAST score
                  295
E value
                  4.0e-27
Match length
                  63
% identity
NCBI Description
                   (AL022223) fructose-bisphosphate aldolase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                  398286
Seq. ID
                  LIB3431-012-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  280
E value
                  3.0e-25
Match length
                  77
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  398287
Seq. No.
                  LIB3431-012-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  429
                  3.0e-42
E value
Match length
                  128
% identity
NCBI Description
                  (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                  398288
                  LIB3431-012-P1-K1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4887617
BLAST score
                  131
E value
                  2.0e-67
Match length
                  142
                  98
% identity
NCBI Description Oryza sativa HOS59 mRNA, partial cds
                  398289
Seq. No.
Seq. ID
                  LIB3431-013-P1-K1-A10
```

```
Method
                  BLASTX
NCBI GI
                  q2673914
BLAST score
                  325
E value
                  8.0e-42
Match length
                  139
                  62
% identity
                  (AC002561) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  398290
                  LIB3431-013-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2660669
BLAST score
                  311
E value
                  2.0e-28
Match length
                  131
% identity
                  47
                  (AC002342) human Mi-2 autoantigen-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  398291
Seq. No.
Seq. ID
                  LIB3431-013-P1-K1-A4
Method
                  BLASTX-
NCBI GI
                  g132105
BLAST score
                  417
E value
                  5.0e-43
Match length
                  130
% identity
                  76
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >qi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  398292
Seq. ID
                  LIB3431-013-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q4206195
BLAST score
                  213
E value
                  5.0e-17
Match length
                  54
% identity
                  (AF071527) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein
                  [Arabidopsis thaliana]
Seq. No.
                  398293
Seq. ID
                  LIB3431-013-P1-K1-A6
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
```

```
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  398294
Seq. ID
                  LIB3431-013-P1-K1-A8
Method
                  BLASTN
                  q4959460
NCBI GI
BLAST score
                  35
E value
                  5.0e-10
Match length
                  35
% identity
                  100
                  Zea mays RACB small GTP binding protein mRNA, complete cds
NCBI Description
Seq. No.
                  398295
Seq. ID
                  LIB3431-013-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q2894534
BLAST score
                  537
E value
                  5.0e-55
Match length
                  116
% identity
                  91
                  (AJ224327) aquaporin [Oryza sativa]
NCBI Description
                  398296
Seq. No.
                  LIB3431-013-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  348
E value
                  4.0e-33
Match length
                  69
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                  398297
                  LIB3431-013-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q479406
BLAST score
                  649
E value
                  4.0e-68
Match length
                  126
% identity
NCBI Description
                  chlorophyll a/b-binding protein - garden pea
                  >gi 20671 emb CAA49149 (X69215) chlorophyll a/b-binding
                  protein [Pisum sativum]
                  398298
Seq. No.
                  LIB3431-013-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  407
                  9.0e-40
E value
Match length
                  89
% identity
                  93
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
```

[Oryza sativa]

NCBI GI

```
Seq. No.
                  398299
Seq. ID
                  LIB3431-013-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q1169798
BLAST score
                  336
E value
                  2.0e-31
Match length
                  85
% identity
                  GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC B (GPI-B)
NCBI Description
                  (PHOSPHOGLUCOSE ISOMERASE B) (PGI-B) (PHOSPHOHEXOSE
                  ISOMERASE B) (PHI-B) >gi 639686 dbj BAA08149 (D45218)
                  phosphoglucose isomerase (Pgi-b) [Oryza sativa]
                  398300
Seq. No.
Seq. ID
                  LIB3431-013-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  501
E value
                  1.0e-52
Match length
                  134
                  81
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  398301
Seq. No.
Seq. ID
                  LIB3431-013-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g6002093
BLAST score
                  52
E value
                  9.0e-21
Match length
                  63
                  97
% identity
                  Zizania latifolia cloroplast rps4 gene for ribosomal
NCBI Description
                  protein S4
Seq. No.
                  398302
Seq. ID
                  LIB3431-013-P1-K1-B4
                  BLASTX
Method
NCBI GI
                  q488573
BLAST score
                  600
E value
                  2.0e-62
Match length
                  122
                  98
% identity
                  (U09463) histone H3.2 [Medicago sativa]
NCBI Description
Seq. No.
                  398303
Seq. ID
                  LIB3431-013-P1-K1-B7
                  BLASTX
Method
```

g3757521

```
BLAST score
                   8.0e-31
E value
                   129
Match length
                   49
% identity
NCBI Description
                   (AC005167) unknown protein [Arabidopsis thaliana]
Seq. No.
                   398304
                   LIB3431-013-P1-K1-B9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4959460
BLAST score
                   35
E value
                   6.0e-10
Match length
                   35
                   100
% identity
                   Zea mays RACB small GTP binding protein mRNA, complete cds
NCBI Description
                   398305
Seq. No.
Seq. ID
                   LIB3431-013-P1-K1-C1
Method
                   BLASTX
                                                                       ď.
NCBI GI
                   g2632254
BLAST score
                   198
                   1.0e-15
E value
Match length
                   78
% identity
                   51
                   (Y12465) serine/threonine kinase [Sorghum bicolor]
NCBI Description
                   398306
Seq. No.
Seq. ID
                   LIB3431-013-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   g170131
BLAST score
                   375
                   6.0e-36
E value
Match length
                   150
                   53
% identity
                  (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
NCBI Description
                   398307
Seq. No.
Seq. ID
                   LIB3431-013-P1-K1-C11
Method
                   BLASTN
NCBI GI
                   g596079
                   42
BLAST score
E value
                   3.0e-14
Match length
                   42
                   100
% identity
NCBI Description
                   Zea mays thiamine biosynthetic enzyme (thi1-2) mRNA,
                   complete cds
                   398308
Seq. No.
Seq. ID
                   LIB3431-013-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   q3789952
BLAST score
                   645
E value
                   1.0e-67
Match length
                   127
% identity
                   98
NCBI Description
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
```

sativa]

2.0e-77

```
Seq. No.
                   398309
 Seq. ID
                   LIB3431-013-P1-K1-C5
 Method
                   BLASTX
 NCBI GI
                   q131225
 BLAST score
                   511
 E value
                    6.0e-52
 Match length
                   111
 % identity
 NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                   V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein
                   precursor - barley >gi 167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
                   398310
 Seq. No.
 Seq. ID
                   LIB3431-013-P1-K1-C6
 Method
                   BLASTX
 NCBI GI
                   q461899
 BLAST score
                   184
 E value
                   1.0e-13
 Match length
                   116
 % identity
 NCBI Description PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR
                    (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING
                   PROTEIN) >gi 1076368 pir_B53422 peptidylprolyl isomerase
                    (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi 405131
                    (L14845) cyclophilin [Arabidopsis thaliana] >gi_1322278
                    (U42724) cyclophilin [Arabidopsis thaliana]
                   398311
 Seq. No.
                   LIB3431-013-P1-K1-C7
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g3914466
 BLAST score
                   199
 E value
                   2.0e-15
 Match length
                   36
 % identity
                   97
 NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                    (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
                   subunit precursor [Zea mays]
 Seq. No.
                   398312
 Seq. ID
                   LIB3431-013-P1-K1-C9
 Method
                   BLASTX
 NCBI GI
                   q4512653
                   225
 BLAST score
                   2.0e-18
 E value
 Match length
                   51
 % identity
                   (AC007048) unknown protein [Arabidopsis thaliana]
 NCBI Description
-Seq. No.
                   398313
 Seq. ID.
                   LIB3431-013-P1-K1-D10
 Method
                   BLASTX
 NCBI GI
                   g121343
 BLAST score
                   729
```

```
Match length
                  138
% identity
                  99
                  GLUTAMINE SYNTHETASE SHOOT ISOZYME, CHLOROPLAST PRECURSOR
NCBI Description
                  (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS31)
                  >gi 68598 pir AJRZQD glutamate--ammonia ligase (EC
                  6.3.1.2) delta precursor, chloroplast - rice
                  >gi_20370_emb_CAA32462_ (X14246) precursor chloroplastic
                  glutamine synthetase (AA -46 to 382) [Oryza sativa]
Seq. No.
                  398314
                  LIB3431-013-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789952
BLAST score
                  566
                  1.0e-58
E value -
                  127
Match length
% identity
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
Seq. No.
                  398315
Seq. ID
                  LIB3431-013-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g3913240
BLAST score
                  401
E value
                  5.0e-39
Match length
                  94
                  90
% identity
NCBI Description
                  MAGNESIUM-CHELATASE SUBUNIT CHLD PRECURSOR
                  (MG-PROTOPORPHYRIN IX CHELATASE) (MG-CHELATASE SUBUNIT D)
                  >gi 2239151_emb_CAA71128_ (Y10022) CHLD magnesium chelatase
                  subunit [Nicotiana tabacum]
Seq. No.
                  398316
Seq. ID
                  LIB3431-013-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  178
E value
                  2.0e-13
Match length
                  55
% identity
                  67
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
      -
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  398317
Seq. ID
                  LIB3431-013-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  383
E value
                  6.0e-37
```

6.0e-74

```
Match length
                  107
% identity
                  67
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  398318
Seq. No.
                  LIB3431-013-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417260
BLAST score
                  421
                  2.0e-41
E value
                  128
Match length
% identity
                  66
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                  lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
Seq. No.
                  398319
                  LIB3431-013-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100615
BLAST score
                  732
                  8.0e-78
E value
Match length
                  143
                  96
% identity
                  ribulose-bisphosphate carboxylase activase A short form
NCBI Description
                  precursor - barley >gi_167091 (M55447) ribulose
                  1,5-bisphosphate carboxylase activase [Hordeum vulgare]
                  398320
Seq. No.
Seq. ID
                  LIB3431-013-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  558
                  2.0e-57
E value
Match length
                  107
                  96
% identity
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
                  398321
Seq. No.
                  LIB3431-013-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  705
                  1.0e-74
E value
Match length
                  133
% identity
NCBI Description
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  398322
Seq. No.
Seq. ID
                  LIB3431-013-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  699
```

Match length

6.0e-64

```
Match length
                  134
                  100
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >qi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                  398323
Seq. ID
                  LIB3431-013-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  362
E value
                  2.0e-34
Match length
                  115
% identity
                  63
NCBI Description
                  (AB016283) carbonic anhydrase [Oryza sativa]
                  398324
Seq. No.
                  LIB3431-013-P1-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q409579
                  55
BLAST score
E value
                  4.0e-22
Match length
                  144
% identity
                  90
NCBI Description Rice cbpl gene for serine carboxypeptidase I, complete cds
                  398325
Seq. No.
Seq. ID
                  LIB3431-013-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g283038
BLAST score
                  357
E value
                  3.0e-34
Match length
                  75
% identity
                  91
NCBI Description
                  chlorophyll a/b-binding protein (cab-m7) precursor - maize
                  >gi_22230_emb_CAA37474_ (X53398) light harvesting
                  chlorophyll a /b binding protein [Zea mays]
Seq. No.
                  398326
Seq. ID
                  LIB3431-013-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g3582333 .
BLAST score
                  539
E value
                  7.0e-62
                  142
Match length
% identity
                  84
NCBI Description
                  (AC005496) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  398327
Seq. ID
                  LIB3431-013-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  614
```

```
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  398328
Seq. ID
                  LIB3431-013-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q1777312
BLAST score
                  259
E value
                  2.0e-22
Match length
                  75
% identity
NCBI Description
                  (D30622) novel serine/threonine protein kinase [Arabidopsis
                  thaliana] -
                  398329
Seq. No.
                  LIB3431-013-P1-K1-E9
Seq. ID
Method
                  BLASTN
                  q4680189
NCBI GI
BLAST score
                  169
                  5.0e-90
E value
                  185
Match length
% identity
                  98
NCBI Description
                  Oryza sativa subsp. indica putative dnaJ-like protein,
                  putative myb-related protein, putative farnesyl
                  pyrophosphate synthase, and hypothetical protein genes,
                  complete cds
Seq. No.
                  398330
Seq. ID
                  LIB3431-013-P1-K1-F10
Method
                  BLASTN
                  q2306980
NCBI GI
BLAST score
                  103
E value
                  6.0e-51
Match length
                  163
% identity
NCBI Description
                  Oryza sativa photosystem I antenna protein (Lhca) mRNA,
                  complete cds
Seq. No.
                  398331
                  LIB3431-013-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914603
BLAST score
                  684
E value
                  3.0e-72
Match length
                  134
% identity
                  98
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
```

(U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase

•

activase [Oryza sativa]

```
398332
Seq. No.
Seq. ID
                   LIB3431-013-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   g2290681
BLAST score
                   178
                   7.0e-25
E value
Match length
                   145
% identity
                   46
NCBI Description
                   (AF000135) acidic cellulase [Citrus sinensis]
Seq. No.
                   398333
                   LIB3431-013-P1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1777312
BLAST score
                   382
E value
                   8.0e-37
Match length
                   108
% identity
                   66
                   (D30622) novel serine/threonine protein kinase [Arabidopsis
NCBI Description
                   thaliana]
                   398334
Seq. No.
                   LIB3431-013-P1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1729971
BLAST score
                   327
E value
                   2.0e-30
                   9.9
Match length
                   69
% identity
                   TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                   rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                   sativa]
                   398335
Seq. No.
                   LIB3431-013-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4079798
                   293
BLAST score
                   2.0e-26
E value
Match length
                   104
                   59
% identity
NCBI Description
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                   sativa]
                   398336
Seq. No.
Seq. ID
                   LIB3431-013-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   228
E value
                   1.0e-18
Match length
                   44
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
```

NCBI GI

```
protein [Oryza sativa]
                   398337
Seq. No.
Seq. ID
                   LIB3431-013-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   q347451
BLAST score
                   536
                   7.0e-55
E value
                   117
Match length
% identity
                   86
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                   sativa]
                   398338
Seq. No.
Seq. ID
                   LIB3431-013-P1-K1-G4
Method
                   BLASTX
                   g132105
NCBI GI
BLAST score
                   665
E value
                   6.0e-70
                  144
Match length
                   88
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4.\overline{1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   398339
Seq. No.
                  LIB3431-013-P1-K1-G6
Seq. ID
Method
                  BLASTN
NCBI GI
                   g20262
BLAST score
                  157
E value
                   4. 0e−83
                  187
Match length
                  96
% identity
                  O.sativa light-induced mRNA
NCBI Description
                   398340
Seq. No.
                  LIB3431-013-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g729668
BLAST score
                  245
E value
                   6.0e-21
                  83
Match length
% identity
                  HISTONE H1 >gi 2147479 pir S65059 histone H1,
NCBI Description
                  drought-inducible - Lycopersicon pennellii >gi 436823
                   (U01890) Solanum pennellii histone H1 [Solanum pennellii]
Seq. No.
                  398341
                  LIB3431-013-P1-K1-G9
Seq. ID
Method
                  BLASTX
```

q4469021

Match length

```
BLAST score
                   245
E value
                   1.0e-20
Match length
                   72
% identity
                   69
NCBI Description
                   (AL035602) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   398342
                   LIB3431-013-P1-K1-H1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3041776
BLAST score
                   60
E value
                   2.0e-25
Match length
                   88
% identity
                   92
NCBI Description
                   Oryza sativa mRNA for fructose-1,6-bisphosphatase
                   (plastidic isoform), complete cds
Seq. No.
                   398343
Seq. ID
                   LIB3431-013-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   q3789954
BLAST score
                   368
                   4.0e-35
E value
Match length
                   110
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
Seq. No.
                   398344
Seq. ID
                   LIB3431-013-P1-K1-H12
                   BLASTX
Method
NCBI GI
                   g4079798
BLAST score
                   376
E value
                   5.0e-36
Match length
                   125
                   62
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   398345
Seq. No.
Seq. ID
                  LIB3431-013-P1-K1-H3
Method
                   BLASTN
NCBI GI
                   g2072554
BLAST score
                   102
E value
                   2.0e-50
                   118
Match length
                   97
% identity
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                   cds
                   398346
Seq. No.
Seq. ID
                  LIB3431-013-P1-K1-H5
Method
                  BLASTX
NCBI GI
                   g2586083
BLAST score
                   206
E value
                   2.0e-17
```

Seq. No.

```
% identity
                  43
NCBI Description
                  (U72725) receptor kinase-like protein [Oryza
                  longistaminata]
Seq. No.
                  398347
                  LIB3431-013-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2407281
BLAST score
                  709
E value
                  4.0e-75
Match length
                  133
% identity
                  99
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
Seq. No.
                  398348
Seq. ID
                  LIB3431-014-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q120657
BLAST score
                  540
E value
                  2.0e-55
Match length
                  135
% identity
                  81
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                  CHLOROPLAST >gi 66024 pir DEZMG3
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  maize >gi 168479 (M18976) glyceraldehyde-3-phosphate
                  dehydrogenase [Zea mays] >gi 763035 emb CAA33455 (X15408)
                  glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.
                  398349
Seq. ID
                  LIB3431-014-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  220
E value
                  4.0e-18
Match length
                  68
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein
          . 3
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  398350
Seq. ID
                  LIB3431-014-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  214
E value
                  3.0e-17
Match length
                  44
% identity
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
```

```
LIB3431-014-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913018
BLAST score
                  321
E value
                  7.0e-30
Match length
                  80
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (ALDP) >qi 218155 dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  398352
Seq. No.
Seq. ID
                  LIB3431-014-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g3551958
BLAST score
                  267
                  1.0e-25
E value
Match length
                  87
% identity
NCBI Description
                  (AF082032) senescence-associated protein 12 [Hemerocallis
                  hybrid cultivar]
Seq. No.
                  398353
Seq. ID
                  LIB3431-014-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g3158476
BLAST score
                  348
E value
                  6.0e-33 →
Match length
                  93
% identity
NCBI Description
                  (AF067185) aquaporin 2 [Samanea saman]
Seq. No.
                  398354
Seq. ID
                  LIB3431-014-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  505
E value
                  3.0e-51
Match length
                  110
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  398355
Seq. ID
                  LIB3431-014-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g4559339
BLAST score
                  610
E value
                  1.0e-63
Match length
                  138
```

Seq. No.

```
% identity
                   (AC007087) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  398356
Seq. ID
                  LIB3431-014-P1-K1-B12
Method
                  BLASTX
NCBI, GI
                  q1001794
BLAST score
                  161
E value
                   4.0e-11
Match length
                  41
% identity
NCBI Description
                  (D64005) hypothetical protein [Synechocystis sp.]
                  398357
Seq. No.
Seq. ID
                  LIB3431-014-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  q5478796
BLAST score
                  57
E value
                  1.0e-23
Match length
                  73
                  96
% identity
                  Oryza sativa CAO mRNA for chlorophyll b synthase, partial
NCBI Description
                  398358
Seq. No.
Seq. ID
                  LIB3431-014-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g19094
BLAST score
                  46
E value
                  6.0e-17
Match length
                  54
                  96
% identity
NCBI Description
                  H.vulgare mRNA PsaN for photosystem I subunit N
Seq. No.
                  398359
Seq. ID
                  LIB3431-014-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g4741205
BLAST score
                  395
                  2.0e-38
E value
                  107
Match length
% identity
NCBI Description
                  (AL049746) putative protein [Arabidopsis thaliana]
                  398360
Seq. No.
Seq. ID
                  LIB3431-014-P1-K1-B8
                  BLASTX
Method
NCBI GI
                  g1262849
                  266
BLAST score
E value
                  1.0e-25
Match length
                  64
% identity
                  95
                  (U51633) type 1 light-harvesting chlorophyll a/b-binding
NCBI Description
                  polypeptide [Pinus palustris]
```

```
LIB3431-014-P1-K1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3063523
BLAST score
                  45
E value
                  6.0e-17
Match length
                  49
                  98
% identity
                  Oryza sativa ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
Seq. No.
                  398362
                  LIB3431-014-P1-K1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3885891
BLAST score
                  41
E value
                  5.0e-14
Match length
                  85
% identity
                  87
NCBI Description
                  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                  mRNA, complete cds
Seq. No.
                  398363
Seq. ID
                  LIB3431-014-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g3122914
BLAST score
                  213
E value
                  6.0e-17
Match length
                  147
% identity
                  31
NCBI Description
                  VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS)
                  >gi 1890130 gb AAB49704.1 (U89986) valyl tRNA synthetase
                  [Arabidopsis thaliana]
Seq. No.
                  398364
Seq. ID
                  LIB3431-014-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g3126854
                                                                            - 70
BLAST score
                  609
E value
                  2.0e-63
Match length
                  119
% identity
NCBI Description
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  398365
Seq. ID
                  LIB3431-014-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  q3126853
BLAST score
                  172
E value
                  7.0e-92
Match length
                  210
                  100
% identity
NCBI Description
                  Oryza sativa chlorophyll a/b binding protein (RCABP89)
                  mRNA, nuclear gene encoding chloroplast protein, complete
                  cds
Seq. No.
                  398366
Seq. ID
                  LIB3431-014-P1-K1-C8
```

1.0e-69

```
BLASTX
Method
NCBI GI
                   g3126854
BLAST score
                   707
E value
                   8.0e-75
Match length
                   137
                   97
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   398367
Seq. No.
Seq. ID
                   LIB3431-014-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g1931640
BLAST score
                   445
E value
                   4.0e-44
Match length
                   125
% identity
NCBI Description
                   (U95973) Serine carboxypeptidase isolog [Arabidopsis
                   thalianal
                   398368
Seq. No.
Seq. ID
                   LIB3431-014-P1-K1-D10
Method
                   BLASTN
NCBI GI
                   q1835730
BLAST score
                   288
E value
                   1.0e-161
Match length
                   308
% identity
                   99
                   Oryza sativa photosystem II 10 kDa polypeptide mRNA,
NCBI Description
                   complete cds
                   398369
Seq. No.
Seq. ID
                   LIB3431-014-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   q19184
BLAST score
                   498
                   4.0e-51
E value
Match length
                   125
% identity
                   82
                   (X61287) Type I (26 kD) CP29 polypeptide [Lycopersicon
NCBI Description
                   esculentum]
Seq. No.
                   398370
Seq. ID
                   LIB3431-014-P1-K1-D12
Method
                   BLASTX
                   q2280518
NCBI GI
                   157
BLAST score
                   2.0e-10
E value
Match length
                   116
% identity
NCBI Description
                   (AB005878) BYJ15 [Nicotiana tabacum]
                   398371
Seq. No.
                   LIB3431-014-P1-K1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g854731
BLAST score
                   662
```

Method

BLASTX

```
Match length
                  140
                  94
% identity
NCBI Description
                  (U19183) acetyl-coenzyme A carboxylase [Zea mays]
                  398372
Seq. No.
                  LIB3431-014-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2306981
BLAST score
                  480
E value
                  4.0e-48
Match length
                  101
% identity
                  83
                  (AF010321) photosystem I antenna protein [Oryza sativa]
NCBI Description
Seq. No.
                  398373
Seq. ID
                  LIB3431-014-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  g1835730
BLAST score
                  73
                                          . 5
E value
                  8.0e-33
Match length
                  89
% identity
                  96
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
NCBI Description
                  complete cds
                  398374
Seq. No.
Seq. ID
                  LIB3431-014-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g2160322
BLAST score
                  281
                  5.0e-25
E value
Match length
                  66
% identity
                  (D16139) cytokinin binding protein CBP57 [Nicotiana
NCBI Description
                  sylvestris]
                  398375
Seq. No.
Seq. ID
                  LIB3431-014-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  304
                  1.0e-27
E value
Match length
                  78
% identity
                  79
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  398376
                  LIB3431-014-P1-K1-E1
Seq. ID
```

Method

BLASTX

```
g3914603
NCBI GI
BLAST score
                   664
                   6.0e-70
E value
Match length
                   130
                   97
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                   activase [Oryza sativa]
                   398377
Seq. No.
                  LIB3431-014-P1-K1-E10
Seq. ID
Method
                  BLASTX
                  g3025189
NCBI GI
BLAST score
                   455
E value
                   3.0e-45
Match length
                   141
% identity
NCBI Description
                  HYPOTHETICAL 67.1 KD PROTEIN SLL1770
                   >gi 1652753 dbj BAA17672 (D90908) ABC1-like [Synechocystis
                  sp.]
Seq. No.
                   398378
Seq. ID
                  LIB3431-014-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2894534
BLAST score
                   746
                   2.0e-79
E value
                   146
Match length
% identity
                   99
NCBI Description
                   (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                   398379
                  LIB3431-014-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3345477
BLAST score
                  534 -
E value
                   1.0e-54
Match length
                   149
% identity
NCBI Description
                   (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                  398380
                  LIB3431-014-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  237
                  9.0e-20
E value
Match length
                   44
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  398381
                  LIB3431-014-P1-K1-E4
Seq. ID
```

```
NCBI GI
                  g115787
BLAST score
                  236
E value
                  5.0e-20
Match length
                  67
% identity
                  81
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  398382
Seq. No.
Seq. ID
                  LIB3431-014-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g3808101
BLAST score
                  306
                  7.0e-28
E value
Match length
                  75
                  85
% identity
                  (AJ012165) chloroplast protease [Capsicum annuum]
NCBI Description
                  398383
Seq. No.
                  LIB3431-014-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82080
BLAST score
                  501
                  1.0e-50
E value
Match length
                  137
% identity
                  69
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >qi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  398384
Seq. No.
                  LIB3431-014-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407279
BLAST score
                  575
E value
                  2.0e-59
Match length
                  117
% identity
                  93
NCBI Description
                  (AF017362) aldolase [Oryza sativa]
                  398385
Seq. No.
                  LIB3431-014-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982362
BLAST score
                  479
E value
                  4.0e-48
Match length
                  103
% identity
                  (AF053311) glutathione peroxidase [Zantedeschia aethiopica]
NCBI Description
Seq. No.
                  398386
                  LIB3431-014-P1-K1-F1
Seq. ID
Method
```

BLASTX

g548605

NCBI GI

Method

NCBI GI

BLASTX

q1346771

```
608
BLAST score
E value
                   3.0e-63
                  133
Match length
% identity
                   91
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                   - barley >qi 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
                  398387
Seq. No.
                  LIB3431-014-P1-K1-F10
Seq. ID
Method
                  BLASTX
                  g3548815
NCBI GI
BLAST score
                  254
E value
                  1.0e-21
Match length
                  109
% identity
                   50
NCBI Description
                   (AC005313) similar to axoneme-associated protein mst101

    [Arabidopsis thaliana]

Seq. No.
                  398388
Seq. ID
                  LIB3431-014-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g1903364
BLAST score
                  296
E value
                  1.0e-26
Match length
                  145
% identity
NCBI Description
                   (AC000104) EST gb T45093 comes from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  398389
Seq. ID
                  LIB3431-014-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q3738285
BLAST score
                  320
E value
                  2.0e-29
Match length
                  101
% identity
                  (AC005309) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  398390
Seq. ID
                  LIB3431-014-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  q3548815
BLAST score
                  255
                  6.0e-22
E value
Match length
                  105
% identity
                   (AC005313) similar to axoneme-associated protein mst101
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  398391
Seq. ID
                  LIB3431-014-P1-K1-F6
```

NCBI GI

```
BLAST score
                  778
                  4.0e-83
E value
Match length
                  158
% identity
                  91
                  PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
NCBI Description
                  >gi 1086117 pir S52988 phosphoenolpyruvate carboxykinase
                   (PCK1) - Urochloa panicoides >gi 607752 (U09241)
                  phosphoenolpyruvate carboxykinase [Urochloa panicoides]
                  398392
Seq. No.
                  LIB3431-014-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789954
BLAST score
                  328
E value
                  7.0e-31
Match length
                  66
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                 .sativa]
Seq. No.
                  398393
                  LIB3431-014-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  464
E value
                  1.0e-46
Match length
                  101
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi 2130146 pir S61419 thiamine biosynthetic enzyme thil-1
                  - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  398394
Seq. ID
                  LIB3431-014-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2626753
BLAST score
                  376
E value
                  4.0e-36
Match length
                  109
% identity
NCBI Description
                  (AB008782) sulfate transporter [Arabidopsis thaliana]
Seq. No.
                  398395
Seq. ID
                  LIB3431-014-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q1769887
BLAST score
                  456
E value
                  1.0e-45
Match length
                  110
% identity
NCBI Description
                  (X95736) amino acid permease 6 [Arabidopsis thaliana]
Seq. No.
                  398396
Seq. ID
                  LIB3431-014-P1-K1-G2
Method
                  BLASTX
```

q3913018

Seq. No.

```
809
BLAST score
E value
                  8.0e-87
Match length
                  154
% identity
                  99
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  3.98397
Seq. No.
Seq. ID
                  LIB3431-014-P1-K1-G4
Method
                  BLASTN
NCBI GI
                  q20262
BLAST score
                  205
                  1.0e-111
E value
                  273
Match length
% identity
                  94
NCBI Description
                  O.sativa light-induced mRNA
Seq. No.
                  398398
                  LIB3431-014-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3288821
BLAST score
                  655
                  1.0e-68
E value
Match length
                  143
                  86
% identity
NCBI Description
                  (AF063901) alanine:glyoxylate aminotransferase;
                  transaminase [Arabidopsis thaliana]
                  >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
                  alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
Seq. No.
                  398399
Seq. ID
                  LIB3431-014-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g462195
BLAST score
                  516
E value
                  2.0e-52
Match length
                  115
                  88
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi_100682_pir__S21636 GOS2 protein - rice
                  >gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                  >gi 3789950 (AF094774) translation initiation factor [Oryza
                  satīva]
Seq. No.
                  398400
Seq. ID
                  LIB3431-014-P1-K1-G7
                  BLASTX
Method
NCBI GI
                  g283039
BLAST score
                  175
E value
                  1.0e-17
                  63
Match length
                  76
% identity
                  gene iojap protein - maize >gi_22349_emb CAA78772_ (Z15063)
NCBI Description
                  putative iojap protein [Zea mays]
```

Match length

```
LIB3431-014-P1-K1-H1
Seq. ID
Method
                  BLASTX
                  g729477
NCBI GI
BLAST score
                  331
E value
                  9.0e-31
Match length
                  133
% identity
                  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR)
NCBI Description
                  >gi_320548_pir_A44974 ferredoxin--NADP+ reductase (EC
                  1.18.1.2) precursor - common ice plant >gi 167256 (M25528)
                  ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
                  [Mesembryanthemum crystallinum] >gi 226768 prf 1604475A
                  ferredoxin NADP reductase [Mesembryanthemum crystallinum]
Seq. No.
                  398402
Seq. ID
                  LIB3431-014-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q266893
BLAST score
                  768
                  5.0e-82
E value
Match length
                  151
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                  >gi 322416 pir S28172 ribulose-bisphosphate carboxylase
                  activase - cucumber >gi 18284 emb CAA47906 (X67674)
                  rubisco activase [Cucumis sativus]
                  398403
Seq. No.
Seq. ID
                  LIB3431-014-P1-K1-H3
Method
                  BLASTN
NCBI GI
                  q3075487
BLAST score
                  281
E value
                  1.0e-157
Match length
                  285
% identity
                  100
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  398404
Seq. ID
                  LIB3431-014-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q4056507
BLAST score
                  267
E value
                  3.0e-23
Match length
                  85
% identity
                  (AC005896) putative RNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  398405
                  LIB3431-014-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  635
E value
                  2.0e-66
```

BLAST score

```
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  398406
Seq. ID
                  LIB3431-014-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g606817
BLAST score
                  649
E value
                  3.0e-71
Match length
                  147
                  95
% identity
NCBI Description
                  (U08404) carbonic anhydrase [Oryza sativa]
                  >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic
                  anhydrase 3 [Oryza sativa]
                  398407
Seq. No.
                  LIB3431-014-P1-K1-H8
Seq. ID
Method
                  BLASTX
                  q4666287
NCBI GI
BLAST score
                  581
                  3.0e-60
E value
Match length
                  121
% identity
                  (D85764) cytosolic monodehydroascorbate reductase [Oryza
NCBI Description
                  sativa]
                  398408
Seq. No.
                  LIB3431-014-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3075488
BLAST score
                  694
                  5.0e-76
E value
                  147
Match length
% identity
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                  398409
Seq. No.
Seq. ID
                  LIB3431-014-P1-N1-A3
Method
                  BLASTN
NCBI GI
                  g3789951
BLAST score
                  88
                  7.0e-42
E value
                  213
Match length
% identity
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein presursor
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
Seq. No.
                  398410
Seq. ID
                  LIB3431-014-P1-N1-A6
Method
                  BLASTN
NCBI GI
                  g218154
```

Match length

```
5.0e-28
E value
Match length
                  80
% identity
                   98
NCBI Description
                  Oryza sativa gene for cytoplasmic aldolase, complete cds,
                  clone:Aldp
Seq. No.
                  398411
Seq. ID
                  LIB3431-014-P1-N1-B10
Method
                  BLASTX
NCBI GI
                  q347451
BLAST score
                  207
E value
                   2.0e-16
Match length
                  39
                  100
% identity
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
Seq. No.
                  398412
                  LIB3431-014-P1-N1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1001794
BLAST score
                  168
E value
                   6.0e-12
Match length
                  41
                  73
% identity
NCBI Description
                  (D64005) hypothetical protein [Synechocystis sp.]
Seq. No.
                  398413
Seq. ID
                  LIB3431-014-P1-N1-B3
Method
                  BLASTX
NCBI GI
                  g3914466
BLAST score
                  302
E value
                  2.0e-27
Match length
                  71
                  79
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi 2981214 (AF052429) photosystem I complex PsaN
                  subunit precursor [Zea mays]
                  398414
Seq. No.
Seq. ID
                  LIB3431-014-P1-N1-B8
Method
                  BLASTN
NCBI GI
                  g20181
BLAST score
                  138
E value
                  1.0e-71
Match length
                  145
                  99
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
                  398415
Seq. No.
Seq. ID
                  LIB3431-014-P1-N1-C1
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  94
E value
                  1.0e-45
```

NCBI Description

```
92
% identity
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS1139
                  398416
Seq. No.
                  LIB3431-014-P1-N1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885892
BLAST score
                  342
                   4.0e-32
E value
Match length
                  66
                  100
% identity
                   (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
Seq. No.
                  398417
                  LIB3431-014-P1-N1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  272
E value
                   6.0e-24
Match length
                  57
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  398418
Seq. No.
Seq. ID
                  LIB3431-014-P1-N1-C7
Method
                  BLASTN
NCBI GI
                  q3126853
BLAST score
                  145
E value
                  8.0e-76
Match length
                  207
% identity
                  97
NCBI Description
                  Oryza sativa chlorophyll a/b binding protein (RCABP89)
                  mRNA, nuclear gene encoding chloroplast protein, complete
                  398419
Seq. No.
Seq. ID
                  LIB3431-014-P1-N1-C8
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  456
E value
                  9.0e-46
Match length
                  103
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  398420
Seq. No.
Seq. ID
                  LIB3431-014-P1-N1-D10
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  236
E value
                  6.0e-20
Match length
                  56
% identity
```

(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.

```
Seq. No.
                  398421
Seq. ID
                  LIB3431-014-P1-N1-D11
Method
                  BLASTX
NCBI GI
                  q733454
BLAST score
                  210
E value
                  1.0e-16
Match length
                  48
% identity
                  85
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
                  398422
Seq. No.
Seq. ID
                  LIB3431-014-P1-N1-D3
Method
                  BLASTX
NCBI GI
                  g99486
BLAST score
                  275
                  4.0e-24
E value
Match length
                  67
                  79
% identity
                  chlorophyll a/b-binding protein (clone pINEab 31) - Scotch
NCBI Description
                  pine >gi 20792 emb CAA41406 (X58516) Type II chlorophyll a
                  /b-binding protein [Pinus sylvestris]
Seq. No.
                  398423
                  LIB3431-014-P1-N1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g168525
BLAST score
                  37
E value
                  3.0e-11
Match length
                  53
% identity
                  92
                  Zea mays nucleic acid-binding protein (NBP)
NCBI Description
Seq. No.
                  398424
                  LIB3431-014-P1-N1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q80783
BLAST score
                  190
E value
                  3.0e-14
Match length
                  120
% identity
                  36
                  hypothetical 31.7K protein (aphE region) - Streptomyces
NCBI Description
                  griseus >gi_153164 (M37378)
                  streptomycin-3'-phosphotransferase [Streptomyces griseus]
                  398425
Seq. No.
Seq. ID
                  LIB3431-014-P1-N1-D9
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  225
E value
                  2.0e-18
Match length
                  44
% identity
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
```

NCBI Description

```
LIB3431-014-P1-N1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132166
BLAST score
                  149
                  1.0e-09
E value
Match length
                  31
                  81
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                  >gi 81660 pir S04048 ribulose-bisphosphate carboxylase
                  activase precursor - Arabidopsis thaliana
                  >gi 16471 emb CAA32429 (X14212) rubisco activase (AA 1 -
                  473) [Arabidopsis thaliana]
Seq. No.
                  398427
Seq. ID
                  LIB3431-014-P1-N1-E11
Method
                  BLASTX
NCBI GI
                  g2696804
BLAST score
                  308
E value
                  4.0e-28
Match length
                  56
% identity
                  100
NCBI Description (AB009665) water channel protein [Oryza sativa]
Seq. No.
                  398428
Seq. ID
                  LIB3431-014-P1-N1-E12
Method
                  BLASTN
NCBI GI
                  g606816
BLAST score
                  350
E value
                  0.0e + 00
Match length
                  364
% identity
                  99
NCBI Description Oryza sativa chloroplast carbonic anhydrase mRNA, complete
Seq. No.
                  398429
Seq. ID
                  LIB3431-014-P1-N1-E2
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  343
E value
                  0.0e + 00
Match length
                  377
% identity
                  98
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
Seq. No.
                  398430
Seq. ID
                  LIB3431-014-P1-N1-E4
Method
                  BLASTX
NCBI GI
                  g3036951
BLAST score
                  233
E value
                  2.0e-19
Match length
                  57
% identity
                  93
                  (AB012639) light harvesting chlorophyll a/b-binding protein
```

[Nicotiana sylvestris]

BLASTX

```
Seq. No.
                  398431
Seq. ID
                  LIB3431-014-P1-N1-E5
Method
                  BLASTX
NCBI GI
                  g3808101
BLAST score
                  181
                   2.0e-13
E value
Match length
                   43
                   84
% identity
                   (AJ012165) chloroplast protease [Capsicum annuum]
NCBI Description
                  398432
Seq. No.
Seq. ID
                  LIB3431-014-P1-N1-E8
Method
                  BLASTX
NCBI GI
                  g2407279
BLAST score
                   200
                   8.0e-25
E value
Match length
                   67
% identity
                   93
NCBI Description
                   (AF017362) aldolase [Oryza sativa]
Seq. No.
                   398433
Seq. ID
                  LIB3431-014-P1-N1-E9
                  BLASTX
Method
NCBI GI
                   g2982362
BLAST score
                   494
                   6.0e-50
E value
                   100
Match length
                   89
% identity
                   (AF053311) glutathione peroxidase [Zantedeschia aethiopica]
NCBI Description
                   398434
Seq. No.
Seq. ID
                  LIB3431-014-P1-N1-F1
Method
                  BLASTX
NCBI GI
                   g548605
                   232
BLAST score
                   1.0e-20
E value
Match length
                   64
                   88
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi 539055 pir A48527 photosystem I protein psaK precursor
                   - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
Seq. No.
                   398435
                  LIB3431-014-P1-N1-F5
Seq. ID
Method
                  BLASTN
NCBI GI
                   g11957
BLAST score
                   63
E value
                   7.0e-27
                   143
Match length
                   43
% identity
                  Rice complete chloroplast genome
NCBI Description
                   398436
Seq. No.
Seq. ID
                  LIB3431-014-P1-N1-F6
```

NCBI GI

BLAST score

g283039

```
NCBI GI
                  q1346771
BLAST score
                   189
E value
                   2.0e-17
Match length
                   67
% identity
NCBI Description
                   PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP]
                  >gi_1086117_pir__S52988 phosphoenolpyruvate carboxykinase
                   (PCK1) - Urochloa panicoides >gi_607752 (U09241)
                  phosphoenolpyruvate carboxykinase [Urochloa panicoides]
Seq. No.
                  398437
                  LIB3431-014-P1-N1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789954
BLAST score
                  277
E value
                  2.0e-24
Match length
                  54
% identity
NCBI Description
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                  sativa]
                  398438
Seq. No.
Seq. ID
                  LIB3431-014-P1-N1-G2
Method
                  BLASTX
NCBI GI
                  g2407279
BLAST score
                  149
                  2.0e-11
E value
Match length
                  45
% identity
                  81
NCBI Description
                  (AF017362) aldolase [Oryza sativa]
                  398439
Seq. No.
Seq. ID
                  LIB3431-014-P1-N1-G4
Method
                  BLASTN
NCBI GI
                  g20262
BLAST score
                  300
E value
                  1.0e-168
                  345
Match length
% identity
                  97
NCBI Description
                  O.sativa light-induced mRNA
                  398440
Seq. No.
Seq. ID
                  LIB3431-014-P1-N1-G6
Method
                  BLASTN
NCBI GI
                  g3789949
BLAST score
                  142
                  2.0e-74
E value
Match length
                  146
% identity
                  99
                  Oryza sativa translation initiation factor (GOS2) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  398441
Seq. ID
                  LIB3431-014-P1-N1-G7
Method
                  BLASTX
```

BLASTX

```
.E value
                   2.0e-10
Match length
                   39
                   79
% identity
                   gene iojap protein - maize >gi_22349_emb_CAA78772_ (Z15063)
NCBI Description
                   putative iojap protein [Zea mays]
Seq. No.
                   398442
Seq. ID
                  LIB3431-014-P1-N1-H1
                 BLASTX
Method
NCBI GI
                   g729478
BLAST score
                   247
E value
                   1.0e-23
Match length
                   60
                   83
% identity
                   FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                   >gi 442481 dbj BAA04616 (D17790) ferredoxin-NADP+
                  reductase [Oryza sativa] >gi 6069649 dbj BAA85425.1
                   (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
                   a region of the predicted gene.; similar to
                   ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
Seq. No.
                   398443
                   LIB3431-014-P1-N1-H3
Seq. ID
                   BLASTN
Method
                   q3075487
NCBI GI
BLAST score
                   80
E value
                   5.0e-37
                   205
Match length
                   90
% identity
                   Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                   mRNA, complete cds
                   398444
Seq. No.
                   LIB3431-014-P1-N1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4666287
BLAST score
                   336
                   1.0e-31
E value
Match length
                   65
                   100
% identity
NCBI Description
                   (D85764) cytosolic monodehydroascorbate reductase [Oryza
                   sativa]
                   398445
Seq. No.
                   LIB3431-014-P1-N1-H9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3075487
BLAST score
                   241
E value
                   1.0e-133
Match length
                   253
% identity
                   99
NCBI Description
                   Oryza sativa chlorophyll a/b-binding protein (RCABP69)
                   mRNA, complete cds
Seq. No.
                   398446
Seq. ID
                   LIB3431-015-P1-K1-A10
```

% identity

```
NCBI GI
                  g2072727
BLAST score
                  700
                  4.0e-74
E value
                  140
Match length
% identity
                  97
NCBI Description
                 (Y12595) Fd-GOGAT protein [Oryza sativa]
                  398447
Seq. No.
Seq. ID
                  LIB3431-015-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  g1398998
BLAST score
                  86
E value
                  8.0e-41
Match length
                  173
                  99
% identity
                  Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II,
NCBI Description
                  complete cds
                  398448
Seq. No.
                  LIB3431-015-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4138179
BLAST score
                  338
E value
                  4.0e-32
                  69
Match length
% identity
                  93
                  (AJ223969) elongation factor 1 alpha subunit [Malus
NCBI Description
                  domestica]
                  398449
Seq. No.
                  LIB3431-015-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g488571
BLAST score
                  515
E value
                  2.0e-52
Match length
                  103
                  99
% identity
                 (U09462) histone H3.2 [Medicago sativa]
NCBI Description
                  398450
Seq. No.
                  LIB3431-015-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4138290
BLAST score
                  576
E value
                  1.0e-59
Match length
                  124
% identity
                  86
                 (AJ005841) thioredoxin M [Oryza sativa]
NCBI Description
                  398451
Seq. No.
Seq. ID
                  LIB3431-015-P1-K1-A6
Method .
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
```

```
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  398452
Seq. No.
Seq. ID
                  LIB3431-015-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q2293480
BLAST score
                  246
                  3.0e-21
E value
Match length
                  48
% identity
NCBI Description
                  (AF011331) glycine-rich protein [Oryza sativa]
                  398453
Seq. No.
Seq. ID
                  LIB3431-015-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g3142698
BLAST score
                  534
E value
                  1.0e-54
Match length
                  129
                                                                                71
% identity
NCBI Description
                  (AF064542) protein farnesyltransferase subunit A
                  [Arabidopsis thaliana]
                  398454
Seq. No.
Seq. ID
                  LIB3431-015-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  570
                  6.0e-59
E value
                  109
Match length
                  99
% identity
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
                  398455
Seq. No.
Seq. ID
                  LIB3431-015-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  438
                  1.0e-43
E value
Match length
                  97
% identity
                  86
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461 pir_S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  398456
Seq. No.
Seq. ID
                  LIB3431-015-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g2501647
BLAST score
                  292
E value
                  3.0e-26
Match length
                  80
% identity
                  69
NCBI Description UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD)
```

NCBI GI

BLAST score

BLASTX

706

g5007084

```
uroporphyrinogen decarboxylase [Nicotiana tabacum]
Seq. No.
                  398457
Seq. ID
                  LIB3431-015-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  q218171
BLAST score
                  236
E value
                  1.0e-130
Match length
                  236
% identity
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                  a/b binding protein of photosystem II (LHCPII), complete
Seq. No.
                  398458
Seq. ID
                  LIB3431-015-P1-K1-B3
Method
                 BLASTX
NCBI GI
                  q3122724
                  313
BLAST score
E value
                  9.0e-29
Match length
                  69
                  86
% identity
                  60S RIBOSOMAL PROTEIN L38 >gi 2289009 (AC002335) ribosomal
NCBI Description
                  protein L38 isolog [Arabidopsis thaliana]
Seq. No.
                  398459
Seq. ID
                  LIB3431-015-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                  173
E value
                  1.0e-12
Match length
                  75
% identity
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
Seq. No.
                  398460
Seq. ID
                  LIB3431-015-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g3193290
BLAST score
                  213
E value
                  3.0e-17
Match length
                  73
% identity
                  (AF069298) contains similarity to a protein kinase domain
NCBI Description
                  (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta
                  domain (Pfam: lectin_legB.hmm, score: 125.64) and legume
                  lectins alpha domain (Pfam: lectin legA.hmm, score: 16.72)
                  [Arabido
Seq. No.
                  398461
Seq. ID
                  LIB3431-015-P1-K1-C10
```

>gi 1362120 pir S55732 uroporphyrinogen decarboxylase -

common tobacco >gi 1009429 emb CAA58040 (X82833)

E value

2.0e-54

```
8.0e-75
E value
Match length
                   137
% identity
                   98
                   (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   398462
Seq. ID
                   LIB3431-015-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g3885513
BLAST score
                   237
E value
                   7.0e-20
Match length
                   59
% identity
                   66
                   (AF084201) similar to chloroplast 50S ribosomal protein L31
NCBI Description
                   [Medicago sativa]
                   398463
Seq. No.
Seq. ID
                   LIB3431-015-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   q2072555
BLAST score
                   348
E value
                   7.0e-33
Match length
                   62
                   98
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                   398464
Seq. No.
Seq. ID
                   LIB3431-015-P1-K1-C4
Method
                   BLASTN
NCBI GI
                   q4519195
BLAST score
                   40
                   5.0e-13
E value
Match length
                   68
% identity
                   90
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MQC12, complete sequence
                   398465
Seq. No.
Seq. ID
                   LIB3431-015-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   g1532135
BLAST score
                   339
                   6.0e-32
E value
Match length
                   112
% identity
NCBI Description
                   (U49442) chloroplast mRNA-binding protein CSP41 precursor
                   [Spinacia oleracea]
Seq. No.
                   398466
Seq. ID
                  LIB3431-015-P1-K1-C8
Method
                  BLASTX
NCBI GI
                   g2623298
BLAST score
                   532
```

% identity

```
Match length
                  116
                   84
% identity
                   (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis
NCBI Description
                  thaliana]
                   398467
Seq. No.
Seq. ID
                  LIB3431-015-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g386875.6
                  494
BLAST score
E value
                   3.0e-50
                  99
Match length
% identity
                   91
NCBI Description
                   (D86611) catalase [Oryza sativa]
                   398468
Seq. No.
Seq. ID
                  LIB3431-015-P1-K1-D1
Method
                  BLASTX
NCBI GI
                   g1055130
BLAST score
                   275
E value
                   3.0e-24
Match length
                  126
% identity
                   (U39998) coded for by C. elegans cDNA yk92b11.3; coded for
NCBI Description
                  by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA
                  yk78c2.5; coded for by C. elegans cDNA cm9a8; coded for by
                  C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA
                  yk78c2.3
Seq. No.
                   398469
Seq. ID
                  LIB3431-015-P1-K1-D11
                  BLASTX
Method
NCBI GI
                   g3126854
BLAST score
                   437
E value
                   4.0e-58
Match length
                  114
                   92
% identity.
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   398470
Seq. No.
                   LIB3431-015-P1-K1-D2
Seq. ID
                  BLASTN
Method
NCBI GI
                   g20262
                   175
BLAST score
E value
                   1.0e-93
Match length
                  175
% identity
                   100
                  O.sativa light-induced mRNA
NCBI Description
Seq. No.
                   398471
                  LIB3431-015-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q347451
BLAST score
                   165
E value
                   1.0e-24
Match length
                  92
```

BLASTN

```
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa]
                  398472
Seq. No.
                  LIB3431-015-P1-K1-D5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2196672
BLAST score
                   444
E value
                   4.0e-44
                  93
Match length
% identity
                  89
                  (Y08807) HMGd1 [Zea mays]
NCBI Description
Seq. No.
                  398473
                  LIB3431-015-P1-K1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4455180
BLAST score
                  184
E value
                   1.0e-13
Match length
                   44
                  82
% identity
                   (AL035521) putative protein [Arabidopsis thaliana]
NCBI Description
                  398474
Seq. No.
                  LIB3431-015-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3885888
BLAST score
                  282
                   3.0e-25
E value
Match length
                   63
% identity
                   90
                   (AF093632) high mobility group protein [Oryza sativa]
NCBI Description
                  398475
Seq. No.
Seq. ID
                  LIB3431-015-P1-K1-E1
                  BLASTN
Method ·
NCBI GI
                  g295500
BLAST score
                   50
E value
                   4.0e-19
Match length
                  102
% identity
                  87
                  Triticum aestivum heat shock protein 16.9C (hsp16.9C) mRNA,
NCBI Description
                  3' end
                  398476
Seq. No.
Seq. ID
                  LIB3431-015-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  37
E value
                   3.0e-11
Match length
                   48
% identity
                   66
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
                   398477
Seq. No.
Seq. ID
                  LIB3431-015-P1-K1-E12
```

NCBI Description

```
NCBI GI
                        g5410347
      BLAST score
                        40
      E value
                        3.0e-13
                        56
      Match length
                        93
      % identity
      NCBI Description
                        Sorghum bicolor BAC clone 110K5, partial sequence
                        398478
      Seq. No.
      Seq. ID
                        LIB3431-015-P1-K1-E2
      Method
                        BLASTN
      NCBI GI
                        g168608
      BLAST score
                        43
      E value -
                        7.0e-15
      Match length
                        67
                        91
      % identity
                        Maize 17S ribosomal RNA gene and flanks
      NCBI Description
                        398479
      Seq. No.
                        LIB3431-015-P1-K1-E3
      Seq. ID
Method
                        BLASTX
      NCBI GI
                        g3292814
      BLAST score
                        169
      E value
                        7.0e-12
                        47
      Match length
      % identity
                         (AL031018) putative protein [Arabidopsis thaliana]
      NCBI Description
                        398480
      Seq. No.
                        LIB3431-015-P1-K1-E6
      Seq. ID
      Method
                        BLASTN
      NCBI GI
                        g304219
      BLAST score
                        33
      E value
                        3.0e-09
      Match length
                        65
      % identity
                        88
      NCBI Description
                        Hordeum vulgare chloroplast photosystem I PSK-I subunit
                        mRNA, complete cds
      Seq. No.
                        398481
      Seq. ID
                        LIB3431-015-P1-K1-E7
      Method
                        BLASTN
      NCBI GI
                        g5410347
      BLAST score
                        41
      E value
                        1.0e-13
                        57
      Match length
      % identity
      NCBI Description
                        Sorghum bicolor BAC clone 110K5, partial sequence
      Seq. No.
                        398482
      Seq. ID
                        LIB3431-015-P1-K1-E9
      Method
                        BLASTX
      NCBI GI
                        q4539333
      BLAST score
                        425
      E value
                        8.0e-42
      Match length
                        129
      % identity
```

(AL035539) putative amino acid transport protein

Seq. ID

Method

[Arabidopsis thaliana] 398483 Seq. No. Seq. ID LIB3431-015-P1-K1-F10 Method BLASTX NCBI GI g399213 BLAST score 501 6.0e-51 E value 119 Match length 82 % identity ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG NCBI Description CD4B PRECURSOR >gi 100190 pir B35905 CD4B protein - tomato >gi 170435 (M32604) ATP-dependent protease (CD4B) [Lycopersicon esculentum] 398484 Seq. No. Seq. ID LIB3431-015-P1-K1-F11 Method BLASTX NCBI GI g3128228 BLAST score 520 E value 1.0e-54 Match length 124 88 % identity (AC004077) putative ribosomal protein L18A [Arabidopsis NCBI Description thaliana] >gi 3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana] 398485 Seq. No. Seq. ID LIB3431-015-P1-K1-F2 Method BLASTX NCBI GI q2497903 220 BLAST score E value 6.0e-18 Match length 59 % identity 68 METALLOTHIONEIN-LIKE PROTEIN TYPE 2 NCBI Description >gi_1752831_dbj_BAA14038.1_ (D89931) metallothionein-like protein [Oryza sativa] >gi_1815628 (U43530) metallothionein-like type 2 [Oryza sativa] Seq. No. 398486 Seq. ID LIB3431-015-P1-K1-F3 Method BLASTX NCBI GI q115787 BLAST score 578 E value 6.0e-60 Match length 112 98 % identity CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] Seq. No. 398487

LIB3431-015-P1-K1-F4

BLASTX

Match length

```
NCBI GI
                   g82080
BLAST score
                   422
                   2.0e-41
E value
                   120
Match length
                   68
% identity
NCBI Description
                   chlorophyll a/b-binding protein type III precursor - tomato
                   >gi_226872_prf__1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                   398488
Seq. No.
Seq. ID
                   LIB3431-015-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   q3885888
BLAST score
                   230
E value
                   4.0e-19
                   93
Match length
                   57
% identity
NCBI Description
                   (AF093632) high mobility group protein [Oryza sativa]
                   398489
Seq. No.
                   LIB3431-015-P1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q100102
BLAST score
                   156
E value
                   3.0e-10
Match length
                   86
% identity
                   38
NCBI Description
                   seed protein precursor - tick bean >gi 22043 emb CAA39696
                   (X56240) unknown seed protein [Vicia faba]
Seq. No.
                   398490
Seq. ID
                   LIB3431-015-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g2281089
BLAST score
                   376
E value
                   4.0e-36
                   79
Match length
% identity
NCBI Description
                   (AC002333) Sm protein F isolog [Arabidopsis thaliana]
                   398491
Seq. No.
Seq. ID
                   LIB3431-015-P1-K1-G11
Method
                  BLASTX
NCBI GI
                   q2306981
BLAST score
                   175
E value
                   8.0e-13
Match length
                  32
% identity
NCBI Description
                   (AF010321) photosystem I antenna protein [Oryza sativa]
                   398492
Seq. No.
Seq. ID
                  LIB3431-015-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g82080
BLAST score
                  322
E value
                   7.0e-30
```

NCBI GI

BLASTN

g1002914

```
% identity
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  398493
Seq. No.
Seq. ID
                  LIB3431-015-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g82080
BLAST score
                  432
                  1.0e-42
E value
                  122
Match length
% identity
                  68
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
Seq. No.
                  398494
Seq. ID
                  LIB3431-015-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  519
E value
                  6.0e-53
Match length
                  113
                  91
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir__A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
Seq. No.
                  398495
Seq. ID
                  LIB3431-015-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g5295988
BLAST score
                  177
E value
                  9.0e-13
Match length
                  51
% identity
                  (AB003327) MADS box-like protein [Oryza sativa]
NCBI Description
Seq. No.
                  398496
                  LIB3431-015-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5734720
BLAST score
                  212
E value
                  6.0e-17
Match length
                  100
% identity
                  48
                  (AC008075) Contains PF 01426 BAH (bromo-adjacent homology)
NCBI Description
                  domain. ESTs gb_N96349, gb_T42710, gb_H77084, gb_AA395147
                  and gb AA605500 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  398497
Seq. ID
                  LIB3431-015-P1-K1-G6
```

NCBI Description

```
BLAST score
                        40
                        4.0e-13
     E value
     Match length
                        56
                        93
     % identity
     NCBI Description Oryza sativa cap-binding protein p26 mRNA, complete cds
                        398498
     Seq. No.
     Seq. ID
                        LIB3431-015-P1-K1-G7
     Method -
                        BLASTX
     NCBI GI
                        q1495768
     BLAST score
                        266
     E value
                        3.0e-23
     Match length
                        108
     % identity
                        51
                        (Z68506) chloroplast inner envelope protein, 110 kD
     NCBI Description
                        (IEP110) [Pisum sativum]
                        398499
     Seq. No.
     Seq. ID
                        LIB3431-015-P1-K1-G8
     Method
                        BLASTX
     NCBI GI
                        g166410
     BLAST score
                        408
     E value
                        7.0e-40
     Match length
                        111
     % identity
                        69
     NCBI Description (L07291) Alfin-1 [Medicago sativa]
                        398500
     Seq. No.
     Seq. ID
                        LIB3431-015-P1-K1-G9
     Method
                        BLASTX
     NCBI GI
                        g3126854
     BLAST score
                        616
     E value
                        3.0e-64
     Match length
                        115
     % identity
                        100
     NCBI Description
                        (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                        398501
     Seq. No.
     Seq. ID
                        LIB3431-015-P1-K1-H11
     Method
                        BLASTN
     NCBI GI
                        g6103440
BLAST score
                        51
     E value
                        2.0e-20
     Match length
                        55
                        98
     % identity
     NCBI Description
                        Oryza sativa metallothionein-like protein (ML2) mRNA,
                        complete cds
     Seq. No.
                        398502
     Seq. ID
                        LIB3431-015-P1-K1-H12
     Method
                        BLASTN
     NCBI GI
                        g3135542
     BLAST score
                        39
     E value
                        1.0e-12
     Match length
                        67
     % identity
```

Oryza sativa aquaporin (PIP2a) mRNA, complete cds

```
398503
   Seq. No.
                     LIB3431-015-P1-K1-H2
   Seq. ID
                     BLASTX
   Method
                     g4455180
   NCBI GI
                     396
   BLAST score
   E value
                     1.0e-38
  Match length
                     108
   % identity
                     71
                      (AL035521) putative protein [Arabidopsis thaliana]
   NCBI Description
                     398504
   Seq. No.
   Seq. ID
                     LIB3431-015-P1-K1-H3
   Method
                     BLASTX
   NCBI GI
                     g3913811
   BLAST score
                     704
                     1.0e-74
   E value
  Match length
                     141
   % identity
                     99
                     GLUTAMYL-TRNA REDUCTASE PRECURSOR (GLUTR)
   NCBI Description
                     >gi_2920320_dbj_BAA25003_ (AB011416) glutamyl-tRNA
                     reductase [Oryza sativa]
   Seq. No.
                     398505
   Seq. ID
                     LIB3431-015-P1-K1-H6
   Method
                     BLASTN
   NCBI GI
                     q2072554
   BLAST score
                     212
   E value
                     1.0e-116
  Match length
                     260
   % identity
                     96
   NCBI Description
                     Oryza sativa metallothionein-like protein mRNA, complete
   Seq. No.
                     398506
   Seq. ID
                     LIB3431-015-P1-K1-H7
   Method'
                     BLASTX
   NCBI GI
                     q3075488
   BLAST score
                     211
   E value
                     6.0e-17
Match length
                     57
   % identity
  NCBI Description
                     (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                     398507
   Seq. No.
   Seq. ID
                     LIB3431-015-P1-K1-H8
  Method
                     BLASTX
  NCBI GI
                     q3915309
   BLAST score
                     159
  E value
                     9.0e-11
  Match length
                     93
                     32
   % identity
  NCBI Description
                     D-XYLOSE-PROTON SYMPORT (D-XYLOSE TRANSPORTER) >qi 2895856
                      (AF045552) D-xylose proton-symporter [Lactobacillus brevis]
   Seq. No.
   Seq. ID
                     LIB3431-015-P1-K1-H9
```

E value

9.0e-65

```
BLASTX
Method
NCBI GI
                  g4803952
BLAST score
                  446
                  2.0e-44
E value
Match length
                  113
% identity
                  76
NCBI Description
                 (AC006202) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  398509
                  LIB3431-016-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6093830
BLAST score
                  155
E value
                  3.0e-10
                  37
Match length
% identity
                  81
                  PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
NCBI Description
                  [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
                  PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor;
                  putative photosytem II peptide [Spinacia oleracea]
Seq. No.
                  398510
Seq. ID
                  LIB3431-016-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q895845
BLAST score
                  165
E value
                  2.0e-11
Match length
                  103
% identity
NCBI Description
                  (X87689) putative start codon [Homo sapiens]
Seq. No.
                  398511
Seq. ID
                  LIB3431-016-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q5912299
BLAST score
                  672
E value
                  7.0e-71
Match length
                  133
% identity
                  100
NCBI Description
                  (AJ133787) gigantea homologue [Oryza sativa]
Seq. No.
                  398512
Seq. ID
                  LIB3431-016-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q4680685
BLAST score
                  214
E value
                  4.0e-17
Match length
                  100
% identity
NCBI Description
                  (AF132957) CGI-23 protein [Homo sapiens]
                  398513
Seq. No.
Seq. ID
                  LIB3431-016-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  620
```

BLASTX

```
116
 Match length
                    100
  % identity
                    (AF061577) chlorophyll a/b binding protein [Oryza sativa]
 NCBI Description
                    398514
  Seq. No.
                    LIB3431-016-P1-K1-A6
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g320618
  BLAST score
                    481
  E value
                    2.0e-48
                    107
 Match length
  % identity
 NCBI Description
                    chlorophyll a/b-binding protein I precursor - rice
                    >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                    chlorophyll a/b-binding protein [Oryza sativa]
                    >gi 227611_prf 1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
                    398515
  Seq. No.
  Seq. ID
                    LIB3431-016-P1-K1-A7
Method
                    BLASTN
  NCBI GI
                    g6015437
  BLAST score
                    34
  E value
                    6.0e-10
 Match length
                    38
  % identity
                    97
                    Homo sapiens PEX1 mRNA, complete cds
 NCBI Description
  Seq. No.
                    398516
                    LIB3431-016-P1-K1-A8
  Seq. ID
 Method
                    BLASTX
  NCBI GI
                    q4079798
  BLAST score
                    342
                    4.0e-32
  E value
                    98
 Match length
  % identity
  NCBI Description
                    (AF052203) 23 kDa polypeptide of photosystem II. [Oryza
                    sativa]
                    398517
  Seq. No.
                    LIB3431-016-P1-K1-A9
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g121343
  BLAST score
                    198
  E value
                    4.0e-24
                    107
 Match length
  % identity
                    63
 NCBI Description
                    GLUTAMINE SYNTHETASE SHOOT ISOZYME, CHLOROPLAST PRECURSOR
                    (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS31)
                    >gi_68598_pir__AJRZQD glutamate--ammonia ligase (EC
                    6.3.1.2) delta precursor, chloroplast - rice
                    >gi_20370_emb_CAA32462 (X14246) precursor chloroplastic
                    glutamine synthetase (AA -46 to 382) [Oryza sativa]
  Seq. No.
                    398518
  Seq. ID
                    LIB3431-016-P1-K1-B1
```

```
g3789954
NCBI GI
BLAST score
                   684
                  3.0e-72
E value
Match length
                  128
% identity
NCBI Description
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                  sativa]
                  398519
Seq. No.
                  LIB3431-016-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3461820
BLAST score
                  212
                  6.0e-17
E value
Match length
                  112
                   44
% identity
NCBI Description
                  (AC004138) unknown protein [Arabidopsis thaliana]
                  398520
Seq. No.
Seq. ID
                                                                            LIB3431-016-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  g2570514
BLAST score
                  178
E value
                  2.0e-95
                  186
Match length
                  99
% identity
NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
Seq. No.
                  398521
                  LIB3431-016-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g871931
BLAST score
                  260
                  2.0e-22
E value
Match length
                  80
% identity
                  66
                  (D30763) ferredoxin [Oryza sativa]
NCBI Description
                  398522
Seq. No.
Seq. ID
                  LIB3431-016-P1-K1-B2
                  BLASTX
Method
NCBI GI
                  g6093869
BLAST score
                  599
E value
                  3.0e-62
Match length
                  128
% identity
                  86
                  60S RIBOSOMAL PROTEIN L13A >gi 2982259 (AF051212) probable
NCBI Description
                  60s ribosomal protein L13a [Picea mariana]
                  398523
Seq. No.
Seq. ID
                  LIB3431-016-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q5006853
BLAST score
                  372
E value
                  7.0e-36
Match length
                  96
% identity
                  80.
```

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```
(AF145728) homeodomain leucine zipper protein [Oryza
NCBI Description
                   sativa]
                   398524
Seq. No.
                   LIB3431-016-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5702015
BLAST score
                   338
E value
                   1.0e-31
Match length
                   105
% identity
                   65
                   (AJ012215) GAL83 protein [Solanum tuberosum]
NCBI Description
Seq. No.
                   398525
Seq. ID
                   LIB3431-016-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g2407281
BLAST score
                   541
E value
                   2.0e-55
Match length
                   109
% identity
NCBI Description
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
                   subunit [Oryza sativa]
                   398526
Seq. No.
Seq. ID
                   LIB3431-016-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   q1346698
BLAST score
                   610
E value
                   1.0e-63
Match length
                   131
                   93
% identity
                   PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_21272_emb_CAA48479_ (X68430) phosphoglycerate kinase
                   [Spinacia oleracea]
Seq. No.
                   398527
Seq. ID
                   LIB3431-016-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   q4666287
BLAST score
                   523
E value
                   2.0e-53
Match length
                   102
                   100
% identity
                   (D85764) cytosolic monodehydroascorbate reductase [Oryza
NCBI Description
                  .sativa]
Seq. No.
                   398528
Seq. ID
                   LIB3431-016-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   q3345477
BLAST score
                   504
E value
                   4.0e-51
Match length
                   96
                   100
% identity
NCBI Description
                   (AB016283) carbonic anhydrase [Oryza sativa]
```

Seq. No.

```
398529
Seq. No.
Seq. ID
                   LIB3431-016-P1-K1-C10
Method
                  BLASTX
NCBI GI
                   g3913641
BLAST score
                   314
                   5.0e-29
E value
Match length
                   61
% identity
                   100
                   FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   >gi 3041777 dbj BAA25423 (AB007194)
                   fructose-1,6-bisphosphatase [Oryza sativa]
Seq. No.
                   398530
Seq. ID
                   LIB3431-016-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g3868756
BLAST score
                   289
E value
                   1.0e-41
Match length
                   120
% identity
                   72
NCBI Description
                   (D86611) catalase [Oryza sativa]
Seq. No.
                   398531
Seq. ID
                   LIB3431-016-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g1617197
BLAST score
                   304
E value
                   1.0e-27
                  76
Match length
                   76
% identity
NCBI Description
                   (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                   398532
Seq. ID
                   LIB3431-016-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g1706260
BLAST score
                   648
E value
                   5.0e-68 ·
Match length
                   132
% identity
                   90
                   CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597
NCBI Description
                   cysteine proteinase 1 precursor - maize
                   >gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea
                   mays]
Seq. No.
                   398533
Seq. ID
                   LIB3431-016-P1-K1-C5
Method
                   BLASTX
                   g3075488
NCBI GI
BLAST score
                   660
E value
                   2.0e-69
                   126
Match length
% identity
                   100
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
```

E value

8.0e-16

```
LIB3431-016-P1-K1-C6
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2072554
BLAST score
                   301
                   1.0e-169
E value
Match length
                   301
                   100
% identity
NCBI Description
                   Oryza sativa metallothionein-like protein mRNA, complete
                   398535
Seq. No.
                   LIB3431-016-P1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3345477
BLAST score
                   371
E value
                   1.0e-35
Match length
                   117
% identity
                   63
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                   398536
Seq. ID
                   LIB3431-016-P1-K1-C8
Method
                   BLASTN
NCBI GI
                   g11957
BLAST score
                   371
E value
                   0.0e + 00
Match length
                   392
                   98
% identity
NCBI Description Rice complete chloroplast genome
Seq. No.
                   398537
Seq. ID
                   LIB3431-016-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   g2330739
BLAST score
                   295
E value
                   1.0e-26
Match length
                   90
% identity
                   58
NCBI Description
                   (Z98598) putative transcriptional regulator
                   [Schizosaccharomyces pombe]
Seq. No.
                   398538
Seq. ID
                   LIB3431-016-P1-K1-D1
Method .
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   36
E value
                   1.0e-10
Match length
                   36
% identity
                   100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   398539
Seq. ID
                  LIB3431-016-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  g20177
BLAST score
                  43
```

```
Match length
                  43
                  100
% identity
                  Rice cab1R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
                  398540
Seq. No.
Seq. ID
                  LIB3431-016-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g4914457
                  303
BLAST score
E value
                  1.0e-27
Match length
                  105
% identity
                  52
                  (AL050400) putative protein [Arabidopsis thaliana]
NCBI Description
                  398541
Seq. No.
Seq. ID
                  LIB3431-016-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q927025
BLAST score
                  196
E value
                  5.0e-15
                  116
Match length
% identity
                  38
                  (L44134) SPF1-like DNA-binding protein [Cucumis sativus]
NCBI Description
                  398542
Seq. No.
                  LIB3431-016-P1-K1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2129950
BLAST score
                  646
E value
                  8.0e-68
Match length
                  132
                  98
% identity
                  inorganic pyrophosphatase (EC 3.6.1.1) (clone TVP9) -
NCBI Description
                  common tobacco
                  398543
Seq. No.
                  LIB3431-016-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115813
BLAST score
                  423
E value
                  1.0e-41
Match length
                  117
                  73
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  398544
Seq. No.
                  LIB3431-016-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789954
                  743
BLAST score
E value
                  4.0e-79
Match length
                  134
% identity
                  100
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
```

E value

9.0e-53

```
398545
Seq. No.
Seq. ID
                    LIB3431-016-P1-K1-D7
Method
                    BLASTX
NCBI GI
                    g3618310
BLAST score
                    331
E value
                    7.0e-31
                    97
Match length
% identity
                    67
                    (AB001883) zinc finger protein [Oryza sativa]
NCBI Description
                    398546
Seq. No.
Seq. ID
                    LIB3431-016-P1-K1-D9
                    BLASTX
Method
NCBI GI
                    g2245136
BLAST score
                    289
                    6.0e-26
E value
Match length
                    92
% identity
                    62
                    (Z97344) trehalose-6-phosphate synthase like protein
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    398547
Seq. ID
                    LIB3431-016-P1-K1-E10
Method
                    BLASTX
NCBI GI
                    q3126854
BLAST score
                    698
E value
                    6.0e-74
Match length
                    129
% identity
                    100
                    (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                    398548
Seq. ID
                    LIB3431-016-P1-K1-E11
Method
                    BLASTX
NCBI GI
                    g132105
BLAST score
                    715
                    7.0e-76
E value
Match length
                    132
% identity
                    99
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
Seq. No.
                    398549
Seq. ID
                    LIB3431-016-P1-K1-E12
Method
                    BLASTX
NCBI GI
                    g115787
BLAST score
                    518
```

sativa]

NCBI GI

BLAST score

```
Match length
                   119
                   87
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi 82461_pir__S03706 chlorophyll a/b-binding
                   protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   398550
Seq. No.
Seq. ID
                   LIB3431-016-P1-K1-E2
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   35
                   5.0e-10
E value
                   35
Match length
                   100
% identity
                   Homo sapiens PEX1 mRNA, complete cds
NCBI Description
Seq. No.
                   398551
Seq. ID
                   LIB3431-016-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g2245120
BLAST score
                   319
                   3.0e-30
E value
Match length
                   128
                   57
% identity
                   (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   398552
Seq. ID
                   LIB3431-016-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   690
                   6.0e-73
E value
Match length
                   129
% identity
                   99
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   398553
Seq. No.
                   LIB3431-016-P1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1617206
BLAST score
                   190
E value
                   2.0e-14
                   54
Match length
% identity
                   69
                   (Z72489) CP12 [Pisum sativum]
NCBI Description
Seq. No.
                   398554
Seq. ID
                   LIB3431-016-P1-K1-E8
Method
                   BLASTN
```

g5410347

```
3.0e-11
E value
Match length
                   57
% identity
                   91
                   Sorghum bicolor BAC clone 110K5, partial sequence
NCBI Description
                   398555
Seq. No.
Seq. ID
                   LIB3431-016-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g730456
BLAST score
                   569
E value
                   9.0e-59
                   108
Match length
                   99
% identity
NCBI Description
                   40S RIBOSOMAL PROTEIN S19
                   398556
Seq. No.
Seq. ID
                   LIB3431-016-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   g2493318
BLAST score
                   171
E value
                   4.0e-12
Match length
                   72
% identity
                   46
                   BLUE COPPER PROTEIN PRECURSOR >gi 562779 emb CAA80963
NCBI Description
                   (Z25471) blue copper protein [Pisum sativum]
                   >gi 1098264 prf 2115352A blue Cu protein [Pisum sativum]
                   398557
Seq. No.
Seq. ID
                   LIB3431-016-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   q2072555
BLAST score
                   232
E value
                   7.0e-20
Match length
                   44
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   398558
Seq. ID
                   LIB3431-016-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   g1707998
BLAST score
                   262
E value
                   2.0e-23
Match length
                   52
% identity
                   98
NCBI Description
                   SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi_481944_pir__S40218 glycine
                   hydroxymethyltransferase (EC 2.1.2.1) - potato
                   >gi_438247_emb_CAA81082_ (Z25863) glycine
hydroxymethyltransferase [Solanum tuberosum]
Seq. No.
                   398559
Seq. ID
                   LIB3431-016-P1-K1-F8
Method
                   BLASTX
```

```
NCBI GI
                   q4220481
BLAST score
                   205
                   4.0e-16
E value
Match length
                   107
                   43
% identity
                   (AC006069) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   398560
                   LIB3431-016-P1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   695
E value
                   2.0e-73
Match length
                   134
                   99
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   398561
Seq. ID
                   LIB3431-016-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   q4455323
BLAST score
                   397
E value
                   1.0e-38
Match length
                   136
% identity
NCBI Description
                   (AL035525) aminopeptidase-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   398562
Seq. ID
                   LIB3431-016-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   q462195
BLAST score
                   423
E value
                   1.0e-41
Match length
                   88
% identity
NCBI Description
                   PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
                   >gi_100682_pir__S21636 GOS2 protein - rice
                   >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                   >gi_3789950 (AF094774) translation initiation factor [Oryza
                   satīva]
Seq. No.
                   398563
Seq. ID
                   LIB3431-016-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   q2501189
BLAST score
                   402
E value
                   3.0e-39
Match length
                   111
% identity
NCBI Description
                   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                   >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
```

- maize >gi_596078 (U17350) thiamine biosynthetic enzyme

```
[Zea mays]
                  398564
Seq. No.
Seq. ID
                  LIB3431-016-P1-K1-G3
Method
                  BLASTX
NCBI GI
                   g115787
BLAST score
                   554
E value
                   6.0e-57
Match length
                  125
                  87
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                  398565
Seq. No.
Seq. ID
                  LIB3431-016-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g710308
BLAST score
                  268
                   1.0e-23
E value
                   49
Match length
                   96
% identity
                   (U11693) victorin binding protein [Avena sativa]
NCBI Description
                   398566
Seq. No.
                  LIB3431-016-P1-K1-G5
Seq. ID
Method
                  BLASTX
                   g2570511
NCBI GI
BLAST score
                   590
E value
                   3.0e-61
Match length
                  111
% identity
                   99
NCBI Description
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
                   398567
Seq. No.
                  LIB3431-016-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789954
BLAST score ·
                  515
E value
                   2.0e-52
Match length
                   96
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  398568
Seq. No.
Seq. ID
                  LIB3431-016-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g1899188
BLAST score
                  359
E value
                   4.0e-34
Match length
                  132
% identity
                  55
```

NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]

BLAST score

```
Seq. No.
                  398569
Seq. ID
                  LIB3431-016-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g556409
BLAST score
                  366
E value
                  6.0e-35
Match length
                  112
                  72
% identity
                  (L34551) transcriptional activator protein [Oryza sativa]
NCBI Description
                  398570
Seq. No.
Seq. ID
                  LIB3431-016-P1-K1-G9
Method
                  BLASTX
                  g4886307
NCBI GI
BLAST score
                  662
                  1.0e-69
E value
Match length
                  133
% identity
                  92
                   (AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase
NCBI Description
                   [Arabidopsis thaliana]
                  398571
Seq. No.
Seq. ID
                  LIB3431-016-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g1778149
BLAST score
                  563
E value
                  4.0e-58
Match length
                  119
                  93
% identity
                   (U66404) phosphate/phosphoenolpyruvate translocator
NCBI Description
                  precursor [Zea mays]
Seq. No.
                  398572
                  LIB3431-016-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3868758
                  370
BLAST score
                  2.0e-35
E value
                  92
Match length
                  77
% identity
                  (D89802) elongation factor 1B gamma [Oryza sativa]
NCBI Description
                  398573
Seq. No.
                  LIB3431-016-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5306269
BLAST score
                  256
E value
                  5.0e-22
                  128
Match length
% identity
                  (AC006233) unknown protein [Arabidopsis thaliana]
NCBI Description
                  398574
Seq. No.
                  LIB3431-016-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g451193
```

```
E value
                  7.0e-44
Match length
                  100
% identity
                  87
NCBI Description
                  (L28008) wali7 [Triticum aestivum]
                  >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]
Seq. No.
                  398575
Seq. ID
                  LIB3431-016-P1-K1-H6
                  BLASTX
Method
NCBI GI
                  q3913018
BLAST score
                  447
                  2.0e-44
E value
Match length
                  90
                  100
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  398576
Seq. No.
                  LIB3431-016-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  525
E value
                  1.0e-53
                  .125
Match length
                  82
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein ....
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  398577
Seq. No.
Seq. ID
                  LIB3431-016-P1-K1-H8
Method
                  BLASTN
NCBI GI
                  q3126853
BLAST score
                  178
E value
                  2.0e-95
Match length
                  216
                  100
% identity
                  Oryza sativa chlorophyll a/b binding protein (RCABP89)
NCBI Description
                  mRNA, nuclear gene encoding chloroplast protein, complete
                  cds
                  398578
Seq. No.
Seq. ID
                  LIB3431-016-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q5824411
BLAST score
                  360
E value
                  3.0e - 34
Match length
                  121
% identity
                  55
NCBI Description
                  (Z68882) Similarity to Bovine inorganic pyrophosphatase
                  (SW:IPYR BOVIN); cDNA EST EMBL:D66533 comes from this gene;
                  cDNA EST EMBL: D70345 comes from this gene; cDNA EST
                  yk338a8.3 comes from this gene; cDNA EST yk338a8.5 comes
```

398579

Seq. No.

```
LIB3431-017-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2498465
BLAST score
                  150
E value
                  1.0e-09
Match length
                  115
% identity
                  43
NCBI Description
                  28 KD HEAT- AND ACID-STABLE PHOSPHOPROTEIN (HASPP28) (PDGF
                  ASSOCIATED PROTEIN) >gi 2143777 pir S62782 heat and
                  acid-stable phosphoprotein, 28K - rat >gi 847785 (U26541)
                  HASPP28 [Rattus norvegicus] >gi 1588241 prf 2208261A
                  casein kinase II substrate [Rattus norvegicus]
                  398580
Seq. No.
Seq. ID
                  LIB3431-017-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  36
E value
                  1.0e-10
Match length
                  88
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  cds
                  398581
Seq. No.
Seq. ID
                  LIB3431-017-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g82080
BLAST score
                  372
                  1.0e-35
E value
                  105
Match length
                  70
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  398582
Seq. No.
Seq. ID
                  LIB3431-017-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
                  7.0e-20
E value
Match length
                  44
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  398583
Seq. No.
Seq. ID
                  LIB3431-017-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  9.0e-20
Match length
                  44
% identity
                  100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
```

```
protein [Oryza sativa]
                    398584
Seq. No.
Seq. ID
                   LIB3431-017-P1-K1-A5
Method
                   BLASTX
NCBI GI
                    g132105
BLAST score
                    548
E value
                    3.0e-56
Match length
                    122
                    84
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >qi 218208 dbj BAA00538
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi_226375_prf 1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
Seq. No.
                    398585
Seq. ID
                    LIB3431-017-P1-K1-A6
Method
                    BLASTX
NCBI GI
                    q510907
BLAST score
                    659
E value
                    3.0e-69
Match length
                    141
% identity
                    80
NCBI Description
                    (Z35108) calnexin [Helianthus tuberosus]
Seq. No.
                    398586
Seq. ID
                    LIB3431-017-P1-K1-A7
Method
                    BLASTX
NCBI GI
                    q132096
BLAST score
                    228
E value
                    2.0e-19
Match length
                    55
% identity
                    82
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR
                   (RUBISCO SMALL SUBUNIT A) >gi_68095_pir__RKRZS6 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS2106) - rice >gi_218210_dbj_BAA00539_
                    (D00644) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa]
Seq. No.
                    398587
Seq. ID
                   LIB3431-017-P1-K1-A8
Method
                   BLASTX
NCBI GI
                    q2497746
BLAST score
                    287
E value
                    1.0e-25
Match length
                    88
% identity
NCBI Description
                   NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2)
                   >gi_951334 (U31766) lipid transfer protein precursor [Oryza
```

>qi 6103441 qb AAF03603.1 (AF147786) metallothionein-like

satīva]

```
Seq. No.
                   398588
Seq. ID
                  LIB3431-017-P1-K1-A9
Method
                  BLASTX
NCBI GI
                   g4337192
BLAST score
                   292
E value
                   3.0e-26
Match length
                   90
                                                               و المعطية ا
% identity
NCBI Description
                   (AC006403) hypothetical protein [Arabidopsis thaliana]
                   398589
Seq. No.
Seq. ID
                  LIB3431-017-P1-K1-B1
Method
                  BLASTX
NCBI GI
                   q2072555
BLAST score
                   237
E value
                   9.0e-20
Match length
                   44
                   100
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                   398590
                   LIB3431-017-P1-K1-B10
Seq. ID
Method
                   BLASTX
                   a733454
NCBI GI
BLAST score
                   589
                   4.0e-61
E value
                   124
Match length
% identity
                   87
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                   398591
Seq. No.
Seq. ID
                   LIB3431-017-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g542200
BLAST score
                   263
                   7.0e-23
E value
Match length
                   98
% identity
                  hypothetical protein - garden asparagus
NCBI Description
                   >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus
                   officinal·is]
Seq. No.
                   398592
Seq. ID
                   LIB3431-017-P1-K1-B2
Method
                  BLASTN
NCBI GI
                   q21843
BLAST score
                   96
                   2.0e-46
E value
Match length
                   312 -
% identity
                  Wheat PsbO mRNA for 33kDa oxygen evolving protein of
NCBI Description
```

photosystem II

```
398593
Seq. No.
Seq. ID
                   LIB3431-017-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   g2618704
BLAST score
                   619
E value
                   1.0e-64
Match length
                   136
% identity
                   85
                   (AC002510) putative thioredoxin reductase [Arabidopsis
NCBI Description
                   thaliana]
                   398594
Seq. No.
Seq. ID
                   LIB3431-017-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g129233
BLAST score
                   491
E value
                   1.0e-49
Match length
                   120
% identity
                   82
                  ORYZAIN GAMMA CHAIN PRECURSOR >gi 67646 pir KHRZOG oryzain
NCBI Description
                   (EC 3.4.22.-) gamma precursor - rice
                   >gi_218185_dbj_BAA14404_ (D90408) oryzain gamma precursor
                   [Oryza sativa]
Seq. No.
                   398595
Seq. ID
                   LIB3431-017-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   q5541681
BLAST score
                   363
E value
                   1.0e-34
Match length
                   133
% identity
                   59
                   (AL096859) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   398596
Seq. ID
                   LIB3431-017-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   g120661
BLAST score
                   228
E value
                   8.0e-19
Match length
                   45
                   93
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
NCBI Description
                   PRECURSOR >gi 170237 (M14417) glyceraldehyde-3-phosphate
                  dehydrogenase A-subunit precursor [Nicotiana tabacum]
Seq. No.
                   398597
                  LIB3431-017-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3184098
BLAST score
                   355
E value
                   1.0e-33
Match length
                  118
% identity
                   (AL023777) coenzyme a synthetase [Schizosaccharomyces
NCBI Description
```

pombe]

Seq. No.

```
398598
Seq. No.
Seq. ID
                   LIB3431-017-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   g2072727
BLAST score
                   699
                   5.0e-74
E value
Match length
                   140
% identity
                   97
NCBI Description
                   (Y12595) Fd-GOGAT protein [Oryza sativa]
                   398599
Seq. No.
                   LIB3431-017-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131225
BLAST score
                   589
E value
                   4.0e-61
                   122
Match length
% identity
                   93
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
Seq. No.
                   398600
Seq. ID
                   LIB3431-017-P1-K1-C12
Method
                   BLASTN
NCBI GI
                   q3885891
BLAST score
                   41
E value
                   1.0e-13
Match length
                   60
% identity
                   93
                   Oryza sativa photosystem-1 F subunit precursor (PSI-F)
NCBI Description
                   mRNA, complete cds
Seq. No.
                   398601
Seq. ID
                   LIB3431-017-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g282833
BLAST score
                   686
E value
                   2.0e-72
Match length
                   143
% identity
                   97
                   phosphoglycerate kinase (EC 2.7.2.3) - spinach (fragment)
NCBI Description
                   398602
Seq. No.
                   LIB3431-017-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g585421
BLAST score
                   429
                   3.0e-42
E value
Match length
                   147
% identity
NCBI Description
                   LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi_541879_pir__JQ2391
                   lipoxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis thaliana
                   >gi_431258 (L23968) lipoxygenase [Arabidopsis thaliana]
```

BLASTX

```
LIB3431-017-P1-K1-C6
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2407281
BLAST score
                    754
                    2.0e-80
E value
Match length
                    142
% identity
                    99
NCBI Description
                    (AF017363) ribulose 1,5-bisphosphate carboxylase small
                    subunit [Oryza sativa]
Seq. No.
                    398604
                    LIB3431-017-P1-K1-C7
Seq. ID
Method
                    BLASTX
NCBI GI
                    q482311
BLAST score
                    634
E value
                    2.0e-66
Match length
                    123
                    98
% identity
NCBI Description
                    photosystem II oxygen-evolving complex protein 1 - rice
                    (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                    complex protein 1 [Oryza sativa]
                    398605
Seq. No.
Seq. ID
                    LIB3431-017-P1-K1-D10
Method
                    BLASTX
NCBI GI
                    q462195
BLAST score
                    405
E value
                    2.0e-39
Match length
                    96
% identity
                    82
                    PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                    >gi_100682_pir__ S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza
                    sativa]
                    398606
Seq. No.
Seq. ID
                    LIB3431-017-P1-K1-D12
Method
                    BLASTX
NCBI GI
                    q132105
BLAST score
                    694
                    2.0e-73
E value
Match length
                    130
% identity
                    98
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
Seq. No.
                    398607
Seq. ID
                    LIB3431-017-P1-K1-D2
```

```
q4581207
NCBI GI
BLAST score
                   504
                   4.0e-51
E value
Match length
                  144
                  73
% identity
                   (Y17914) cyclic nucleotide and calmodulin-regulated ion
NCBI Description
                  channel [Arabidopsis thaliana]
                   398608
Seq. No.
                  LIB3431-017-P1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3075488
                  533
BLAST score
                  2.0e-54
E value
                  120
Match length
% identity
                   85
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   398609
                  LIB3431-017-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3927827
BLAST score
                  190
                   3.0e-14
E value
Match length
                  104
% identity
                   43
                   (AC005727) osmotin-like protein precursor [Arabidopsis
NCBI Description
                  thaliana]
                   398610
Seq. No.
                  LIB3431-017-P1-K1-D6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g11957
BLAST score
                  292
E value
                   1.0e-163
Match length
                  308
                  99
% identity
                  Rice complete chloroplast genome
NCBI Description
                   398611
Seq. No.
                  LIB3431-017-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5902390
BLAST score
                   386
                   3.0e-37
E value
Match length
                  126
% identity
                   60
                   (AC008148) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   398612
Seq. No.
Seq. ID
                  LIB3431-017-P1-K1-D8
                  BLASTX
Method
NCBI GI
                  g400879
BLAST score
                  211
E value
                   6.0e-17
Match length
                  103
% identity
                   50
```

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```
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                   (PSI-N) >gi_479690_pir__S35159 photosystem I chain psaN -
                  barley >gi_19095_emb_CAA47056_ (X66428) photosystem I
                  subunit N [Hordeum vulgare]
                  398613
Seq. No.
Seq. ID
                  LIB3431-017-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g3341648
BLAST score
                  566
                  2.0e-58
E value
Match length
                  115
% identity
                  90
                  (AJ005343) DNA directed RNA polymerase [Zea mays]
NCBI Description
                  398614
Seq. No.
                  LIB3431-017-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129233
BLAST score
                  739
E value
                  1.0e-78
Match length
                  145
                  98
% identity
                  ORYZAIN GAMMA CHAIN PRECURSOR >gi 67646 pir KHRZOG oryzain
NCBI Description
                   (EC 3.4.22.-) gamma precursor - rice
                  >gi_218185_dbj_BAA14404_ (D90408) oryzain gamma precursor
                   [Oryza sativa]
Seq. No.
                  398615
Seq. ID
                  LIB3431-017-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g517500
BLAST score
                  535
E value
                  8.0e-55
Match length
                  132
% identity
                  77
NCBI Description
                  (M87435) precursor of the oxygen evolving complex 17 kDa
                  protein [Zea mays] >gi_444338_prf__1906386A photosystem II
                  OE17 protein [Pisum sativum]
Seq. No.
                  398616
Seq. ID
                  LIB3431-017-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q517500
BLAST score
                  250
E value
                  2.0e-21
Match length
                  113
% identity
NCBI Description
                  (M87435) precursor of the oxygen evolving complex 17 kDa
                  protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
Seq. No.
                  398617
Seq. ID
                  LIB3431-017-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q5903092
```

Method

BLASTX

```
1.0e-33
E value
Match length
                   110
% identity
                   70
                   (AC008017) Highly similar to developmental protein DG1118
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   398618
Seq. ID
                   LIB3431-017-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   q1703200
BLAST score
                   377
E value
                   3.0e-36
Match length
                   119
% identity
                   62
NCBI Description
                   PROTEIN KINASE AFC2 >gi 601789 (U16177) protein kinase
                   [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353)
                   protein kinase [Arabidopsis thaliana]
                   >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2)
                   [Arabidopsis thaliana]
                  398619
Seq. No.
                   LIB3431-017-P1-K1-E6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q20270
BLAST score
                   147
E value
                   8.0e-77
Match length
                   162
                   99
% identity
                   Rice nial gene for nitrate reductase apoenzyme (exon 1-2)
NCBI Description
Seq. No.
                   398620
                   LIB3431-017-P1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115772
BLAST score
                   535
E value
                   6.0e-55
Match length
                   101
                   100
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108_
                   (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                   [Oryza sativa]
                   398621
Seq. No.
                   LIB3431-017-P1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3885888
BLAST score
                   165
                   2.0e-11
E value
                   78
Match length
% identity
NCBI Description
                   (AF093632) high mobility group protein [Oryza sativa]
Seq. No.
                   398622
Seq. ID
                   LIB3431-017-P1-K1-F1
```

Method

BLASTX

```
NCBI GI
                  g1617197
BLAST score
                  245
                  1.0e-20
E value
Match length
                   66
                  73
% identity
NCBI Description
                   (272488) CP12 [Nicotiana tabacum]
Seq. No.
                  398623
                  LIB3431-017-P1-K1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1706260
BLAST score
                  561
E value
                   9.0e-58
                  121
Match length
                  85
% identity
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597
NCBI Description
                  cysteine proteinase 1 precursor - maize
                  >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                  mays]
                  398624
Seq. No.
Seq. ID
                  LIB3431-017-P1-K1-F4
Method
                  BLASTN
NCBI GI
                  g2773153
BLAST score
                  418
E value
                  0.0e + 00
Match length
                   450
% identity
                   98
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                   (Asr1) mRNA, complete cds
Seq. No.
                  398625
Seq. ID
                  LIB3431-017-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  q2072554
BLAST score
                  161
E value
                   3.0e-85
Match length
                  161
% identity
                  100
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
Seq. No.
                  398626
Seq. ID
                  LIB3431-017-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  9.0e-20
Match length
                  44
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  398627
                  LIB3431-017-P1-K1-F8
Seq. ID
```

E value

660

2.0e-69

```
NCBI GI
                  q4585882
BLAST score
                  611
E value
                  1.0e-63
                  135
Match length
                  79
% identity
                  (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  398628
Seq. ID
                  LIB3431-017-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g68843
BLAST score
                  342
E value
                  4.0e-32
Match length
                  86
% identity
                  80
NCBI Description
                  phospholipid transfer protein homolog - rice
                  >gi_4139635_pdb_1RZL_ Rice Nonspecific Lipid Transfer
                  Protein >gi_5107522_pdb_1BV2_ Lipid Transfer Protein From
                  Rice Seeds, Nmr, 14 Structures
                  398629
Seq. No.
Seq. ID
                  LIB3431-017-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  a2072555
BLAST score
                  237
                  6.0e-20
E value
Match length
                  44
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  398630
                  LIB3431-017-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  595
                  9.0e-62
E value
                  128
Match length
                  88
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  398631
Seq. ID
                  LIB3431-017-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g2570511
```

Seq. ID

```
126
Match length
% identity
                   98
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                   398632
Seq. No.
                  LIB3431-017-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2293480
BLAST score
                   337
E value
                   9.0e-32
Match length
                   71
                   92
% identity
                   (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
                   398633
Seq. No.
                  LIB3431-017-P1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3135543
BLAST score
                   553
E value
                   8.0e-57
Match length
                   136
% identity
                   82
                  (AF062393) aquaporin [Oryza sativa]
NCBI Description
Seq. No.
                   398634
                   LIB3431-017-P1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2570511
BLAST score
                   607
E value
                   3.0e-63
Match length
                   115
% identity
                   99
                  (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   398635
Seq. ID
                   LIB3431-017-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   q3063524
BLAST score
                   168
E value
                   8.0e-12
Match length
                  107
% identity
                   47
                   (AF052305) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
                   398636
Seq. No.
Seq. ID
                  LIB3431-017-P1-K1-G9
Method
                  BLASTX
NCBI GI
                   g1236961
BLAST score
                   280
E value
                   7.0e-25
Match length
                   97
% identity
                   (U50201) prunasin hydrolase precursor [Prunus serotina]
NCBI Description
Seq. No.
                   398637
                  LIB3431-017-P1-K1-H10
```

Match length

```
Method
                   BLASTX
NCBI GI
                   g3789952
BLAST score
                   383
                   3.0e-37
E value
Match length
                   85
                   98
% identity
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                   satival
                   398638
Seq. No.
Seq. ID
                   LIB3431-017-P1-K1-H11
                   BLASTX
Method
NCBI GI
                   q5919219
                   202
BLAST score
E value
                   1.0e-15
                   133
Match length
                   13
% identity
                   (AF186273) leucine-rich repeats containing F-box protein
NCBI Description
                   FBL3 [Homo sapiens]
                  398639
Seq. No.
                   LIB3431-017-P1-K1-H12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g6015437
BLAST score
                   33
                   4.0e-09
E value
Match length
                   33
% identity
                   100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                   398640
Seq. No.
                  LIB3431-017-P1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3885892
BLAST score
                   442
E value
                   8.0e-44
Match length
                   85
% identity
                   98
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
                   398641
Seq. No.
                   LIB3431-017-P1-K1-H3
Seq. ID
Method
                   BLASTX
                   g3075488
NCBI GI
                   426
BLAST score
E value
                   6.0e-42
Match length
                   82
% identity
                   99
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   398642
Seq. ID
                   LIB3431-017-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g1173189
BLAST score
                   220
                   8.0e-18
E value
```

```
100
% identity
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
NCBI Description
                   >gi_2119091_pir__S58629 ribosomal protein S12 - maize
chloroplast >gi_342619 (M17841) ribosomal protein S12 [Zea
                    mays] >gi 12161\overline{4}1 emb CAA60309 (X86563) ribosomal protein
                    S12 [Zea mays]
Seq. No.
                    398643
Seq. ID
                    LIB3431-017-P1-K1-H5
Method
                    BLASTN
NCBI GI
                    g4105560
BLAST score
                    37
E value
                    5.0e-12
Match length
                    37
% identity
                    100
                    Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mRNA,
NCBI Description
                    complete cds
Seq. No.
                    398644
Seq. ID
                    LIB3431-017-P1-K1-H6
Method
                    BLASTX
NCBI GI
                    g1617197
BLAST score
                    305
E value
                    1.0e-27
Match length
                    76
% identity
                    76
                    (Z72488) CP12 [Nicotiana tabacum]
NCBI Description
                    398645
Seq. No.
Seq. ID
                    LIB3431-017-P1-K1-H7
Method
                    BLASTX
NCBI GI
                    q4126473
BLAST score
                    252
                    1.0e-21
E value
Match length
                    140
% identity
NCBI Description
                    (AB014884) adenylyl cyclase associated protein [Gossypium
                    hirsutum]
Seq. No.
                    398646
Seq. ID
                    LIB3431-017-P1-K1-H8
Method
                    BLASTN
NCBI GI
                    q487317
BLAST score
                    97
E value
                    5.0e-47
Match length
                    101
% identity
                    99
NCBI Description
                    Rice mRNA EN56, partial sequence
                    398647
Seq. No.
Seq. ID
                    LIB3431-017-P1-N1-A12
Method
                    BLASTX
NCBI GI
                    q115813
BLAST score
                    171
E value
                    4.0e-12
Match length
                    40
% identity
                    80
```

```
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi 19182 emb CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  398648
Seq. No.
Seq. ID
                  LIB3431-017-P1-N1-A4
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  361
                  0.0e+00
E value
                  369
Match length
                  99
% identity
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                  cds
                  398649
Seq. No.
                  LIB3431-017-P1-N1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                  365
                  6.0e-35
E value
Match length
                  69
                  99
% identity
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
Seq. No.
                  398650
                  LIB3431-017-P1-N1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218209
BLAST score
                  187
                  1.0e-101
E value
                  235
Match length
% identity
                  95
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
Seq. No.
                  398651
                  LIB3431-017-P1-N1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g886692
BLAST score
                  377
E value
                  0.0e+00
Match length
                  385
% identity
                  99
NCBI Description
                  O.sativa mRNA for lipid transfer protein, b1
Seq. No.
                  398652
                  LIB3431-017-P1-N1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  160
E value
                  8.0e-85
Match length
                  244
% identity
                  91
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
```

cds 398653 Seq. No. Seq. ID LIB3431-017-P1-N1-B10 BLASTX Method NCBI GI g733454 BLAST score 317 E value 3.0e-29 67 Match length % identity 93 (U23188) chlorophyll a/b-binding apoprotein CP26 precursor NCBI Description [Zea mays] 398654 Seq. No. LIB3431-017-P1-N1-B2 Seq. ID BLASTX Method NCBI GI q482311 BLAST score 260 E value. 1.0e-22 Match length 51 100 % identity NCBI Description photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving complex protein 1 [Oryza sativa] Seq. No. 398655 LIB3431-017-P1-N1-B4 Seq. ID BLASTX Method · NCBI GI g1841466 BLAST score 205 E value 4.0e-16 Match length 37 % identity (Y11003) putative pre-pro-cysteine proteinase [Nicotiana NCBI Description tabacum] 398656 Seq. No. LIB3431-017-P1-N1-B5 Seq. ID Method BLASTX NCBI GI g5541681 BLAST score 182 2.0e-13 E value 79 Match length % identity (AL096859) putative protein [Arabidopsis thaliana] NCBI Description 398657 Seq. No. LIB3431-017-P1-N1-C1 Seq. ID BLASTX Method NCBI GI q586339 BLAST score 182 2.0e-13 E value Match length 67 % identity PEROXISOMAL-COENZYME A SYNTHETASE >gi 626794 pir \$46098 NCBI Description

probable AMP-binding protein - yeast (Saccharomyces

cerevisiae) >gi_536615_emb_CAA85185_ (Z36091) ORF YBR222c

NCBI Description

[Saccharomyces cerevisiae]

```
Seq. No.
                    398658 -
                   LIB3431-017-P1-N1-C10
Seq. ID
Method
                    BLASTN
NCBI GI
                    g2072726
BLAST score
                    350
E value
                    0.0e + 00
Match length
                    369
% identity
                    99
                   O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2
NCBI Description
Seq. No.
                    398659
Seq. ID
                   LIB3431-017-P1-N1-C11
Method
                   BLASTX
NCBI GI
                    g131225
BLAST score
                    284
E value
                    2.0e-25
                                                                 19.00
Match length
                    70
% identity
                    77
NCBI Description
                    PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
Seq. No.
                    398660
Seq. ID
                   LIB3431-017-P1-N1-C12
Method
                   BLASTX
NCBI GI
                    g3885892
BLAST score
                    272
E value
                    5.0e-24
Match length
                    55
% identity
NCBI Description
                    (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.
                    398661
Seq. ID
                   LIB3431-017-P1-N1-C2
Method
                   BLASTX
NCBI GI
                   q2499497
BLAST score
                    236
E value
                    8.0e-20
Match length
                   70
                   76
% identity
                   PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_1161600_emb_CAA88841_ (Z48977) phosphoglycerate kinase
                    [Nicotiana tabacum]
Seq. No.
                   398662
Seq. ID
                   LIB3431-017-P1-N1-C3
Method
                   BLASTX
NCBI GI
                   q450231
BLAST score
                   186
E value
                   8.0e-14
Match length
                   56
% identity
                   59
```

4,0

(U05041) lipoxygenase [Cuscuta reflexa]

E value

234

1.0e-19

```
398663
Seq. No.
                  LIB3431-017-P1-N1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  174
E value
                  1.0e-20
Match length
                  57
% identity
                  95
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  398664
Seq. ID
                  LIB3431-017-P1-N1-C7
Method
                  BLASTX
NCBI GI
                  g482311
BLAST score
                  175
E value
                  1.0e-12
Match length
                  34
% identity
                  100
NCBI Description
                  photosystem II oxygen-evolving complex protein 1 - rice
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                  398665
Seq. No.
                  LIB3431-017-P1-N1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4678346
BLAST score
                  187
E value
                  5.0e-14
Match length
                  44
                  77
% identity
NCBI Description
                   (AL049659) putative protein [Arabidopsis thaliana]
Seq. No.
                  398666
                  LIB3431-017-P1-N1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341699
BLAST score
                  238
E value
                  7.0e-20
Match length
                  153
% identity
                  37
NCBI Description
                   (AC003672) putative giberellin beta-hydroxylase
                   [Arabidopsis thaliana]
Seq. No.
                  398667
Seq. ID
                  LIB3431-017-P1-N1-D10
Method
                  BLASTX
NCBI GI
                  g462195
```

```
45
Match length
                    100
% identity
                    PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                    >gi_100682_pir__S21636 GOS2 protein - rice
>gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
>gi_3789950 (AF094774) translation initiation factor [Oryza
                    sativa]
Seq. No.
                    398668
Seq. ID
                    LIB3431-017-P1-N1-D12
Method
                    BLASTX
NCBI GI
                    q671740
BLAST score
                    179
E value
                    4.0e-13
Match length
                    34
                    100
% identity
NCBI Description
                    (X84730) ribulose-bisphosphate carboxylase [synthetic
                    construct]
                                4.5
Seq. No.
                    398669
                    LIB3431-017-P1-N1-D3
Seq. ID
Method
                    BLASTN
NCBI GI
                    q3075487
BLAST score
                    309
E value
                    1.0e-173
Match length
                    325
% identity
                    99
                    Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                    mRNA, complete cds
Seq. No.
                    398670
                    LIB3431-017-P1-N1-D6
Seq. ID
Method
                    BLASTN
NCBI GI
                    g11957
                    94
BLAST score
E value
                    2.0e-45
Match length
                    209
% identity
                    86
NCBI Description
                    Rice complete chloroplast genome
                    398671
Seq. No.
Seq. ID
                    LIB3431-017-P1-N1-D8
Method
                    BLASTX
NCBI GI
                    g3914466
BLAST score
                    369
E value
                    2.0e-35
Match length
                    67
% identity
                    99
                    PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                    (PSI-N) >gi 2981214 (AF052429) photosystem I complex PsaN
                    subunit precursor [Zea mays]
Seq. No.
                    398672
Seq. ID
                    LIB3431-017-P1-N1-D9
Method
                    BLASTN
                    g2239152
NCBI GI
```

```
0.0e+00
E value
Match length
                   380
% identity
                   98
                   O.sativa mRNA for putative T3/T7-like RNA polymerase,
NCBI Description
                   partial
                   398673
Seq. No.
Seq. ID
                   LIB3431-017-P1-N1-E1
Method
                   BLASTX
NCBI GI
                   g129233
BLAST score
                   240
E value
                   3.0e-26
Match length
                   60
% identity
                   98
NCBI Description
                   ORYZAIN GAMMA CHAIN PRECURSOR > qi 67646 pir KHRZOG oryzain
                   (EC 3.4.22.-) gamma precursor - rice
                   >gi 218185 dbj BAA14404 (D90408) oryzain gamma precursor
                   [Oryza satīva]
Seq. No.
                   398674
                   LIB3431-017-P1-N1-E10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q169133
BLAST score
                   56
                   1.0e-22
E value
Match length
                   168
                   83
% identity
                   Zea mays precursor of the oxygen evolving complex 17 kDa
NCBI Description
                   protein mRNA, complete cds
Seq. No.
                   398675
                   LIB3431-017-P1-N1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g347451
BLAST score
                   173
E value
                   2.0e-12
Match length
                   33
% identity
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   398676
                   LIB3431-017-P1-N1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1703199
BLAST score
                   150
E value
                   9.0e-10
Match length
                   45
% identity
                   62
                   PROTEIN KINASE AFC1 >gi 601787 (U16176) protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   398677
Seq. ID
                   LIB3431-017-P1-N1-E4
Method
                   BLASTN
                   g3789953
NCBI GI
```

```
E value
                   9.0e-23
Match length
                   248
% identity
                   82
NCBI Description
                   Oryza sativa chlorophyll a/b-binding protein precursor
                   (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
                   398678
Seq. No.
Seq. ID
                   LIB3431-017-P1-N1-E6
Method
                   BLASTX
NCBI GI
                   q128186
BLAST score
                   251
                   1.0e-21
E value
Match length
                   50
% identity
                   90
                   NITRATE REDUCTASE 1 (NR1) >gi 82490 pir S07554 nitrate
NCBI Description
                   reductase (NADH) (EC 1.6.6.1) - rice
Seq. No.
                   398679
                   LIB3431-017-P1-N1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q421916
BLAST score
                   195
E value
                   6.0e-15
Match length
                   36
                   100
% identity
                   chlorophyll a/b-binding protein - English ivy (fragment)
>gi_12582_emb_CAA48410_ (X68333) light harvesting
NCBI Description
                   chlorophyll a /b binding protein [Hedera helix]
Seq. No.
                   398680
                   LIB3431-017-P1-N1-E8
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3885887
BLAST score
                   405
E value
                   0.0e + 00
Match length
                   456
                   97
% identity
                   Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   398681
Seq. ID
                   LIB3431-017-P1-N1-F12
Method
                   BLASTX
NCBI GI
                   q482311
BLAST score
                   307
E value
                   4.0e-28
Match length
                   61
                   100
% identity
                   photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                   complex protein 1 [Oryza sativa]
Seq. No.
                   398682
Seq. ID
                   LIB3431-017-P1-N1-F8
Method
                   BLASTX
NCBI GI
                   q115813
```

% identity

```
BLAST score
                   152
E value
                   6.0e-10
Match length
                   33
% identity
                   85
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                   CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                   398683
Seq. ID
                   LIB3431-017-P1-N1-G10
Method
                   BLASTN
NCBI GI
                   q1619603
BLAST score
                   306
E value
                   1.0e-172
Match length
                   322
                   99
% identity
NCBI Description
                   O.sativa mRNA for lipid transfer protein
                   >gi 1667589 gb U77295 OSU77295 Oryza sativa lipid transfer
                   protein (LTP) mRNA, complete cds
                   398684
Seq. No.
                   LIB3431-017-P1-N1-G12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2072554
BLAST score
                   290
E value
                   1.0e-162
Match length
                   290
% identity
                   100
                   Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   398685
Seq. No.
                   LIB3431-017-P1-N1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   251
E value
                   4.0e-32
Match length
                   71
                   99
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4\overline{.1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   398686
Seq. No.
Seq. ID
                   LIB3431-017-P1-N1-G3
Method
                   BLASTX
NCBI GI
                   q2570511
BLAST score
                   163
E value
                   8.0e-22
Match length
                   63
```

```
(AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   398687
                  LIB3431-017-P1-N1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g482311
BLAST score
                  193
E value
                   1.0e-14
Match length
                   48
% identity
                   81
NCBI Description
                  photosystem II oxygen-evolving complex protein 1 - rice
                   (strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
Seq. No.
                   398688
                  LIB3431-017-P1-N1-G5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5381215
BLAST score
                  116
E value
                  8.0e-59
Match length
                  152
                   95
% identity
NCBI Description
                  Oryza sativa rwc-2 mRNA for water channel protein, partial
Seq. No.
                  398689
                  LIB3431-017-P1-N1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q479406
BLAST score
                   307
E value
                   3.0e-28
Match length
                  66
                  89
% identity
                  chlorophyll a/b-binding protein - garden pea
NCBI Description
                  >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding
                  protein [Pisum sativum]
Seq. No.
                  398690
Seq. ID
                  LIB3431-017-P1-N1-G8
Method
                  BLASTX
NCBI GI
                  q4741942
BLAST score
                  221
E value
                  5.0e-18
Match length
                  60
                  72
% identity
NCBI Description
                   (AF134121) Lhca5 protein [Arabidopsis thaliana]
Seq. No.
                  398691
Seq. ID
                  LIB3431-017-P1-N1-G9
Method
                  BLASTX
NCBI GI
                  q1236961
BLAST score
                  231
E value
                  3.0e-19
Match length
                  64
% identity
                  64
NCBI Description
                  (U50201) prunasin hydrolase precursor [Prunus serotina]
```

```
Seq. No.
                   398692
                   LIB3431-017-P1-N1-H2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3885891
BLAST score
                   207
E value
                   1.0e-113
Match length
                   247
% identity
                   96
NCBI Description
                   Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                   mRNA, complete cds
                   398693
Seq. No.
Seq. ID
                   LIB3431-017-P1-N1-H3
Method
                   BLASTX
NCBI GI
                   q3075488
BLAST score
                   176
E value
                   9.0e-13
Match length
                   33
                   100
% identity
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                   398694
Seq. No.
Seq. ID
                   LIB3431-017-P1-N1-H4
Method
                   BLASTN
NCBI GI
                   q2072554
BLAST score
                   140
E value
                   7.0e-73
Match length
                   248
                   88
% identity
                   Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   398695
Seq. No.
                   LIB3431-017-P1-N1-H5
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4105560
BLAST score
                   141
E value
                   2.0e-73
Match length
                   190
% identity
                   Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mRNA,
NCBI Description
                   complete cds
                   398696
Seq. No.
Seq. ID
                   LIB3431-017-P1-N1-H7
Method
                   BLASTX
NCBI GI
                   q4126473
BLAST score
                   195
E value
                   5.0e-15
Match length
                   47
% identity
NCBI Description
                   (AB014884) adenylyl cyclase associated protein [Gossypium
                   hirsutum]
Seq. No.
                   398697
Seq. ID
                   LIB3431-017-P1-N1-H9
Method
                   BLASTN
```

E value

3.0e-37

```
q2267594
NCBI GI
BLAST score
                  101
E value
                  1.0e-49
                  196
Match length
                  99
% identity
NCBI Description
                  Oryza sativa plastocyanin precursor, mRNA, complete cds
Seq. No.
                  398698
Seq. ID
                  LIB3431-018-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  56
E value
                  6.0e-23
Match length
                  111
% identity
                  89
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
Seq. No.
                  398699
Seq. ID
                  LIB3431-018-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  q3821780
BLAST score
                  36
E value
                  1.0e-10
Match length
                  47
% identity
                  66
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  398700
Seq. No.
Seq. ID
                  LIB3431-018-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q4038034
BLAST score
                  273
                  6.0e-24
E value
Match length
                  76
% identity
                  68
                  (AC005936) unknown protein [Arabidopsis thaliana]
NCBI Description
                  398701
Seq. No.
Seq. ID
                  LIB3431-018-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q3914603
                  1128
BLAST score
                  1.0e-124
E value
Match length
                  220
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
Seq. No.
                  398702
Seq. ID
                  LIB3431-018-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2088647
BLAST score
                  388
```

```
127
Match length
% identity
                   58
NCBI Description
                   (AF002109) hypothetical protein [Arabidopsis thaliana]
                   >gi 3158394 (AF036340) LRR-containing F-box protein
                   [Arabidopsis thaliana]
Seq. No.
                   398703
Seq. ID
                   LIB3431-018-P1-K1-B4
Method
                   BLASTN
NCBI GI
                   q473980
BLAST score
                   56
E value
                   2.0e-22
Match length
                   83
                   90
% identity
NCBI Description
                  Rice mRNA, partial homologous to glycine-rich protein gene
                   398704
Seq. No.
                   LIB3431-018-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1839022
BLAST score
                  269
E value
                   1.0e-23
Match length
                   65
% identity
                   71
NCBI Description
                   (Y11121) amino acid carrier [Ricinus communis]
Seq. No.
                   398705
                  LIB3431-018-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g417154
BLAST score
                   910
E value
                   2.0e-98
Match length
                   201
% identity
                   90
NCBI Description
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                  398706
Seq. No.
                  LIB3431-018-P1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g11957
BLAST score
                  487
E value
                  0.0e+00
Match length
                  543
                  97
% identity
NCBI Description
                  Rice complete chloroplast genome
Seq. No.
                  398707
Seq. ID
                  LIB3431-018-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q115793
BLAST score
                  688
E value
                  1.0e-72
Match length
                  154
```

84

% identity

% identity

```
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR
                   (CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_
                   (X63197) type III LHCII CAB precursor protein [Hordeum
                   vulgare]
                   398708
Seq. No.
Seq. ID
                   LIB3431-018-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q2501578
BLAST score
                   515
E value
                   3.0e-52
Match length
                   125
% identity
                   82
                   ETHYLENE-INDUCIBLE PROTEIN HEVER >qi 2129913 pir $60047
NCBI Description
                   ethylene-responsive protein 1 - Para rubber tree
                   >gi 1209317 (M88254) ethylene-inducible protein [Hevea
                   brasiliensis]
Seq. No.
                   398709
Seq. ID
                   LIB3431-018-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   739
E value
                   2.0e-78
Match length
                   137
                   99
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   398710
Seq. No.
Seq. ID
                   LIB3431-018-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g2497746
BLAST score
                   380
E value
                   2.0e-36
Match length
                   99
                   76
% identity
NCBI Description
                   NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2)
                   >qi 951334 (U31766) lipid transfer protein precursor [Oryza
                   sativa]
                   398711
Seq. No.
Seq. ID
                   LIB3431-018-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   q3789952
BLAST score
                   252
E value
                   2.0e-21
Match length
                   151
```

```
(AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
                  398712
Seq. No.
                  LIB3431-018-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3980400
BLAST score
                  489
E value
                  3.0e-49
Match length
                  142
% identity
                   (AC004561) putative tropinone reductase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  398713
                  LIB3431-018-P1-K1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4959460
BLAST score
                  36
E value
                   1.0e-10
Match length
                  36
                  100
% identity
NCBI Description
                  Zea mays RACB small GTP binding protein mRNA, complete cds
                  398714
Seq. No.
Seq. ID
                  LIB3431-018-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q170131
BLAST score
                  276
                   3.0e-24
E value
Match length
                  75
% identity
                   65
                  (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
NCBI Description
                  398715
Seq. No.
Seq. ID
                  LIB3431-018-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q115813
BLAST score
                  424
                  1.0e-41
E value
Match length
                  118
% identity
                  73
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                  398716
Seq. ID
                  LIB3431-018-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  782
E value
                  2.0e-83
Match length
                  170
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
```

protein 2R precursor - rice >gi_20182_emb_CAA32109_

Seq. No.

398721

```
[Oryza sativa]
                  398717
Seq. No.
                  LIB3431-018-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548603
BLAST score
                  690
E value
                  1.0e-72
Match length
                  136
% identity
                  96
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                  barley >qi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                  398718
Seq. ID
                  LIB3431-018-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  767
E value
                  9.0e-82
Match length
                  169
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  398719
Seq. ID
                  LIB3431-018-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g121343
BLAST score
                  871
E value
                  5.0e-94
Match length
                  177
% identity
NCBI Description
                  GLUTAMINE SYNTHETASE SHOOT ISOZYME, CHLOROPLAST PRECURSOR
                  (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS31)
                  >gi_68598_pir__AJRZQD glutamate--ammonia ligase (EC
                  6.3.1.2) delta precursor, chloroplast - rice
                  >gi 20370 emb CAA32462 (X14246) precursor chloroplastic
                  glutamine synthetase (AA -46 to 382) [Oryza sativa]
                  398720
Seq. No.
Seq. ID
                  LIB3431-018-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q2130069
BLAST score
                  1038
E value
                  1.0e-113
Match length
                  199
% identity
                  96
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
```

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

Seq. No.

```
LIB3431-018-P1-K1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4803952
BLAST score
                   461
E value
                   8.0e-46
Match length
                   115
                   77
% identity
                   (AC006202) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   398722
                   LIB3431-018-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q125580
BLAST score
                   791
E value
                   2.0e-84
Match length
                   181
                   85
% identity
                   PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >gi_100839_pir__S15743 phosphoribulokinase (EC 2.7.1.19) - wheat >gi_5924030_emb_CAB56544.1_ (X51608)
                   phosphoribulokinase [Triticum aestivum]
Seq. No.
                   398723
Seq. ID
                   LIB3431-018-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   q671740
BLAST score
                   342
E value
                   4.0e-32
Match length
                   63
% identity
                   100
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
Seq. No.
                   398724
Seq. ID
                   LIB3431-018-P1-K1-E3
Method
                   BLASTX
                   g2072555 📑
NCBI GI
                                                                  · 2 . .
BLAST score
                   237
E value
                   1.0e-19
Match length
                   44
% identity
                   100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   398725
Seq. ID
                   LIB3431-018-P1-K1-E7
Method
                   BLASTN
NCBI GI
                   g2331140
BLAST score
                   279
E value
                   1.0e-155
Match length
                   420
                   97
% identity
NCBI Description
                   Oryza sativa water-stress inducible protein (WSI) mRNA,
                   complete cds
```

```
Seq. ID
                   LIB3431-018-P1-K1-E9
                   BLASTX
Method
NCBI GI
                   q320618
BLAST score
                   746
                   2.0e-79
E value
                   159
Match length
                   90
% identity
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
Seq. No.
                   398727
Seq. ID
                   LIB3431-018-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   q548605
BLAST score
                   595
E value
                   1.0e-61
Match length
                   130
                   91
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                    (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi_539055_pir__A48527 photosystem I protein psaK precursor
                   - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                    [Hordeum vulgare]
Seq. No.
                   398728
                   LIB3431-018-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131388
BLAST score
                   658
                   6.0e-69
E value
                   189
Match length
% identity
                   72
NCBI Description
                   OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                   THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__$16260
                   photosystem II oxygen-evolving complex protein 1 - common
                   wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
33kDa oxygen evolving protein of photosystem II [Triticum
                   aestivuml
                   398729
Seq. No.
                   LIB3431-018-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g548605
BLAST score
                   377
E value
                   3.0e-36
Match length
                   78
                   95
% identity
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                    (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi 539055 pir A48527 photosystem I protein psaK precursor
```

[Hordeum vulgare]

- barley >gi_304220 (L12707) photosystem I PSI-K subunit

```
398730
Seq. No.
Seq. ID
                   LIB3431-018-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g2570499
BLAST score
                   191
E value
                   1.0e-14
Match length
                   38
% identity
                   100
                   (AF022732) 23kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   398731
Seq. No.
Seq. ID
                   LIB3431-018-P1-K1-G10
Method
                   BLASTX
                   q5305740
NCBI GI
BLAST score
                   759
E value
                   8.0e-81
Match length
                   186
% identity
                   84
                   (AF135862) precursor monofunctional aspartokinase [Glycine
NCBI Description
Seq. No.
                   398732
Seq. ID
                   LIB3431-018-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   q115787
BLAST score
                   691
E value
                   7.0e-73
Match length
                   133
                   99
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                   protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   398733
Seq. ID
                   LIB3431-018-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   q5921185
BLAST score
                   395
E value
                   6.0e-47
Match length
                   213
% identity
                   CYTOCHROME P450 76C1 >qi 2979548 (AC003680) putative
NCBI Description
                   7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]
Seq. No.
                   398734
Seq. ID
                   LIB3431-018-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   q1173347
BLAST score
                   932
E value
                   1.0e-101
Match length
                   185
                   95
% identity
NCBI Description
                   SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7) P2ASE)
```

```
(X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                   aestivum]
                   398735
Seq. No.
Seq. ID
                   LIB3431-018-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g132096
BLAST score
                   803
                    6.0e-86
E value
Match length
                   150
% identity
                    99
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT A) >gi_68095_pir__RKRZS6 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS2106) - rice >gi 218210 dbj BAA00539
                    (D00644) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa]
Seq. No.
                   398736
Seq. ID
                   LIB3431-018-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g6014904
BLAST score
                   296
E value
                   1.0e-26
Match length
                   74
% identity
                   DAG PROTEIN, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_1200205_emb_CAA65064 (X95753) DAG [Antirrhinum majus]
Seq. No.
Seq. ID
                   LIB3431-018-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   q2501189
BLAST score
                   643
E value
                   3.0e-67
Match length
                   164
                   79
% identity
                   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                   >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
Seq. No.
                   398738
Seq. ID
                   LIB3431-018-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   728
E value
                   3.0e-77
Match length
                   156
% identity
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
```

>gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
3.1.3.37) precursor - wheat >gi 14265 emb CAA46507

[Oryza sativa]

```
398739
Seq. No.
Seq. ID
                    LIB3431-018-P1-K1-G9
Method
                    BLASTX
NCBI GI
                    g3885888
BLAST score
                    326
E value
                    4.0e-30
Match length
                    89
% identity
                    76
NCBI Description
                    (AF093632) high mobility group protein [Oryza sativa]
                    398740
Seq. No.
Seq. ID
                    LIB3431-018-P1-K1-H10
Method
                    BLASTX
NCBI GI
                    q115793
BLAST score
                    869
E value
                    1.0e-93
Match length
                    192
                    85
% identity
                    CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR
NCBI Description
                    (CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_
                    (X63197) type III LHCII CAB precursor protein [Hordeum
                    vulgare]
Seq. No.
                    398741
                    LIB3431-018-P1-K1-H12
Seq. ID
Method
                    BLASTX
                    q710308
NCBI GI
                    987
BLAST score
E value
                    1.0e-107
                    224
Match length
% identity
                    (U11693) victorin binding protein [Avena sativa]
NCBI Description
Seq. No.
                    398742
Seq. ID
                    LIB3431-018-P1-K1-H3
Method
                    BLASTX
NCBI GI
                    q113466
BLAST score
                    282
                    8.0e-25
E value
Match length
                    82
                    65
% identity
                    ADP, ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE
NCBI Description
                    NUCLEOTIDE TRANSLOCATOR) (ANT) >gi_72020_pir__XWNC ADP,ATP carrier protein - Neurospora crassa >gi_2977_emb_CAA25104_
                    (X00363) ADP/ATP carrier protein [Neurospora crassa]
Seq. No.
                    398743
                    LIB3431-018-P1-K1-H4
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3126854
BLAST score
                    731
E value
                    2.0e-77
Match length
                    186
% identity
NCBI Description
                    (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

NCBI Description

```
Seq. No.
                   398744
Seq. ID
                   LIB3431-018-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g121530
BLAST score
                   866
E value
                   3.0e-93
Match length
                   194
% identity
NCBI Description
                   (S)-2-HYDROXY-ACID OXIDASE, PEROXISOMAL (GLYCOLATE OXIDASE)
                   (GOX) (SHORT CHAIN ALPHA-HYDROXY ACID OXIDASE)
                   >gi_65974_pir__OXSPH (S)-2-hydroxy-acid oxidase (EC
                   1.1.3.15), peroxisomal - spinach >gi_229945_pdb_1GOX_Glycolate Oxidase (E.C.1.1.3.1) >gi_170113 (J03492)
                   glycolate oxidase (EC 1.1.3.15) [Spinacia oleracea]
                   398745
Seq. No.
Seq. ID
                   LIB3431-018-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g3345477
                   813
BLAST score
E value
                   4.0e-87
Match length
                   201
                   79
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                   398746
Seq. No.
                   LIB3431-018-P1-N1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g70772
BLAST score
                   292
E value
                   2.0e-26
Match length
                   58
                   100
% identity
                   histone H4 - wheat >gi_70773 pir HSPM4 histone H4 - garden
NCBI Description
                   pea
                   398747
Seq. No.
                   LIB3431-018-P1-N1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3789954
BLAST score
                   390
E value
                   1.0e-37
Match length
                   72
                   100
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
Seq. No.
                   398748
                   LIB3431-018-P1-N1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4038034
BLAST score
                   222
E value
                   4.0e-19
Match length
                   76
% identity
                   68
```

(AC005936) unknown protein [Arabidopsis thaliana]

```
398749
Seq. No.
                  LIB3431-018-P1-N1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132166
BLAST score
                  158
E value
                  1.0e-10
Match length
                  -31
% identity
                  87
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                  >qi 81660 pir S04048 ribulose-bisphosphate carboxylase
                  actīvase precursor - Arabidopsis thaliana
                  >gi 16471 emb CAA32429 (X14212) rubisco activase (AA 1 -
                  473) [Arabidopsis thaliana]
Seq. No.
                  398750
Seq. ID
                  LIB3431-018-P1-N1-A7
Method
                  BLASTX
NCBI GI
                  q4836912
BLAST score
                  238
                  5.0e-20
E value
Match length
                  73
% identity
                  66
                  (AC007153) 60811 [Arabidopsis thaliana]
NCBI Description
                  398751
Seq. No.
Seq. ID
                  LIB3431-018-P1-N1-A8
Method
                  BLASTX
NCBI GI
                  q2326947
BLAST score
                  158
                  1.0e-10
E value
Match length
                  29
                  100
% identity
                  (Z50801) Chlorophyll a/b-binding protein CP29 precursor
NCBI Description
                  [Zea mays]
                  398752
Seq. No.
Seq. ID
                  LIB3431-018-P1-N1-A9
Method
                  BLASTN
NCBI GI
                  q2570514
BLAST score
                  259
                  1.0e-143
E value
                  332
Match length
                  97
% identity
NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
Seq. No.
                  398753
                  LIB3431-018-P1-N1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172818
BLAST score
                  179
E value
                  2.0e-25
Match length
                  67
                  97
% identity
                  40S RIBOSOMAL PROTEIN S16 >gi 538428 (L36313) ribosomal
NCBI Description
```

protein S16 [Oryza sativa] >gi_1096552_prf__2111468A

ribosomal protein S16 [Oryza sativa]

```
Seq. No.
                  398754
                  LIB3431-018-P1-N1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2331130
BLAST score
                  171
                  2.0e-91
E value
Match length
                  191
                  98
% identity
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
                  398755
Seq. No.
Seq. ID
                  LIB3431-018-P1-N1-B6
Method
                  BLASTX
NCBI GI
                  g115813
                  224
BLAST score
                  3.0e-18
E value
Match length
                  78
                  69
% identity -
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  398756
Seq. No.
                  LIB3431-018-P1-N1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g829283
BLAST score
                  200
E value
                  1.0e-15
Match length
                  51
% identity
NCBI Description
                  (Z15018) heat shock protein hsp82 [Oryza sativa]
Seq. No.
                  398757
Seq. ID
                  LIB3431-018-P1-N1-B9
Method
                  BLASTN
NCBI GI
                  q11957
BLAST score
                  68
E value
                  4.0e-30
                  156
Match length
                  87
% identity
NCBI Description Rice complete chloroplast genome
Seq. No.
                  398758
Seq. ID
                  LIB3431-018-P1-N1-C3
Method
                  BLASTX
NCBI GI
                  g6063542
BLAST score
                  253
E value
                  2.0e-40
Match length
                  88
% identity
                  (AP000615) EST C74302(E30840) corresponds to a region of
NCBI Description
                  the predicted gene.; similar to glyceraldehyde-3-phosphate
```

dehydrogenase. (M64118) [Oryza sativa]

```
398759
Seq. No.
Seq. ID
                  LIB3431-018-P1-N1-C4
                  BLASTX
Method
NCBI GI
                  g671740
BLAST score
                  244
                  8.0e-21
E value
Match length
                  58
% identity
                  79
NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
                  398760
Seq. No.
Seq. ID
                  LIB3431-018-P1-N1-C5
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  338
E value
                  9.0e-32
                  73
Match length
% identity
                  92
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir__A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
Seq. No.
                  398761
Seq. ID
                  LIB3431-018-P1-N1-C6
Method
                  BLASTX
NCBI GI
                  g2407273
BLAST score
                  268
E value
                  1.0e-23
Match length
                  53
% identity
NCBI Description
                  (AF017359) lipid transfer protein LPT II [Oryza sativa]
Seq. No.
                  398762
Seq. ID
                  LIB3431-018-P1-N1-C8
Method
                  BLASTX
NCBI GI
                  q3980406
BLAST score
                  313
E value
                  8.0e-29
Match length
                  93 👵
% identity
NCBI Description
                  (AC004561) putative tropinone reductase [Arabidopsis
                  thaliana]
Seq. No.
                  398763
Seq. ID
                  LIB3431-018-P1-N1-D12
Method
                  BLASTX
NCBI GI
                  q115813
BLAST score
                  267
E value
                  3.0e-23
Match length
                  83
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
```

```
Seq. No.
                  398764
                  LIB3431-018-P1-N1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3036951
BLAST score
                  243
E value
                  3.0e-27
Match length
                  65
                  100
% identity
                   (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
                  398765
Seq. No.
Seq. ID
                  LIB3431-018-P1-N1-D3
                  BLASTX
Method
NCBI GI
                  q548603
BLAST score
                  325
                  3.0e-30
E value
Match length
                  63
                  97
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                  barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                  398766
Seq. ID
                  LIB3431-018-P1-N1-D4
Method
                  BLASTN
NCBI GI
                  g20181
BLAST score
                  183
E value
                  2.0e-98
Match length
                  190
                  99
% identity
NCBI Description
                  Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
Seq. No.
                  398767
Seq. ID
                  LIB3431-018-P1-N1-D5
Method
                  BLASTN
NCBI GI
                  q20369
BLAST score
                  252
E value
                  1.0e-139
Match length
                  263
                  99
% identity
NCBI Description
                  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
                  synthetase (EC 6.3.1.2) (clone lambda-GS31)
                  >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of
                  chloroplast localising glutamine synthetase
Seq. No.
                  398768
Seq. ID
                  LIB3431-018-P1-N1-D6
Method
                  BLASTN
NCBI GI
                  q20191
BLAST score
                  430
E value
                  0.0e + 00
Match length
                  466
% identity
                  98
```

% identity

```
NCBI Description O.sativa mRNA for catalase
                   398769
Seq. No.
Seq. ID
                  LIB3431-018-P1-N1-E1
Method
                   BLASTX
NCBI GI
                   q3913641
BLAST score
                   434
E value
                   1.0e-60
Match length
                   126
% identity
                   96
NCBI Description
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                   (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi 3041777 dbj_BAA25423_ (AB007194)
                   fructose-1,6-bisphosphatase [Oryza sativa]
Seq. No.
                  398770
Seq. ID
                  LIB3431-018-P1-N1-E10
Method
                  BLASTN
NCBI GI
                  g21838
BLAST score
                   67
E value
                   3.0e-29
                  204
Match length
                  85
% identity
NCBI Description
                  T.aestivum PRK gene for ribulose-5-phosphate kinase
                  398771
Seq. No.
Seq. ID
                  LIB3431-018-P1-N1-E11
Method
                  BLASTX
NCBI GI
                  g2864617
BLAST score
                  200
E value
                  2.0e-15
Match length
                  85
% identity
NCBI Description
                   (AL021811) H+-transporting ATP synthase chain9 - like
                  protein [Arabidopsis thaliana] >gi_5730141_emb_CAB52473.1
                   (AJ245574) ATP synthase beta chain precursor (subunit II)
                   [Arabidopsis thaliana]
Seq. No.
                  398772
Seq. ID
                  LIB3431-018-P1-N1-E12
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  284
E value
                  3.0e-25
Match length
                  63
% identity
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                  398773
Seq. ID
                  LIB3431-018-P1-N1-E2
Method
                  BLASTX
NCBI GI .
                  q2407279
BLAST score
                  279
E value
                  4.0e-42
Match length
                  94
```

```
NCBI Description (AF017362) aldolase [Oryza sativa]
                   398774
Seq. No.
Seq. ID
                  LIB3431-018-P1-N1-E3
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                   455
E value
                   0.0e+00
Match length
                   483
                   99
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  cds
                   398775
Seq. No.
Seq. ID
                  LIB3431-018-P1-N1-E5
Method
                  BLASTX
NCBI GI
                  g2582822
BLAST score
                  285
E value
                   3.0e - 34
Match length
                   90
                   82
% identity
NCBI Description
                   (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
                  Protein of 32kDa) [Solanum tuberosum]
Seq. No.
                   398776
                  LIB3431-018-P1-N1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2331130
BLAST score
                  162
E value
                   6.0e-86
Match length
                   254
% identity
                   91
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
Seq. No.
                   398777
Seq. ID
                  LIB3431-018-P1-N1-E9
Method
                  BLASTX
NCBI GI
                  q3036951
BLAST score
                  291
E value
                   3.0e-26
Match length
                   56
% identity
                   100
                   (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
Seq. No.
                  398778
Seq. ID
                  LIB3431-018-P1-N1-F1
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  140
E value
                  7.0e-73
Match length
                  272
% identity
                  88
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
```

% identity

```
398779
Seq. No.
                  LIB3431-018-P1-N1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  368
E value
                  3.0e - 35
Match length
                  76
% identity
                  95
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
                  398780
Seq. No.
Seq. ID
                  LIB3431-018-P1-N1-F11
Method
                  BLASTX
NCBI GI
                  g482311
BLAST score
                  297
                  3.0e-41
E value
                  91
Match length
                  99
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
Seq. No.
                  398781
Seq. ID
                  LIB3431-018-P1-N1-F5
Method
                  BLASTN
NCBI GI
                  g20369
BLAST score
                  382
E value
                  0.0e + 00
Match length
                  382
                  100
% identity
NCBI Description
                  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
                  synthetase (EC 6.3.1.2) (clone lambda-GS31)
                  >gi 2170909 dbj E02681 E02681 cDNA encoding precursor of
                  chloroplast localising glutamine synthetase
Seq. No.
                  398782
Seq. ID
                  LIB3431-018-P1-N1-F7
                  BLASTX
Method ·
NCBI GI
                  q1477428
BLAST score
                  294
E value
                  2.0e-26
Match length
                  59
% identity
NCBI Description
                  (X99623) alpha-tubulin 1 [Hordeum vulgare]
                  398783
Seq. No.
Seq. ID
                  LIB3431-018-P1-N1-F8
Method
                  BLASTX
NCBI GI
                  q4079798
BLAST score
                  298
E value
                  8.0e-43
Match length
                  93
```

```
NCBI Description
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                   sativa]
                   398784
Seq. No.
Seq. ID
                   LIB3431-018-P1-N1-G10
Method
                   BLASTX
NCBI GI
                   g4376158
                   227
BLAST score
                   2.0e-18
E value
                   75
Match length
% identity
                   63
NCBI Description
                   (X98873) aspartate kinase [Arabidopsis thaliana]
Seq. No.
                   398785
                   LIB3431-018-P1-N1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g421916
BLAST score
                   154
E value
                   3.0e-10
                   29
Match length
                   97
% identity
                   chlorophyll a/b-binding protein - English ivy (fragment)
>gi_12582_emb_CAA48410_ (X68333) light harvesting
NCBI Description
                   chlorophyll a /b binding protein [Hedera helix]
                   398786
Seq. No.
Seq. ID
                   LIB3431-018-P1-N1-G4
Method
                   BLASTN
NCBI GI
                   g218209
BLAST score
                   57
E value
                   2.0e-23
Match length
                   153
% identity
                   85
NCBI Description
                   Oryza sativa mRNA for the small subunit of
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS2106
Seq. No.
                   398787
Seq. ID
                   LIB3431-018-P1-N1-G7
Method
                   BLASTX
NCBI GI
                   g3036951
BLAST score
                   282
E value
                   3.0e-25
Match length
                   54
% identity
                   100
NCBI Description
                   (AB012639) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
Seq. No.
                   398788
                   LIB3431-018-P1-N1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5262756
BLAST score
                   221
E value
                   5.0e-27
Match length
                   80
% identity
NCBI Description
                   (AL080283) putative protein [Arabidopsis thaliana]
```

% identity

```
Seq. No.
                   398789
Seq. ID
                   LIB3431-018-P1-N1-G9
Method
                   BLASTN
NCBI GI
                   g3885887
BLAST score
                   365
E value
                   0.0e+00
Match length
                   365
% identity
                   100
NCBI Description
                   Oryza sativa high mobility group protein (HMG) mRNA,
                   complete cds
                   398790
Seq. No.
Seq. ID
                   LIB3431-018-P1-N1-H10
Method
                   BLASTX
NCBI GI
                   q115794
BLAST score
                   542
                   2.0e-55
E value
Match length
                   114
% identity
                   90
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
                   III CAB-13) >gi_72748_pir_CDT033 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato
                   >gi_19277_emb_CAA42818_ (X60275) LHCII type III
                   [Lycopersicon esculentum]
Seq. No.
                   398791
Seq. ID
                   LIB3431-018-P1-N1-H12
Method
                   BLASTN
NCBI GI
                   q710307
BLAST score
                   36
E value
                   1.0e-10
Match length
                   52
                   92
% identity
NCBI Description Avena sativa victorin binding protein mRNA, complete cds
Seq. No.
                   398792
Seq. ID
                   LIB3431-018-P1-N1-H2
Method
                   BLASTX
NCBI GI
                   q3881189
BLAST score
                   146
E value
                   2.0e-15
Match length
                   93
% identity
                   43
                   (Z99281) similar to ADP-ribosylation factor; cDNA EST
NCBI Description
                   EMBL: C08179 comes from this gene; cDNA EST EMBL: C08337
                   comes from this gene; cDNA EST EMBL: C09829 comes from this
                   gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST y
                   398793
Seq. No.
Seq. ID
                   LIB3431-018-P1-N1-H4
Method
                   BLASTX
NCBI GI
                   q115802
BLAST score
                   195
E value
                   5.0e-15
Match length
                   40
```

```
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
                  CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll
                  a/b-binding protein (cab-36) - common tobacco
                  >gi 19827 emb CAA41188 (X58230) chlorophyll a/b binding
                  protein [Nicotiana tabacum]
Seq. No.
                  398794
                  LIB3431-018-P1-N1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2570514
                  266
BLAST score
E value
                  1.0e-148
                  325
Match length
                  98
% identity
NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
                  398795
Seq. No.
Seq. ID
                  LIB3431-018-P1-N1-H6
Method
                  BLASTX
NCBI GI
                  q5042409
BLAST score
                  148
E value
                  3.0e-09
                  39
Match length
                  72
% identity
NCBI Description
                  (AC006193) Putative membrane related protein [Arabidopsis
                  thaliana]
                  398796
Seq. No.
                  LIB3431-018-P1-N1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g606817
BLAST score
                  188
E value
                  5.0e-25
Match length
                  61
% identity
                  78
NCBI Description
                  (U08404) carbonic anhydrase [Oryza sativa]
                  >gi 5917783 gb AAD56038.1_AF182806_1 (AF182806) carbonic
                  anhydrase 3 [Oryza sativa]
Seq. No.
                  398797
Seq. ID
                  LIB3431-018-P1-N1-H8
Method
                  BLASTN
NCBI GI
                  g4206059
BLAST score
                  34
E value
                  2.0e-09
Match length
                  34
% identity
                  100
                  Homo sapiens map 20q13.3; 51cR from D20S173 repeat region,
NCBI Description
                  complete sequence
Seq. No.
                  398798
Seq. ID
                  LIB3431-019-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  239
E value
                  1.0e-132
Match length
                  239
```

.

E value

1.0e-37

```
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  cds
                  398799
Seq. No.
Seq. ID
                  LIB3431-019-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g1085987
BLAST score
                  231
E value
                  2.0e-19
                  45
Match length
                  98
% identity
NCBI Description
                  light harvesting chlorophyll a protein precursor - Norway
                  spruce >gi_607148_emb_CAA57407_ (X81808) light harvesting
                  chlorophyll a /b-binding protein Lhcb1*1 [Picea abies]
                  398800
Seq. No.
Seq. ID
                  LIB3431-019-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  q4761113
BLAST score
                  47
E value
                  3.0e-17
                  51
Match length
                  98
% identity
NCBI Description
                  Allium grayi 5S ribosomal RNA gene, complete sequence
Seq. No.
                  398801
                  LIB3431-019-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789954
BLAST score
                  691
E value
                  4.0e-73
                  127
Match length
% identity
                  100
NCBI Description
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                  sativa]
                  398802
Seq. No.
                  LIB3431-019-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g126894
                  535
BLAST score
E value
                  1.0e-54
Match length
                  137
                  78
% identity
NCBI Description
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
                  >gi_319832_pir__DEPUGW malate dehydrogenase (EC 1.1.1.37)
                  precursor, glyoxysomal - watermelon >gi_167284 (M33148)
                  glyoxysomal malate dehydrogenase precursor (EC 1.1.1.37)
                  [Citrullus vulgaris]
Seq. No.
                  398803
Seq. ID
                  LIB3431-019-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g5442410
BLAST score
                  390
```

E value

7.0e-38

```
137
Match length
                    57
% identity
                    (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]
NCBI Description
                   398804
Seq. No.
Seq. ID
                   LIB3431-019-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                    689
                    9.0e-73
E value
                   150
Match length
                   87
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
Seq. No.
                   398805
Seq. ID
                   LIB3431-019-P1-K1-A9
Method
                   BLASTX'
NCBI GI
                   g2982453
BLAST score
                   149
E value
                    9.0e-15
                   77
Match length
% identity
NCBI Description
                    (AL022223) fructose-bisphosphate aldolase-like protein
                    [Arabidopsis thaliana]
Seq. No.
                   398806
Seq. ID
                   LIB3431-019-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g2809245
BLAST score
                   298
E value
                    6.0e-27
Match length
                   78
% identity
NCBI Description
                    (AC002560) F21B7.14 [Arabidopsis thaliana]
                   398807
Seq. No.
Seq. ID
                   LIB3431-019-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g4038594
BLAST score
                   280
E value
                   8.0e-25
Match length
                   84
% identity
NCBI Description
                    (AJ222798) tDET1 protein [Lycopersicon esculentum]
                   >gi_4454332_emb_CAA11914_ (AJ224356) tDET1 protein
                    [Lycopersicon esculentum]
Seq. No.
                   398808
Seq. ID
                   LIB3431-019-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   g3885882
BLAST score
                   390
```

```
Match length
                  74
                  100
% identity
NCBI Description
                  (AF093629) inorganic pyrophosphatase [Oryza sativa]
                  398809
Seq. No.
Seq. ID
                  LIB3431-019-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q4585882
BLAST score
                  590
E value
                  3.0e-61
Match length
                  134
% identity
                  78
NCBI Description
                  (AC005850) PSI type III chlorophyll a/b-binding protein
                  [Arabidopsis thaliana]
                  398810
Seq. No.
Seq. ID
                  LIB3431-019-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q2921158
BLAST score
                  554
E value
                  4.0e-57
Match length
                  122
% identity
                  89
NCBI Description
                  (AF022909) ClpC [Arabidopsis thaliana]
Seq. No.
                  398811
                  LIB3431-019-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q320618
BLAST score
                  753
E value
                  3.0e-80
Match length
                  142
                  99
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  398812
Seq. No.
Seq. ID
                  LIB3431-019-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  427
                  3.0e-42
E value
Match length
                  103
% identity
                  83
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
```

carboxylase S [Oryza sativa]

```
398813
Seq. No.
Seq. ID
                   LIB3431-019-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g2982453
BLAST score
                   568
E value
                   1.0e-58
                   129
Match length
% identity
                   86
NCBI Description
                    (AL022223) fructose-bisphosphate aldolase-like protein
                    [Arabidopsis thaliana]
                   398814
Seq. No.
                   LIB3431-019-P1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q126201
BLAST score
                   409
E value
                    6.0e-40
Match length
                   117
% identity
                   68
NCBI Description
                   3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM
                   DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_81676_pir_S20510 3-isopropylmalate dehydrogenase (EC \overline{1.1.1.85}) precursor -
                   rape >gi_17827_emb_CAA42596_ (X59970) 3-isopropylmalate
                   dehydrogenase [Brassica napus]
Seq. No.
                   398815
                   LIB3431-019-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5031281
BLAST score
                   345
E value
                   2.0e-32
Match length
                   115
% identity
NCBI Description
                    (AF139499) unknown [Prunus armeniaca]
Seq. No.
                   398816
Seq. ID
                   LIB3431-019-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   q3292814
BLAST score
                   248
E value
                   4.0e-21
Match length
                   117
% identity
NCBI Description
                   (AL031018) putative protein [Arabidopsis thaliana]
                   398817
Seq. No.
Seq. ID
                   LIB3431-019-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   q2072555
BLAST score
                   237
E value
                   9.0e-20
Match length
                   44
% identity
                   100
                    (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
```

protein [Oryza sativa]

```
398818
Seq. No.
Seq. ID
                  LIB3431-019-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g3913018
BLAST score
                  712
                   2.0e-75
E value
Match length
                  136
% identity
                   99
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
                   398819
Seq. No.
Seq. ID
                  LIB3431-019-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g3776005
BLAST score
                   372
E value
                   1.0e-35
Match length
                  76
% identity
NCBI Description
                   (AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  398820
Seq. ID
                  LIB3431-019-P1-K1-C6
Method
                  BLASTX
NCBI GI
                   q37.76005
BLAST score
                  287
E value
                   1.0e-25
Match length
                  76
% identity
NCBI Description
                   (AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.
                   398821
Seq. ID
                  LIB3431-019-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q1173347
BLAST score
                   473
E value
                   2.0e-47
Match length
                  107
                   89
% identity
NCBI Description
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7) P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  398822
Seq. ID
                  LIB3431-019-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  538
E value
                   4.0e-55
Match length
                  120
                  85
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
```

NCBI GI

BLAST score

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

```
Seq. No.
                  398823
Seq. ID
                  LIB3431-019-P1-KI 109
Method
                  BLASTX
NCBI GI
                  q2239089
BLAST score
                  218
                  1.0e-17
E value
Match length
                  100
% identity
                  41
                   (Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase
NCBI Description
                   [Dianthus caryophyllus] >gi 3288180_emb_CAB11466_ (Z98758)
                  anthranilate N-hydroxycinnamoyl/benzoyltransferase
                  [Dianthus caryophyllus]
Seq. No.
                  398824
                  LIB3431-019-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1835731
BLAST score
                  512
E value
                  4.0e-52
Match length
                  97
% identity
                  100
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                  LIB3431-019-P1-K1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q6015437
BLAST score
                  36
                                                               43.
E value
                  6.0e-11
Match length
                  47
% identity
                  65
NCBI Description
                  Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  398826
                  LIB3431-019-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  588
E value
                  5.0e-61
Match length
                  108
% identity
                  100
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                  398827
Seq. ID
                  LIB3431-019-P1-K1-D3
Method
                  BLASTX
```

g2501646

```
E value
                    5.0e-66
Match length
                    139
                    91
 % identity
                    UROPORPHYRINOGEN DECARBOXYLASE (UPD)
NCBI Description
                    >gi 1362169_pir S55733 uroporphyrinogen decarboxylase -
                    barley >gi 1016347 emb CAA58039 (X82832) uroporphyrinogen
                    decarboxylase [Hordeum vulgare]
Seq. No.
                    398828
                    LIB3431-019-P1-K1-D4
Method
                    BLASTN
                    g6015437
NCBI GI
BLAST score
                    38
                    7.0e-12
E value
Match length
                    38
                    100
 % identity
                    Homo sapiens PEX1 mRNA, complete cds
NCBI Description
 Seq. No.
                    398829
                    LIB3431-019-P1-K1-D5
Seq. ID
Method
                    BLASTN
NCBI GI
                    q3821780
BLAST score
                    36
                    1.0e-10
E value
                    47
Match length
                    66
 % identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                    398830
Seq. No.
                    LIB3431-019-P1-K1-D7
Seq. ID
Method
                    BLASTX
NCBI GI
                    g115787
BLAST score
                    508
E value
                    1.0e-51
Match length
                    117
 % identity
                    87
                    CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                    CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
                    398831
 Seq. No.
Seq. ID
                    LIB3431-019-P1-K1-D8
Method
                    BLASTX
NCBI GI
                    g132105
BLAST score
                    609
E value
                    2.0e-63
                    131
Match length
 % identity
                    88
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                    ribulose-bisphosphate carboxylase (\overrightarrow{EC} 4.1.1.39) small chain
                    precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
```

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

NCBI GI

E value

BLAST score

q1871192

9.0e-26

288

```
carboxylase S [Oryza sativa]
                                                                         1
                   398832
Seq. No.
                   LIB3431-019-P1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   380
E value
                   2.0e-36
                   96
Match length
% identity
                   83
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   398833
Seq. No.
Seq. ID
                   LIB3431-019-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g4874311
BLAST score
                   433
E value
                   8.0e-43
Match length
                   132
% identity
NCBI Description
                   (AC006053) unknown protein [Arabidopsis thaliana]
Seq. No.
                   398834
Seq. ID
                   LIB3431-019-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   q5103831
BLAST score
                   221
E value
                   6.0e-18
Match length
                   66
% identity
NCBI Description
                   (AC007591) ESTs gb H37032, gb R6425, gb Z34651, gb N37268,
                   gb AA713172 and gb Z34241 come from this gene. [Arabidopsis
                   thaliana]
Seq. No.
                   398835
Seq. ID
                   LIB3431-019-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g1076724
BLAST score
                   601
E value
                   2.0e-62
Match length
                   127
% identity
                   84
NCBI Description
                   LHCI-680, photosystem I antenna protein - barley
                   >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                   antenna protein [Hordeum vulgare]
                   398836
Seq. No.
Seq. ID
                   LIB3431-019-P1-K1-E3
Method
                   BLASTX
```

sativa] >gi_226375_prf__1508256A ribulose bisphosphate

```
137
  Match length
   % identity
                     45
                     (U90439) Cys3His zinc finger protein isolog [Arabidopsis
  NCBI Description
                     thaliana]
                     398837
  Seq. No.
  Seq. ID
                     LIB3431-019-P1-K1-E4
  Method
                     BLASTX
NCBI GI
                     ,g4539332
                     296
  BLAST score
                     1.0e-26
  E value
  Match length
                     90
                     68
   % identity
                     (AL035539) glycosyltransferase like protein (fragment)
  NCBI Description
                     [Arabidopsis thaliana]
                     398838
   Seq. No.
                     LIB3431-019-P1-K1-E5
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     g6015437
                     39
  BLAST score
  E value
                     2.0e-12
  Match length
                     39
   % identity
                     100
  NCBI Description Homo sapiens PEX1 mRNA, complete cds
                                      ×2...
                     398839
  Seq. No.
  Seq. ID
                     LIB3431-019-P1-K1-E6
  Method
                     BLASTX
  NCBI GI
                     g2293480
  BLAST score
                     416
  E value
                     7.0e-41
  Match length
                     85
   % identity
  NCBI Description
                     (AF011331) glycine-rich protein [Oryza sativa]
                                80
  Seq. No.
                     398840
  Seq. ID
                     LIB3431-019-P1-K1-E7
  Method
                     BLASTX
  NCBI GI
                     q2623298
  BLAST score
                     512
  E value
                     5.0e-52
  Match length
                     143
   % identity
                     (AC002409) putative 4-alpha-glucanotransferase [Arabidopsis
  NCBI Description
                     thaliana]
  Seq. No.
                     398841
  Seq. ID
                     LIB3431-019-P1-K1-E9
  Method
                     BLASTX
  NCBI GI
                     g1076746
  BLAST score
                     163
  E value
                     3:0e-11
  Match length
                     30
                     97
   % identity
                     heat shock protein 70 - rice (fragment)
  NCBI Description
```

>gi_763160_emb_CAA47948_ (X67711) heat shock protein 70

Seq. ID LIB3431-019-P1-K1-F1 BLASTX Method NCBI GI g134034 BLAST score 261 E value 1.0e-22 110. Match length % identity 50 30S RIBOSOMAL PROTEIN \$30, CHLOROPLAST PRECURSOR (CS-S5) NCBI Description (CS5) (S22) (RIBOSOMAL PROTEIN 1) (PSRP-1) >gi_279640_pir__R3SPS5 ribosomal protein CS-S22 precursor, chloroplast - spinach >gi_12316_emb_CAA41960_ (X59270) chloroplast ribosomal protein S22 [Spinacia oleracea] >gi_18031_emb_CAA33403_ (X15344) spinach S22 r-protein [Spinacia oleracea] 398843 Seq. No. LIB3431-019-P1-K1-F10 Seq. ID Method BLASTX NCBI GI ÿ3075488 BLAST score 439 E value 2.0e-43 104 Match length 82 % identity (AF058796) chlorophyll a/b-binding protein [Oryza sativa] NCBI Description 398844 Seq. No. LIB3431-019-P1-K1-F11 Seq. ID BLASTX Method NCBI GI g3914005 BLAST score 314 E value 8.0e-29 Match length 70 % identity MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 1816586 NCBI Description (U85494) LON1 protease [Zea mays] 398845 Seq. No. LIB3431-019-P1-K1-F2 Seq. ID BLASTX Method g1777961 NCBI GI BLAST score 482 2.0e-48 E value Match length 152 % identity (U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum NCBI Description vulgare] 398846 Seq. No. LIB3431-019-P1-K1-F4 Seq. ID Method BLASTX NCBI GI g82080 BLAST score 336 E value 2.0e-31

[Oryza sativa]

398842

Seq. No.

Match length

% identity

```
% identity
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
Seq. No.
                  398847
                  LIB3431-019-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                 g2130082
BLAST score
                  260
E value
                  2.0e-22
Match length
                  128
% identity
                  41
                  protein kinase Xa21 (EC 2.7.1.-) - rice >gi 1122443
NCBI Description
                  (U37133) receptor kinase-like protein [Oryza sativa]
                  >gi 2586085 (U72723) receptor kinase-like protein [Oryza
                  longistaminata] >gi_1586408_prf__2203451A receptor
                  kinase-like protein [Oryza sativa]
                  398848
Seq. No.
                  LIB3431-019-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q710308
BLAST score
                  716
                  7.0e-76
E value
Match length
                  156
                  88
% identity
                  (U11693) victorin binding protein [Avena sativa]
NCBI Description
Seq. No.
                  398849
                  LIB3431-019-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  583
E value
                  2.0e-60
Match length
                  111
                  98
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  398850
                  LIB3431-019-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  531
E value
                  3.0e-54
Match length
                  101
% identity
                  100
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  398851
Seq. No.
Seq. ID
                  LIB3431-019-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g3075488
BLAST score
                  500
E value
                  1.0e-50
Match length
                  117
```

```
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                  398852
Seq. No.
Seq. ID
                  LIB3431-019-P1-K1-G1
                  BLASTX
Method
NCBI GI
                  q4996602
BLAST score
                  316
E value
                  5.0e-29
Match length
                  142
                  50
% identity
                  (AB022273) thylakoid-bound ascorbate peroxidase [Nicotiana
NCBI Description
                  tabacum
                  398853
Seq. No.
                  LIB3431-019-P1-K1-G3
Seq. ID
Method
                  BLASTX
                  g5834807
NCBI GI
BLAST score
                  161
E value
                  7.0e-11
Match length
                  50
% identity
                 (AL117212) hypothetical protein [Schizosaccharomyces pombe]
NCBI Description
                  398854
Seq. No.
                  LIB3431-019-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  380
E value
                  4.0e-44
Match length
                  108
                  86
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  398855
Seq. No.
Seq. ID
                  LIB3431-019-P1-K1-G7
                  BLASTX
Method
NCBI GI
                  g132105
BLAST score
                  390
E value
                  3.0e-52
                  125
Match length
                  81
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  398856
Seq. ID
                  LIB3431-019-P1-K1-G8
```

BLAST score

```
BLASTX
Method
NCBI GI
                  g4506221
BLAST score
                  206
                  3.0e-16
E value
                  102
Match length
                  45
% identity
                  proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
NCBI Description
                  >gi 1945611_dbj_BAA19749 (AB003103) 26S proteasome subunit
                  p55 [Homo sapiens]
                  398857
Seq. No.
Seq. ID
                  LIB3431-019-P1-K1-H1
Method
                  BLASTX
                  g4079800
NCBI GI
BLAST score
                  502
                  7.0e-51
E value
Match length
                  101
% identity
                  96
NCBI Description
                   (AF052503) S-phase-specific ribosomal protein [Oryza
                  sativa]
Seq. No.
                  398858
Seq. ID
                  LIB3431-019-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q3885882
BLAST score
                  317
E value
                  2.0e-29
Match length
                  83
% identity
                  75
NCBI Description
                  (AF093629) inorganic pyrophosphatase [Oryza sativa]
                  398859
Seq. No.
                  LIB3431-019-P1-K1-H2
Seq. ID
Method
                  -BLASTX
NCBI GI
                  q5903092
BLAST score
                  382
E value
                  8.0e-37
Match length
                  114
% identity
                  72
                   (AC008017) Highly similar to developmental protein DG1118
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  398860
                  LIB3431-019-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3885888
BLAST score
                  316
E value
                  5.0e-29
Match length
                  142
% identity
NCBI Description
                  (AF093632) high mobility group protein [Oryza sativa]
Seq. No.
                  398861
                  LIB3431-019-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885882
```

Match length

```
3.0e-42
   E value
                      95
   Match length
   % identity
                      (AF093629) inorganic pyrophosphatase [Oryza sativa]
   NCBI Description
                      398862
   Seq. No.
   Seq. ID
                      LIB3431-019-P1-K1-H6
   Method
                      BLASTX
                      g2795806
 NCBI GI
A BLAST score
                      498
   E value
                      2.0e-50
   Match length
                      141
                      70
   % identity
   NCBI Description
                      (AC003674) unknown protein [Arabidopsis thaliana]
   Seq. No.
                      398863
                      LIB3431-019-P1-K1-H7
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                      g1164988
   BLAST score
                      345
   E value
                      2.0e-32
   Match length
                      124
   % identity
                      55
   NCBI Description
                      (X94335) YOR3513c [Saccharomyces cerevisiae]
   Seq. No.
                      398864
                      LIB3431-019-P1-K1-H9
   Seq. ID
   Method
                      BLASTX
   NCBI GI
                      g266893
   BLAST score
                      661
   E value
                      1.0e-69
   Match length
                      130
   % identity
                      95
   NCBI Description
                      RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                      CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                      >gi_322416_pir__S28172 ribulose-bisphosphate carboxylase
                      activase - cucumber >gi 18284 emb CAA47906 (X67674)
                      rubisco activase [Cucumis sativus]
   Seq. No.
                      398865
   Seq. ID
                      LIB3431-019-P1-N1-A10
   Method
                      BLASTN
   NCBI GI
                      g2072554
   BLAST score
                      233
   E value
                      1.0e-128
   Match length
                      237
   % identity
                      100
   NCBI Description
                      Oryza sativa metallothionein-like protein mRNA, complete
   Seq. No.
                      398866
   Seq. ID
                     LIB3431-019-P1-N1-A11
   Method
                      BLASTX
   NCBI GI
                      g1085987
   BLAST score
                      231
   E value
                      2.0e-19
```

BLAST score

```
% identity
NCBI Description
                   light harvesting chlorophyll a protein precursor - Norway
                   spruce >gi 607148 emb CAA57407 (X81808) light harvesting
                   chlorophyll a /b-binding protein Lhcb1*1 [Picea abies]
                   398867
Seq. No.
Seq. ID
                   LIB3431-019-P1-N1-A2
Method
                   BLASTN
NCBI GI
                   g218207
BLAST score
                   161
E value
                   2.0e-85
Match length
                   245
                   91
% identity
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS1139
                   398868
Seq. No.
                   LIB3431-019-P1-N1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3789954
BLAST score
                   390
E value
                   1.0e-37
Match length
                   72
% identity
                   100
NCBI Description
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                   sativa]
Seq. No.
                   398869
Seq. ID
                   LIB3431-019-P1-N1-A6
Method
                   BLASTX
NCBI GI
                   g5442410
BLAST score
                   179
E value
                   5.0e-13
Match length
                   78
% identity
NCBI Description
                   (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]
Seq. No.
                   398870
Seq. ID
                   LIB3431-019-P1-N1-A7
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   409
E value
                   6.0e-40
Match length
                   77
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   398871
Seq. ID
                   LIB3431-019-P1-N1-A9
Method
                   BLASTX
NCBI GI
                   g2191138
```

E value

1.0e-39

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```
1.0e-25
E value
Match length
                   64
% identity
                   (AF007269) A IG002N01.18 gene product [Arabidopsis
NCBI Description
                  thaliana]
                   398872
Seq. No.
Seq. ID
                  LIB3431-019-P1-N1-B1
Method
                  BLASTX
NCBI GI
                  g2809245
BLAST score
                  283
                   3.0e-25
E value
                   64
Match length
% identity
                   83
                   (AC002560) F21B7.14 [Arabidopsis thaliana]
NCBI Description
                   398873
Seq. No.
                  LIB3431-019-P1-N1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4038594
BLAST score
                   233
E value
                   2.0e-19
Match length
                   67
% identity
NCBI Description
                   (AJ222798) tDET1 protein [Lycopersicon esculentum]
                  >gi_4454332_emb_CAA11914_ (AJ224356) tDET1 protein
                   [Lycopersicon esculentum]
                   398874
Seq. No.
Seq. ID
                  LIB3431-019-P1-N1-B12
Method
                  BLASTN
NCBI GI
                   q3885881
BLAST score
                   345
E value
                   0.0e+00
                                100
Match length
                   373
% identity
                   98
NCBI Description
                  Oryza sativa inorganic pyrophosphatase (IPP) mRNA, complete
                   398875
Seq. No.
Seq. ID
                  LIB3431-019-P1-N1-B4
Method
                  BLASTX
NCBI GI
                   q115813
BLAST score
                   176
                   1.0e-12
E value
Match length
                   41
% identity
                  80
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                   398876
Seq. No.
Seq. ID
                  LIB3431-019-P1-N1-B6
Method
                  BLASTX
NCBI GI
                  q461753
BLAST score
                  406
```

E value

4.0e-19

```
103
Match length
                   77
% identity
NCBI Description
                   ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
                   PRECURSOR >gi 419773 pir S31164 ATP-dependent ClpB
                   proteinase regulatory chain homolog precursor, chloroplast
                   - garden pea >gi 169128 (L09547) nuclear encoded precursor
                   to chloroplast protein [Pisum sativum]
Seq. No.
                   398877
Seq. ID
                   LIB3431-019-P1-N1-B7
Method
                   BLASTN
NCBI GI
                   g20181
BLAST score
                   139
E value
                   3.0e-72
Match length
                   150
% identity
                   98
NCBI Description
                   Rice cab2R gene for light harvesting chlorophyll
                   a/b-binding protein
Seq. No.
                   398878
Seq. ID
                   LIB3431-019-P1-N1-B8
Method
                   BLASTX
NCBI GI
                   q671740
BLAST score
                   363
                   2.0e-34
E value
Match length
                   72
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
Seq. No.
                   398879
Seq. ID
                   LIB3431-019-P1-N1-C11
Method
                   BLASTX
NCBI GI
                   q5031281
BLAST score
                   237
E value
                   9.0e-20
Match length
                   51
% identity
                   (AF139499) unknown [Prunus armeniaca]
NCBI Description
                   398880
Seq. No.
Seq. ID
                   LIB3431-019-P1-N1-C3
Method
                   BLASTN
NCBI GI
                   q2072554
BLAST score
                   282
                   1.0e-157
E value
Match length
                   286
% identity
                   100
NCBI Description
                   Oryza sativa metallothionein-like protein mRNA, complete
                   398881
Seq. No.
Seq. ID
                   LIB3431-019-P1-N1-C4
Method
                   BLASTN
NCBI GI
                   g218154
BLAST score
                   50
```

```
78
Match length
                   91
% identity
NCBI Description
                  Oryza sativa gene for cytoplasmic aldolase, complete cds,
                  clone:Aldp
                   398882
Seq. No.
                  LIB3431-019-P1-N1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3776005
BLAST score
                   162
E value
                   6.0e-11
Match length
                   36
                   89
% identity
NCBI Description
                   (AJ010466) RNA helicase [Arabidopsis thaliana]
                   398883
Seq. No.
                  LIB3431-019-P1-N1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                   g14264
BLAST score
                   51
E value
                   1.0e-19
Match length
                  87
% identity
                   90
NCBI Description
                  T.aestivum gene for sedoheptulose-1,7-bisphoshatase
Seq. No.
                   398884
Seq. ID
                  LIB3431-019-P1-N1-C8
Method
                  BLASTN
NCBI GI
                   g218207
BLAST score
                   163
E value
                   1.0e-86
Match length
                   279
                   90
% identity
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
Seq. No.
                   398885
Seq. ID
                  LIB3431-019-P1-N1-D10
Method
                  BLASTX
NCBI GI
                   g1835731
BLAST score
                  280
E value
                   6.0e-25
Match length
                   64
% identity
NCBI Description
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                  398886
Seq. ID
                  LIB3431-019-P1-N1-D11
Method
                  BLASTX
NCBI GI
                  q517500
BLAST score
                  176
E value
                  8.0e-13
Match length
                  53
% identity
                   68
NCBI Description
                   (M87435) precursor of the oxygen evolving complex 17 kDa
                  protein [Zea mays] >gi_444338 prf_ 1906386A photosystem II
```

OE17 protein [Pisum sativum]

```
Seq. No.
                  398887
Seq. ID
                  LIB3431-019-P1-N1-D3
                  BLASTX
Method
NCBI GI
                  q6014938
BLAST score
                  173
E value
                  2.0e-12
                . 34
Match length
% identity
                  94
                  UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD) >gi 3420233
NCBI Description
                   (AF058763) uroporphyrinogen decarboxylase [Zea mays]
Seq. No.
                  398888
                  LIB3431-019-P1-N1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g421916
BLAST score
                  162
E value
                  4.0e-11
Match length
                  29
% identity
                  100
NCBI Description
                  chlorophyll a/b-binding protein - English ivy (fragment)
                  >gi_12582_emb_CAA48410_ (X68333) light harvesting
                  chlorophyll a /b binding protein [Hedera helix]
Seq. No.
                  398889
Seq. ID
                  LIB3431-019-P1-N1-D8
Method
                  BLASTX
NCBI GI
                  q347451
BLAST score
                  387
E value
                  2.0e-37
Match length
                  72
% identity
                  97
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa].
Seq. No.
                  398890
Seq. ID
                  LIB3431-019-P1-N1-D9
Method
                  BLASTX
NCBI GI
                  q3036951
BLAST score
                  310
E value
                  2.0e-28
Match length
                  61
% identity
NCBI Description
                   (AB012639) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
Seq. No.
                  398891
Seq. ID
                  LIB3431-019-P1-N1-E4
Method
                  BLASTX
NCBI GI
                  q5764049
BLAST score
                  252
E value
                  2.0e-21
Match length
                  67
                  70
% identity
NCBI Description
                  (Y16832) alpha-1,3-mannosyl-glycoprotein
                  beta-1,2-N-acetylglucosaminyltransferase [Nicotiana
```

NCBI Description

tabacum] Seq. No. 398892 Seq. ID LIB3431-019-P1-N1-E6 Method BLASTN NCBI GI g2331130 BLAST score 189 E value 1.0e-102 Match length 193 % identity 99 Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete NCBI Description Seq. No. 398893 Seq. ID LIB3431-019-P1-N1-F10 Method BLASTN NCBI GI g3075487 BLAST score 240 E value 1.0e-132 Match length 260 % identity 98 NCBI Description Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds Seq. No. 398894 Seq. ID LIB3431-019-P1-N1-F2 Method BLASTX NCBI GI q1777961 BLAST score 194 E value 1.0e-14 Match length 73 % identity NCBI Description (U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum vulgare] Seq. No. 398895 Seq. ID LIB3431-019-P1-N1-F4 Method' BLASTX NCBI GI q115813 BLAST score 243 E value 1.0e-20 Match length 55 % identity 85 CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III NCBI Description CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum] Seq. No. 398896 Seq. ID LIB3431-019-P1-N1-F6 Method BLASTX NCBI GI q710308 BLAST score 147 E value 2.0e-09 27 Match length % identity 96

(U11693) victorin binding protein [Avena sativa]

```
398897
Seq. No.
                   LIB3431-019-P1-N1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3126854
BLAST score
                   345
E value
                   1.0e-32
Match length
                   65
% identity
                   100
NCBI Description
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   398898
                   LIB3431-019-P1-N1-F8
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1835730
BLAST score
                   219
E value
                   1.0e-120
Match length
                   255
% identity
NCBI Description
                   Oryza sativa photosystem II 10 kDa polypeptide mRNA,
                   complete cds
                   398899
Seq. No.
Seq. ID
                   LIB3431-019-P1-N1-F9
Method
                   BLASTN
NCBI GI
                   q3075487
BLAST score
                   338 -
E value
                   0.0e + 00
Match length
                   338
                   100
% identity
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
                   mRNA, complete cds
Seq. No.
                   398900
Seq. ID
                   LIB3431-019-P1-N1-G1
Method
                   BLASTX
NCBI GI
                   q1321627
BLAST score
                   231
E value
                   3.0e-19
Match length
                   55
% identity
NCBI Description
                   (D83656) thylakoid-bound ascorbate peroxidase [Cucurbita
Seq. No.
                   398901
Seq. ID
                   LIB3431-019-P1-N1-G10
Method
                   BLASTX
NCBI GI
                   q289920
BLAST score
                   286
E value
                   1.0e-25
Match length
                   58
% identity
                   95
NCBI Description
                   (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
Seq. No.
                   398902
                  LIB3431-019-P1-N1-G2
Seq. ID
Method
```

BLASTX

```
q120661
NCBI GI
BLAST score
                  251
                  2.0e-21
E value
                  50
Match length
                  92
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
NCBI Description
                  PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
                  dehydrogenase A-subunit precursor [Nicotiana tabacum]
                  398903
Seq. No.
Seq. ID
                  LIB3431-019-P1-N1-G5
Method
                  BLASTN
NCBI GI
                  g218171
BLAST score
                  215
E value
                   1.0e-117
Match length
                  243
                   97
% identity
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                  a/b binding protein of photosystem II (LHCPII), complete
Seq. No.
                  398904
Seq. ID
                  LIB3431-019-P1-N1-G6
Method
                  BLASTX
NCBI GI
                  q1652203
BLAST score
                  153
E value
                   5.0e-10
Match length
                  78
% identity
NCBI Description
                   (D90903) hypothetical protein [Synechocystis sp.]
                  398905
Seq. No.
Seq. ID
                  LIB3431-019-P1-N1-G7
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  310
E value
                   1.0e-30
Match length
                  68
% identity
                  100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  398906
Seq. ID
                  LIB3431-019-P1-N1-H11
Method
                  BLASTX
NCBI GI
                  q3789954
BLAST score
                  184
E value
                  9.0e-14
Match length
                  33
% identity
                  97
```

```
NCBI Description
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                  sativa]
                  398907
Seq. No.
Seq. ID
                  LIB3431-019-P1-N1-H4
Method
                  BLASTN
NCBI GI
                  q3885887
BLAST score
                  374
E value .
                  0.0e+00
Match length
                  378
                  100
% identity
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                  complete cds
                  398908
Seq. No.
                  LIB3431-019-P1-N1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885882
BLAST score
                  189
E value
                  3.0e-14
Match length
                  39
% identity
                  97
NCBI Description
                  (AF093629) inorganic pyrophosphatase [Oryza sativa]
Seq. No.
                  398909
Seq. ID
                  LIB3431-019-P1-N1-H7
Method
                  BLASTX
NCBI GI
                  q1164988
BLAST score
                  341
E value
                  6.0e-32
Match length
                  94
% identity
NCBI Description
                  (X94335) YOR3513c [Saccharomyces cerevisiae]
Seq. No.
                  398910
Seq. ID
                  LIB3431-019-P1-N1-H8
Method
                  BLASTN
NCBI GI
                  g12470
BLAST score
                  76
E value
                  5.0e-35
Match length
                  99
% identity
NCBI Description Z.mays chloroplast rRNA-operon
                  398911
Seq. No.
Seq. ID
                  LIB3431-019-P1-N1-H9
Method
                  BLASTX
NCBI GI
                  q132166
BLAST score
                  160
E value
                  6.0e-11
Match length
                  31
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                  >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase
                  activase precursor - Arabidopsis thaliana
                  >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 -
```

473) [Arabidopsis thaliana] 398912

Seq. ID LIB3431-020-P1-K1-A1 Method BLASTX NCBI GI g2494116

BLAST score 171 E value 8.0e-26 Match length **67** . % identity 75

Seq. No.

(AC002376) Similar to Synechocystis hypothetical protein NCBI Description

(qb D90915). [Arabidopsis thaliana]

Seq. No. 398913

Seq. ID LIB3431-020-P1-K1-A12

Method BLASTX NCBI GI g115787 BLAST score 516 E value 2.0e-52 Match length 120 86

% identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_

×2.

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 398914

LIB3431-020-P1-K1-A7 Seq. ID

Method BLASTX NCBI GI g5931655 BLAST score 199 E value 2.0e-15 Match length 100 % identity 41

NCBI Description (AJ011629) squamosa promoter binding protein-like 1

[Arabidopsis thaliana]

398915 Seq. No.

Seq. ID LIB3431-020-P1-K1-A8

Method BLASTX NCBI GI g3550982 BLAST score 156 2.0e-10 E value 82 Match length % identity

NCBI Description (AB010690) mutM homologue-1 [Arabidopsis thaliana]

> >gi 5903053 gb AAD55612.1 AC008016 22 (AC008016) Identical to gb AB010690 mutM homologue-1 (formamidopyrimidine-DNA glycosylase 1) from Arabidopsis thaliana. EST gb Z18192

comes from this gene

398916 Seq. No.

LIB3431-020-P1-K1-B12 Seq. ID

Method BLASTX NCBI GI q121446 BLAST score 160

BLAST score

E value

262

1.0e-22

```
2.0e-11
E value
Match length
                   60
                   58
% identity
                   FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE PRECURSOR
NCBI Description
                   (FD-GOGAT) >gi_100877_pir__A38596 glutamate synthase (ferredoxin) (EC 1.4.7.1) - maize >gi_168477 (M59190)
                   ferredoxin-dependent glutamate synthase [Zea mays]
Seq. No.
                   398917
Seq. ID
                   LIB3431-020-P1-K1-B4
                   BLASTX
Method
NCBI GI
                   q417260
BLAST score
                   421
E value
                   3.0e-41
                   128
Match length
% identity
                   66
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                   lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                   light-regulated gene [Oryza sativa]
Seq. No.
                   398918
                   LIB3431-020-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4063821
BLAST score
                   756
E value
                   1.0e-80
Match length
                   144
% identity
                   99
                   (AB015204) plastidic ATP sulfurylase [Oryza sativa]
NCBI Description
                   398919
Seq. No.
                   LIB3431-020-P1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3789952
BLAST score
                   588
E value
                   7.0e-61
Match length
                   115
% identity
                   95
                    (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
                   398920
Seq. No.
Seq. ID
                   LIB3431-020-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   g4138290
BLAST score
                   582
E value
                   2.0e-60
Match length
                   125
% identity
                   (AJ005841) thioredoxin M [Oryza sativa]
NCBI Description
Seq. No.
                   398921
Seq. ID
                   LIB3431-020-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   g2673912
```

Seq. No.

```
90
Match length
% identity
                   58
                   (AC002561) unknown protein [Arabidopsis thaliana]
NCBI Description
                  398922
Seq. No.
Seq. ID
                  LIB3431-020-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  391
E value
                  7.0e-38
Match length
                  124
                   64
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (\overrightarrow{EC} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >qi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  398923
Seq. ID
                  LIB3431-020-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q170404
BLAST score
                   565
E value
                   3.0e-68
Match length
                  137
% identity
NCBI Description
                   (M14444) chlorophyll a/b-binding protein Cab-3C
                   [Lycopersicon esculentum]
Seq. No.
                   398924
Seq. ID
                  LIB3431-020-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q1346874
BLAST score
                  152
E value
                  8.0e-10
Match length
                   49
% identity
                   61
                  PHOTOSYSTEM II REACTION CENTER W PROTEIN >gi 1016177
NCBI Description
                   (U30821) subunit of the water oxidation complex on the
                   lumenal surface of the photosystem II reaction center
                  complex [Cyanophora paradoxa]
Seq. No.
                  398925
Seq. ID
                  LIB3431-020-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  646
E value
                  1.0e-67
Match length
                  140
% identity
                  89
                 (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
```

```
LIB3431-020-P1-K1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g473878
BLAST score
                  168
                  3.0e-12
E value
Match length
                  46
                  70
% identity
NCBI Description (U08315) calnexin homolog [Arabidopsis thaliana]
                  398927
Seq. No.
                  LIB3431-020-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5729754
BLAST score
                  175
E value
                  1.0e-12
                  77
Match length
                  49
% identity
                  transcription factor CA150 >gi 2460124 (AF017789) putative
NCBI Description
                  transcription factor CA150 [Homo sapiens]
                  398928
Seq. No.
                  LIB3431-020-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q500734
BLAST score
                  374
                  7.0e-36
E value
Match length
                  131
% identity
                   (U10414) Contains similarity to Pfam domain: PF00005
NCBI Description
                   (ABC_tran), Score=245.2, E-value=3e-70, N=2 [Caenorhabditis
                  elegans]
Seq. No.
                  398929
Seq. ID
                  LIB3431-020-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  9.0e-20
Match length
                  44
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  398930
Seq. No.
Seq. ID
                  LIB3431-020-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g1519251
BLAST score
                  537
E value
                  4.0e-55
Match length
                  108
% identity
NCBI Description
                  (U65957) GF14-c protein [Oryza sativa]
Seq. No.
                  398931
                  LIB3431-020-P1-K1-D10
Seq. ID
Method
                  BLASTX
```

Seq. No.

```
q3915131
NCBI GI
BLAST score
                   582
                   3.0e-60
E value
                   112
Match length
                   100
% identity
                  THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)
NCBI Description
                  >gi 426442 dbj_BAA04864 (D21836) thioredoxin h [Oryza
                   satīva] >gī 454882 dbj BAA05546 (D26547) rice thioredoxin
                  h [Oryza sativa] >gi 1930072 (U92541) thioredoxin h [Oryza
                  sativa]
                   398932
Seq. No.
Seq. ID
                  LIB3431-020-P1-K1-D4
Method
                  BLASTX
NCBI GI
                   g2570511
BLAST score
                   662
E value
                   1.0e-69
                   127
Match length
% identity
                   98
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   398933
Seq. ID
                  LIB3431-020-P1-K1-D5
Method
                  BLASTX
NCBI GI
                   q3047117
BLAST score
                   740
E value
                   1.0e-78
Match length
                   144
% identity
                   97
NCBI Description
                   (AF058919) similar to ATP-dependent RNA helicases
                   [Arabidopsis thaliana]
Seq. No.
                   398934
Seq. ID
                  LIB3431-020-P1-K1-D7
Method
                  BLASTX
NCBI GI
                   q1617206
BLAST score
                  180
E value
                   3.0e-13
Match length
                   49
% identity
NCBI Description
                   (Z72489) CP12 [Pisum sativum]
Seq. No.
                   398935
Seq. ID
                  LIB3431-020-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                   632
E value
                   5.0e-66
                  137
Match length
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf_1707316A chlorophyll a/b binding protein 1
                   [Oryza satīva]
```

```
LIB3431-020-P1-K1-D9
Seq. ID
Method
                    BLASTX
                    q2582822
NCBI GI
BLAST score
                    458
E value
                    1.0e-45
Match length
                    108
% identity
                    80
NCBI Description
                    (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
                    Protein of 32kDa) [Solanum tuberosum]
Seq. No.
                    398937
Seq. ID
                   LIB3431-020-P1-K1-E1
Method
                   BLASTX
NCBI GI
                    g4886307
BLAST score
                    543
E value
                    1.0e-55
Match length
                    123
% identity
                    87
                    (AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase
NCBI Description
                    [Arabidopsis thaliana]
                    398938
Seq. No.
Seq. ID
                   LIB3431-020-P1-K1-E10
Method
                   BLASTX
NCBI GI
                    q2570515
BLAST score
                    219
E value
                    1.0e-17
Match length
                    47
                    91
% identity
NCBI Description
                    (AF022740) glycolate oxidase [Oryza sativa]
                    398939
Seq. No.
Seq. ID
                   LIB3431-020-P1-K1-E11
Method
                   BLASTX
NCBI GI
                    q320618
BLAST score
                    607
E value
                    4.0e-63
Match length
                    133
                    87
% identity
                    chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
Seq. No.
                    398940
Seq. ID
                   LIB3431-020-P1-K1-E12
Method
                   BLASTX
NCBI GI
                    g132105
BLAST score
                    759
E value
                    6.0e-81
Match length
                   139
% identity
                    100
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
```

precursor (clone pOSSS1139) - rice >gi_218208_dbj BAA00538_

BLAST score

559

(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

```
Seq. No.
                   398941
Seq. ID
                  LIB3431-020-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g3345477
BLAST score
                   491
E value
                   2.0e-49
Match length
                   140
                   69
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                   398942
Seq. No.
Seq. ID
                  LIB3431-020-P1-K1-E3
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   35
E value
                   6.0e-10
Match length
                   35
% identity
                   100
NCBI Description
                  Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   398943
Seq. ID
                  LIB3431-020-P1-K1-E5
Method
                  BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
                   1.0e-19
E value
Match length
                   44
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                   398944
Seq. No.
Seq. ID
                  LIB3431-020-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                   417
E value
                  7.0e-41
Match length
                  121
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                  398945
Seq. No.
Seq. ID
                  LIB3431-020-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g1835731
```

% identity

```
2.0e-57
E value
                  106
Match length
% identity
                  100
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                  398946
Seq. No.
Seq. ID
                  LIB3431-020-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  625
                  3.0e-65
E value
Match length
                  117
                  99
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  398947
Seq. No.
                  LIB3431-020-P1-K1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2565305
                  605
BLAST score
E value
                  5.0e-63
                  119
Match length
% identity
                  96
                   (AF024589) glycine decarboxylase P subunit [Hordeum sp. x
NCBI Description
                  Triticum sp.]
                  398948
Seq. No.
                  LIB3431-020-P1-K1-F1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3789951
BLAST score
                  188
E value
                  1.0e-101
Match length
                  380
% identity
                  96
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
Seq. No.
                  398949
Seq. ID
                  LIB3431-020-P1-K1-F11
                  BLASTX
Method
NCBI GI
                  g1661160
BLAST score
                  523
E value
                  3.0e-53
Match length
                  115
                  85
% identity
                  (U74295) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  398950
Seq. No.
Seq. ID
                  LIB3431-020-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g728744
BLAST score
                  338
E value
                  1.0e-54
Match length
                  152
```

Match length

```
NCBI Description AUXIN-INDUCED PROTEIN PCNT115 >gi 100305 pir S16390
                   auxin-induced protein - common tobacco
                   >gi 19799 emb CAA39708 (X56267) auxin-induced protein
                   [Nicotiana tabacum]
                   398951
Seq. No.
Seq. ID
                   LIB3431-020-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   g3789952
BLAST score
                   788
E value
                   2.0e-84
Match length
                   152
% identity
                   96
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
                   398952
Seq. No.
Seq. ID
                   LIB3431-020-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g115772
BLAST score
                   211
E value
                   2.0e-17
                   57
Match length
                   77
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-1) (LHCP) | >gi_82460_pir__S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108_
                   (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                   [Oryza sativa]
                   398953
Seq. No.
                   LIB3431-020-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g6002055
BLAST score
                   634
E value
                   3.0e-66
Match length
                   151
                   77
% identity
                   (AJ249794) lipoxygenase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   398954
                   LIB3431-020-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3345477
BLAST score
                   316
E value
                   5.0e-29
Match length
                   59
                   100
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                   398955
Seq. No.
                   LIB3431-020-P1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131225
BLAST score
                   570
E value
                   7.0e-59
```

Match length

```
% identity
                   93
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi 100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  398956
Seq. ID
                  LIB3431-020-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                   9.0e-20
Match length
                   44
                  100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  398957
Seq. No.
                  LIB3431-020-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462763
                  322
BLAST score
E value
                   2.0e-44
Match length
                  124
                   79
% identity
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                  398958
                  LIB3431-020-P1-K1-G12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g871931
BLAST score
                   490
E value
                  2.0e-49
Match length
                  125
                  80
% identity
NCBI Description
                   (D30763) ferredoxin [Oryza sativa]
                  398959
Seq. No.
                  LIB3431-020-P1-K1-G6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g5670155
BLAST score
                  43
E value
                   4.0e-15
Match length
                  75
% identity
                  89
                  Oryza sativa subsp. japonica BAC clone 34K24, complete
NCBI Description
                  sequence
Seq. No.
                  398960
                  LIB3431-020-P1-K1-G7
Seq. ID
Method
                  BLASTN
                  g21810
NCBI GI
BLAST score
                  38
E value
                  9.0e-12
```

```
100
% identity
NCBI Description
                    T.aestivum mRNA for heat shock protein 26.6B
                    398961
Seq. No.
                    LIB3431-020-P1-K1-H1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g2072555
BLAST score
                    237
                    6.0e-20
E value
Match length
                    44
                    100
% identity
                    (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                    >gi 6103441 gb_AAF03603.1 (AF147786) metallothionein-like
                    protein [Oryza sativa]
                    398962
Seq. No.
Seq. ID
                    LIB3431-020-P1-K1-H10
Method
                    BLASTX
NCBI GI
                    g3915131
BLAST score
                    592
E value
                    2.0e-61
Match length
                    114
% identity
                    100
                    THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)
NCBI Description
                    >gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza
sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin
                    h [Oryza sativa] >gi 1930072 (U92541) thioredoxin h [Oryza
                    satival
Seq. No.
                    398963
Seq. ID
                    LIB3431-020-P1-K1-H11
Method
                    BLASTX
NCBI GI
                    q115787
BLAST score
                    529
E value
                    5.0e-54
Match length
                    121
% identity
                    88
                    CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                    CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
Seq. No.
                    398964
Seq. ID
                    LIB3431-020-P1-K1-H2
Method
                    BLASTX
NCBI GI
                    q132105
BLAST score
                    185
E value
                    9.0e-14
Match length
                    105
% identity
                    48
NCBI Description
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
```

carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)

NCBI Description

```
carboxylase S [Oryza sativa]
                   398965
Seq. No.
Seq. ID
                  LIB3431-020-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   g4583546
BLAST score
                   145
                   6.0e-09
E value
                  -70
Match length
% identity
                   (AJ010819) GrpE protein [Arabidopsis thaliana]
NCBI Description
                   398966
Seq. No.
Seq. ID
                  LIB3431-020-P1-K1-H4
Method
                  BLASTX
NCBI GI
                   g2270994
BLAST score
                   231
E value
                   4.0e-19
Match length
                   125
% identity
                   42
                   (AF004809) Ca+2-binding EF hand protein [Glycine max]
NCBI Description
Seq. No.
                   398967 ...
                  LIB3431-020-P1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4097587
BLAST score
                   250
E value
                   3.0e-21
Match length
                   69
                   72
% identity
NCBI Description
                   (U64926) NTGP5 [Nicotiana tabacum]
Seq. No.
                   398968
Seq. ID
                  LIB3431-020-P1-K1-H7
Method
                  BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   9.0e-20
Match length
                   44
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                   398969
Seq. ID
                  LIB3431-020-P1-N1-A2
Method
                  BLASTN
NCBI GI
                   q3342030
BLAST score
                  85
E value
                   7.0e-40
Match length
                   109
% identity
```

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375 prf _1508256A ribulose bisphosphate

complete sequence

Joinvillea ascendens 18S small subunit ribosomal RNA gene,

```
398970
Seq. No.
                   LIB3431-020-P1-N1-A8
Seq. ID
                   BLASTX.
Method
NCBI GI
                   g5932555
                   287
BLAST score
E value
                   1.0e-25
Match length
                   87
% identity
                    66
                    (AC009465) putative ribose 5-phosphate isomerase
NCBI Description
                    [Arabidopsis thaliana]
                   398971
Seq. No.
Seq. ID
                   LIB3431-020-P1-N1-B10
Method
                   BLASTX
NCBI GI
                   g421916
                   190
BLAST score
E value
                   2.0e-14
                   35
Match length
% identity
                   100
                   chlorophyll a/b-binding protein - English ivy (fragment)
>gi_12582_emb_CAA48410_ (X68333) light harvesting
NCBI Description
                   chlorophyll a /b binding protein [Hedera helix]
Seq. No.
                   398972
Seq. ID
                   LIB3431-020-P1-N1-B5
Method
                   BLASTX
NCBI GI
                   q417260
BLAST score
                   313
E value
                    7.0e-29
Match length
                   78
% identity
                   76
NCBI Description
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
                   lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                   light-regulated gene [Oryza sativa]
Seq. No.
                   398973
Seq. ID
                   LIB3431-020-P1-N1-B6
Method
                   BLASTX
NCBI GI
                   q4063821
BLAST score
                   192
E value
                   2.0e-14
Match length
                   67
% identity
NCBI Description
                    (AB015204) plastidic ATP sulfurylase [Oryza sativa]
                   398974
Seq. No.
Seq. ID
                   LIB3431-020-P1-N1-B8
Method
                   BLASTX
NCBI GI
                   q4138290
BLAST score
                   307
E value
                   4.0e-28
Match length
                   60
% identity
                   100
NCBI Description
                   (AJ005841) thioredoxin M [Oryza sativa]
Seq. No.
                   398975
Seq. ID
                   LIB3431-020-P1-N1-C11
```

```
Method
                  BLASTX
NCBI GI
                  g1346875
BLAST score
                  251
                  2.0e-21
E value
Match length
                  79
% identity
                  57
NCBI Description
                  PHOTOSYSTEM II REACTION CENTER W PROTEIN
                  >gi_1185169_emb_CAA91652_ (Z67753) PSII, protein W, 13 kDa
                   [Odontella sinensis]
                  398976
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-C2
Method
                  BLASTN
NCBI GI
                  g20181
BLAST score
                  63
                  6.0e-27
E value
Match length
                  91
% identity
                  92
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
Seq. No.
                  398977
                  LIB3431-020-P1-N1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3789951
BLAST score
                  223
E value
                  1.0e-122
Match length
                  358
                  90
% identity
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein presursor
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
Seq. No.
                  398978
Seq. ID
                  LIB3431-020-P1-N1-C8
Method
                  BLASTN
NCBI GI
                  g2072554
                                                         244-
BLAST score
                  269
E value
                  1.0e-149
Match length
                  357
% identity
                  94
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  398979
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-C9
Method
                  BLASTN
NCBI GI
                  g1519250
BLAST score
                  212
E value
                  1.0e-115
Match length
                  323
% identity
                  91
NCBI Description Oryza sativa GF14-c protein mRNA, complete cds
                  398980
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-D11
Method
                  BLASTX
```

```
NCBI GI
                  g3915131
BLAST score
                  360
                   4.0e-34
E value
                  74
Match length
                  96
% identity
NCBI Description
                  THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)
                  >gi 426442 dbj BAA04864 (D21836) thioredoxin h [Oryza
                  satīva] >gī 454882 dbj BAA05546 (D26547) rice thioredoxin
                  h [Oryza sativa] >gi 1930072 (U92541) thioredoxin h [Oryza
                  satival
                  398981
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-D3
Method
                  BLASTN
NCBI GI
                  g3695004
BLAST score
                  38
E value
                  1.0e-11
                  54
Match length
% identity
                  93
                  Zea mays pyruvate dehydrogenase kinase isoform 2 mRNA,
NCBI Description
                  nuclear gene encoding mitochondrial protein, complete cds
Seq. No.
                  398982
                  LIB3431-020-P1-N1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                  163
E value
                  2.0e-21
Match length
                  63
% identity
                  80
NCBI Description
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
Seq. No.
                  398983
Seq. ID
                  LIB3431-020-P1-N1-D8
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  160
E value
                  7.0e-11
Match length
                  31
% identity
NCBI Description
                  (272488) CP12 [Nicotiana tabacum]
                  398984
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-D9
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  483
E value
                  1.0e-48
Match length
                  100
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding.
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

Seq. No.

NCBI GI

```
Seq. ID
                  LIB3431-020-P1-N1-E1
                  BLASTN
Method
                  g218171
NCBI GI
BLAST score
                  69
                  2.0e-30
E value
Match length
                  167
% identity
                  86
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                  a/b binding protein of photosystem II (LHCPII), complete
                  398986
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-E11
                  BLASTN
Method
                  g2570514
NCBI GI
BLAST score
                  266
E value
                  1.0e-148
Match length
                  326
% identity
                  98
NCBI Description
                  Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
Seq. No.
                  398987
                  LIB3431-020-P1-N1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3036946
BLAST score
                  319
E value
                  2.0e-29
Match length
                  61
                  100
% identity
NCBI Description
                   (AB012637) light harvesting chlorophyll a/b-binding protein
                  [Nicotiana sylvestris]
                  398988
Seq. No.
                  LIB3431-020-P1-N1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4886307
BLAST score
                  480
E value
                  3.0e-48
                  108
Match length
% identity
                  85
NCBI Description
                   (AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase
                  [Arabidopsis thaliana]
                  398989
Seq. No.
                  LIB3431-020-P1-N1-E3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3345476
BLAST score
                  310
E value
                  1.0e-174
Match length
                  362
% identity
                  96
NCBI Description
                  Oryza sativa gene for carbonic anhydrase, complete cds
Seq. No.
                  398990
                  LIB3431-020-P1-N1-E5
Seq. ID
Method
                  BLASTX
```

g5916444

Seq. No.

```
BLAST score
                   289
                   8.0e-26
E value
                   89
Match length
                   57
% identity
                   (ACO07633) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   398991
                  LIB3431-020-P1-N1-E6
Seq. ID
                  BLASTN
Method
NCBI GI
                   g6103440
BLAST score
                   54
                   2.0e-21
E value
Match length
                   94
                   89
% identity
                  Oryza sativa metallothionein-like protein (ML2) mRNA,
NCBI Description
                   complete cds
                   398992
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-E8
Method
                  BLASTX
NCBI GI
                   g1835731
BLAST score
                   402
E value
                   4.0e-39
                   92
Match length
% identity
                   85
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                   398993
Seq. No.
                  LIB3431-020-P1-N1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g671740
BLAST score
                   473
E value
                   1.0e-47
Match length
                   86
% identity
                   100
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
Seq. No.
                   398994
                  LIB3431-020-P1-N1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g132105
BLAST score
                   360
E value
                   1.0e-48
Match length
                   98
                   98
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi 68094_pir__RKRZS9
                  ribulose-bisphosphate carboxy\overline{l}ase (\overline{EC} 4\overline{.1}.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

```
Seq. ID
                  LIB3431-020-P1-N1-F12
Method
                  BLASTX
NCBI GI
                  g115800
BLAST score
                  180
E value
                  3.0e-13
Match length
                  45
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 3 PRECURSOR (LHCII TYPE I
NCBI Description
                  %CAB-3) (LHCP) >gi 81771 pir S01962 chlorophyll a/b-binding
                  protein 3 precursor - soybean >gi 18552 emb CAA31419
                  (X12981) chlorophyll a/b binding preprotein (AA - 32 to
                  231) [Glycine max]
                  398996
Seq. No.
                  LIB3431-020-P1-N1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3789951
BLAST score
                  154
E value
                  4.0e-81
Match length
                  348
                  95
% identity
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  398997
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-F3
Method
                  BLASTN
NCBI GI
                  g3789951
BLAST score
                  69
E value
                  2.0e-30
Match length
                  121
                  89
% identity
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  398998
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-F4
                  BLASTX
Method
NCBI GI
                  g3036951
BLAST score
                  211
                  3.0e-32
E value
Match length
                  78
% identity
NCBI Description
                  (AB012639) light harvesting chlorophyll a/b-binding protein
                  [Nicotiana sylvestris]
                  398999
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-F5
Method
                  BLASTX
NCBI GI
                  g1654140
BLAST score
                  355
E value
                  7.0e-35
Match length
                  119
% identity
                  66
                 (U37840) lipoxygenase [Lycopersicon esculentum]
NCBI Description
```

```
399000
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-F6
Method
                  BLASTX
NCBI GI
                  g4079798
BLAST score
                  153
E value
                   3.0e-10
Match length
                   32
% identity 🛞
NCBI Description
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                   sativa]
Seq. No.
                   399001
                  LIB3431-020-P1-N1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g710308
                   381
BLAST score
E value
                   1.0e-36
                  79
Match length
% identity
                   86
                  (U11693) victorin binding protein [Avena sativa]
NCBI Description
                   399002
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-F9
Method
                  BLASTX
NCBI GI
                   q3345477
BLAST score
                  204
                   7.0e-16
E value
                   46
Match length
% identity
                   80
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                   399003
Seq. No.
                  LIB3431-020-P1-N1-G10
Seq. ID -
Method
                  BLASTX
NCBI GI
                   g2462750
BLAST score
                  269
                   1.0e-23
E value ·
Match length
                  71
                   70
% identity
NCBI Description
                   (AC002292) Highly similar to auxin-induced protein
                   (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                   399004
Seq. ID
                  LIB3431-020-P1-N1-G11
Method
                  BLASTX
NCBI GI
                   g2072555
BLAST score
                  237
                   1.0e-19
E value
Match length
                   44
% identity
                   100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                   399005
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-G12
```

NCBI GI

```
Method
                  BLASTX
NCBI GI
                  g2462762
BLAST score
                  341
                  6.0e-32
E value
                  85
Match length
                  73
% identity
NCBI Description
                   (AC002292) Highly similar to auxin-induced protein
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                  399006
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-G7
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  187
                  5.0e-14
E value
Match length
                  49
                  71
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi 100605 pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  399007
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-H10
Method
                  BLASTX
NCBI GI
                  g871931
                  220
BLAST score
                  8.0e-18
E value
Match length
                  55
% identity
NCBI Description
                 (D30763) ferredoxin [Oryza sativa]
                  399008
Seq. No.
                  LIB3431-020-P1-N1-H12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q20181
BLAST score
                  119
                  3.0e-60
E value
                  139
Match length
                  96
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
                  399009
Seq. No.
Seq. ID
                  LIB3431-020-P1-N1-H5
Method
                  BLASTN
NCBI GI
                  q505134
BLAST score
                  185
E value
                  1.0e-100
                  217
Match length
                  97
% identity
NCBI Description Rice mRNA for ferredoxin, complete cds
Seq. No.
                  399010
Seq. ID
                  LIB3431-020-P1-N1-H7
Method
                  BLASTX
```

g1617197

Seq. ID

```
BLAST score
                   213
                   7.0e-19
E value
Match length
                   67
                   73
% identity
NCBI Description
                   (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                   399011
                   LIB3431-020-P1-N1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   213
                   7.0e-17
E value
Match length
                   44
% identity
                   91
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                   399012
Seq. ID
                  LIB3431-021-P1-K1-A1
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   35
E value
                   6.0e-10
Match length
                   35
% identity
                   100
NCBI Description
                  Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   399013
Seq. ID
                   LIB3431-021-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   g1709846
BLAST score
                   235
E value
                   2.0e-19
Match length
                   134
% identity
                   PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi 706853 (U04336)
NCBI Description
                   22 kDa component of photosystem II [Lycopersicon
                  esculentum]
Seq. No.
                   399014
Seq. ID
                   LIB3431-021-P1-K1-A11
Method
                  BLASTX
NCBI GI
                   q1350742
BLAST score
                  176
E value
                   1.0e-12
Match length
                   46
% identity
NCBI Description
                  PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi_1086831 (U41264)
                  coded for by C. elegans cDNA yk64g10.5; coded for by C.
                  elegans cDNA yk51f3.5; coded for by C. elegans cDNA
                  yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for
                  by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA
                  yk64g1
Seq. No.
                  399015
```

LIB3431-021-P1-K1-A12

Seq. No.

```
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  304
                  1.0e-27
E value
Match length
                  76
% identity
                  76
                  (Z72488) CP12 [Nicotiana tabacum]
NCBI Description
                  399016
Seq. No.
                                                                        7.
Seq. ID
                  LIB3431-021-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q4455169
BLAST score
                  180
E value
                  4.0e-13
                  71
Match length
                  45
% identity
                  (AL035521) putative aldehyde dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  399017
Seq. ID
                  LIB3431-021-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g6016678
BLAST score
                  324
E value
                  6.0e-30
               ----77
Match length
% identity
                  (AC009991) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  399018
Seq. ID
                  LIB3431-021-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g131388
BLAST score
                  417
E value
                  6.0e-41
Match length
                  137
                  65
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
                  33kDa oxygen evolving protein of photosystem II [Triticum
                  aestivum]
Seq. No.
                  399019
Seq. ID
                  LIB3431-021-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g4455169
BLAST score
                  235
E value
                  2.0e-19
Match length
                  71
% identity
                  (AL035521) putative aldehyde dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
```

```
LIB3431-021-P1-K1-A8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1632831
BLAST score
                   315
E value
                   7.0e-36
Match length
                   139
% identity
                   58
NCBI Description
                  (Z49698) orf [Ricinus communis]
                   399021
Seq. No.
Seq. ID
                   LIB3431-021-P1-K1-A9
                   BLASTX
Method
NCBI GI
                   q6016678
BLAST score
                   184
E value
                   1.0e-13
Match length
                   63
% identity
                   54
NCBI Description
                   (AC009991) unknown protein [Arabidopsis thaliana]
Seq. No.
                   399022
                   LIB3431-021-P1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4689380
BLAST score
                   424
E value
                   8.0e-42
Match length
                   121
% identity
                   70
                   (AF139465) LHCII type III chlorophyll a/b binding protein
NCBI Description
                   [Vigna radiata]
                   399023
Seq. No.
                   LIB3431-021-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3377805
BLAST score
                   406
E value
                   1.0e-39
Match length
                   154
% identity
NCBI Description
                   (AF075597) contains similarity to several apoptosis or
                   programmed cell death proteins such as rat apoptosis
                   protein RP-8 (GB:M80601) [Arabidopsis thaliana]
                   >qi 3912928 gb AAC78712.1 (AF001308) putative zinc finger
                   protein [Arabidopsis thaliana]
Seq. No.
                   399024
Seq. ID
                   LIB3431-021-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   657
E value
                   5.0e-69
Match length
                   140
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
```

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

Seq. No. 399025

Seq. ID LIB3431-021-P1-K1-B12

Method BLASTX
NCBI GI g2306981
BLAST score 467
E value 1.0e-46
Match length 84
% identity 96

NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No. 399026

Seq. ID LIB3431-021-P1-K1-B2

Method BLASTX
NCBI GI g5762457
BLAST score 652
E value 2.0e-68
Match length 123
% identity 98

NCBI Description (AF176040) ubiquitin-conjugating enzyme UBC2

[Mesembryanthemum crystallinum]

Seq. No. 399027

Seq. ID LIB3431-021-P1-K1-B4-

Method BLASTX
NCBI GI g131225
BLAST score 404
E value 1.0e-48
Match length 116
% identity 81

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT

V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein

precursor - barley >gi 167087 (M61146) photosystem I

hydrophobic protein [Hordeum vulgare]

Seq. No. 399028

Seq. ID LIB3431-021-P1-K1-B6

Method BLASTX
NCBI GI g4689380
BLAST score 678
E value 2.0e-71
Match length 137
% identity 90

NCBI Description (AF139465) LHCII type III chlorophyll a/b binding protein

[Vigna radiata]

Seq. No. 399029

Seq. ID LIB3431-021-P1-K1-B7

Method BLASTX
NCBI GI g115794
BLAST score 724
E value 7.0e-77
Match length 142

E value

Match length

8.0e-19

```
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
                   III CAB-13) >gi 72748 pir CDTO33 chlorophyll a/b-binding
                  protein type III precursor (cab-13) - tomato
                  >gi 19277 emb CAA42818 (X60275) LHCII type III
                   [Lycopersicon esculentum]
Seq. No.
                   399030
Seq. ID
                  LIB3431-021-P1-K1-B8
Method
                  BLASTN
NCBI GI
                   q20181
BLAST score
                   192
E value
                   1.0e-104
Match length
                   196
                   99
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
Seq. No.
                   399031
Seq. ID
                   LIB3431-021-P1-K1-B9
Method
                  BLASTN
NCBI GI
                   g218209
BLAST score
                   117
E value
                   3.0e-59
Match length
                   157
% identity
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
Seq. No.
                   399032
Seq. ID
                  LIB3431-021-P1-K1-C1
Method
                  BLASTN
NCBI GI
                   g2062705
BLAST score
                   35
E value
                   5.0e-10
Match length
                   35
                   100
% identity
NCBI Description
                  Human butyrophilin (BTF5) mRNA, complete cds
                   399033
Seq. No.
Seq. ID
                  LIB3431-021-P1-K1-C10
Method
                  BLASTX
NCBI GI
                   q5106775
BLAST score
                   545
E value
                   5.0e-56
Match length
                   109
% identity
NCBI Description
                   (AF067732) ribosomal protein S12 [Hordeum vulgare]
                   399034
Seq. No.
Seq. ID
                  LIB3431-021-P1-K1-C11
Method
                  BLASTX
NCBI GI
                   q2289907
BLAST score
                  229
```

BLAST score

425

```
% identity
                  (AC002397) C2F [Mus musculus]
NCBI Description
                   399035
Seq. No.
                   LIB3431-021-P1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g129916
BLAST score
                   481
E value
                   2.0e-48
Match length
                   152
                   67
% identity
                   PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911 pir TVWTGY
NCBI Description
                   phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                   >gi 21835 emb CAA33302 (X15232) phosphoglycerate kinase
                   (AA 1 - 401) [Triticum aestivum]
                   399036
Seq. No.
Seq. ID
                   LIB3431-021-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   8.0e-20
Match length
                   44
% identity
                   100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   399037
Seq. No.
Seq. ID
                   LIB3431-021-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   666
                   5.0e-70
E value
Match length
                   146
% identity
                   90
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   399038
Seq. No.
Seq. ID
                   LIB3431-021-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g3885882
BLAST score
                   492
E value
                   9.0e-50
                   94
Match length
% identity
                   (AF093629) inorganic pyrophosphatase [Oryza sativa]
NCBI Description
Seq. No.
                   399039
                   LIB3431-021-P1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q417260
```

```
7.0e-42
E value
Match length
                   122
                   70
% identity
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                   lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                   light-regulated gene [Oryza sativa]
Seq. No.
                   399040
Seq. ID
                   LIB3431-021-P1-K1-C7
                   BLASTN
Method
NCBI GI
                   g6015437
BLAST score
                   38
E value
                   9.0e-12
Match length
                   38
                   100
% identity
                   Homo sapiens PEX1 mRNA, complete cds
NCBI Description
Seq. No.
                   399041
Seq. ID
                   LIB3431-021-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g2407281
BLAST score
                   423
E value
                   1.0e-41
Match length
                   129
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq. No.
                   399042
Seq. ID
                   LIB3431-021-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   623
E value
                   5.0e-65
Match length
                   134
% identity
                   88
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
```

Seq. No. 399043

Seq. ID LIB3431-021-P1-K1-D10

Method BLASTX
NCBI GI 94336608
BLAST score 190
E value 9.0e-28
Match length 109
% identity 71

NCBI Description (AF099111) sigma factor; Sig2 [Zea mays]

Seq. No. 399044

Seq. ID

```
Seq. ID
                   LIB3431-021-P1-K1-D11
                   BLASTX
Method
NCBI GI
                   q4980489
BLAST score
                   174
                   2.0e-12
E value
Match length
                   100
% identity
                   (AE001689) muconate cycloisomerase [Thermotoga maritima]
NCBI Description
                   399045
Seq. No.
Seq. ID
                   LIB3431-021-P1-K1-D2
Method
                   BLASTX
                   q6015065
NCBI GI
BLAST score
                   704
                   1.0e-74
E value
                   144
Match length
                   91
% identity
NCBI Description
                   ELONGATION FACTOR 2 (EF-2) >gi 2369714 emb CAB09900_
                   (Z97178) elongation factor 2 [Beta vulgaris]
                   399046
Seq. No.
                   LIB3431-021-P1-K1-D3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3885886
BLAST score
                   666
E value
                   4.0e-70
Match length
                   130
% identity
                   100
NCBI Description
                   (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
                   399047
Seq. No.
Seq. ID
                   LIB3431-021-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g125580
BLAST score
                   611
E value
                   1.0e-63
                   137
Match length
                   87
% identity
                   PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >gi_100839_pir__S15743 phosphoribulokinase (EC 2.7.1.19) - wheat >gi_5924030_emb_CAB56544.1_ (X51608)
                   phosphoribulokinase [Triticum aestivum]
Seq. No.
                   399048
Seq. ID
                   LIB3431-021-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   g2494320
BLAST score
                   252
E value
                   2.0e-21
Match length
                   58
                   78
% identity
NCBI Description
                   EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)
                   >gi 1806575 emb CAA67868 (X99517) Eukaryotic initiation
                   factor-5 [Zea mays]
                   399049
Seq. No.
```

LIB3431-021-P1-K1-D6

```
BLASTX
Method
NCBI GI
                   g482311
BLAST score
                   571
E value
                   4.0e-59
Match length
                   115
                   97
% identity
NCBI Description
                  photosystem II oxygen-evolving complex protein 1 - rice
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                   complex protein 1 [Oryza sativa]
                   399050
Seq. No.
Seq. ID
                  LIB3431-021-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   q1346109
BLAST score
                   318
E value
                   3.0e-29
Match length
                   59
                   100
% identity
NCBI Description
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                   PROTEIN (GPB-LR) (RWD) >gi 540535 dbj BAA07404 (D38231)
                   RWD [Oryza sativa]
Seq. No.
                   399051
                   LIB3431-021-P1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q131225
BLAST score
                   578
E value
                   1.0e-59
Match length
                   124
                   90
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                   precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                   399052
Seq. ID
                   LIB3431-021-P1-K1-D9
Method
                  BLASTX
NCBI GI
                   q4467099
BLAST score
                   482
E value
                   2.0e-48
Match length
                   119
% identity
                   (AL035538) glycine hydroxymethyltransferase like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   399053
Seq. ID
                  LIB3431-021-P1-K1-E1
Method
                  BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   9.0e-20
Match length
                   44
% identity
                   100
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
```

```
399054
Seq. No.
                  LIB3431-021-P1-K1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1835731
BLAST score
                   484
E value
                  1.0e-48
Match length
                  93
% identity
NCBI Description
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  399055
Seq. No.
Seq. ID
                  LIB3431-021-P1-K1-E11
                  BLASTX
Method
NCBI GI
                  g2072555
BLAST score
                  237
                   9.0e-20
E value
Match length
                   44
% identity
                  100
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  399056
Seq. No.
Seq. ID
                  LIB3431-021-P1-K1-E12
Method.
                  BLASTX
NCBI GI
                  q2499497
BLAST score
                   689
E value
                   9.0e-73
Match length
                  144
                   97
% identity
                  PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 1161600 emb CAA88841 (Z48977) phosphoglycerate kinase
                   [Nicotiana tabacum]
Seq. No.
                  399057
Seq. ID
                  LIB3431-021-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q3063453
BLAST score
                  207
E value
                  1.0e-18
Match length
                  61
% identity
NCBI Description
                   (AC003981) F22013.15 [Arabidopsis thaliana]
                  399058
Seq. No.
Seq. ID
                  LIB3431-021-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  q1835731
BLAST score
                  580
E value
                  5.0e-60
Match length
                  123
% identity
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  399059
Seq. No.
Seq. ID
                  LIB3431-021-P1-K1-E5
```

Method

BLASTX

```
BLASTN
Method
NCBI GI
                  g2072554
BLAST score
                  330
                  0.0e+00
E value
Match length
                  330
                  100
% identity
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                  399060
Seq. No.
Seq. ID
                  LIB3431-021-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q3914603
BLAST score
                   671
E value
                   1.0e-70
                  131
Match length
                   99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
                  399061
Seq. No.
                  LIB3431-021-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2582822
BLAST score
                   462
E value
                   3.0e-46
                  128
Match length
% identity
                  70
                   (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
NCBI Description
                  Protein of 32kDa) [Solanum tuberosum]
Seq. No.
                  399062
Seq. ID
                  LIB3431-021-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g3789952
BLAST score
                  177
E value
                   7.0e-13
Match length
                  32
% identity
                  100
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
                  399063
Seq. No.
Seq. ID
                  LIB3431-021-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g551047
BLAST score
                  222
E value
                  4.0e-18
Match length
                  43
% identity
NCBI Description
                  (X79277) type II LHCI [Lolium temulentum]
Seq. No.
                  399064
                  LIB3431-021-P1-K1-F3
Seq. ID
```

51000

.

Match length

```
q2130069
NCBI GI
                   750
BLAST score
                   6.0e-80
E value
                   136
Match length
                   99
% identity
NCBI Description
                   catalase (EC 1.11.1.6) catA - rice
                   >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                   399065
Seq. ID
                  LIB3431-021-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g4539423
BLAST score
                   487
                   3.0e-49
E value
Match length
                  126
                   75
% identity
                   (AL049171) pyrophosphate-dependent phosphofructo-1-kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   399066
Seq. ID
                   LIB3431-021-P1-K1-F6
Method
                  BLASTX
NCBI GI
                   q2570515
BLAST score
                   447
E value
                   2.0e-68
Match length
                  146
                   96
% identity
NCBI Description
                   (AF022740) glycolate oxidase [Oryza sativa]
Seq. No.
                   399067
                  LIB3431-021-P1-K1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3789954
BLAST score
                   387
E value
                   2.0e-37
Match length
                  98
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
Seq. No.
                   399068
                  LIB3431-021-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                   448
E value
                   2.0e-44
Match length
                  96
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                   399069
Seq. No.
                  LIB3431-021-P1-K1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  36
E value
                  1.0e-10
```

NCBI Description

```
% identity
                   100
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
                  399070
Seq. No.
Seq. ID
                  LIB3431-021-P1-K1-G1
Method
                  BLASTN
NCBI GI
                  g304219
BLAST score
                   53
E value
                   6.0e-21
Match length
                   129
% identity
                   85
                  Hordeum vulgare chloroplast photosystem I PSK-I subunit
NCBI Description
                  mRNA, complete cds
                   399071
Seq. No.
                  LIB3431-021-P1-K1-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                   g20262
BLAST score
                  95
                   9.0e-46
E value
                  190
Match length
% identity
                  88
NCBI Description O.sativa light-induced mRNA
Seq. No.
                   399072
                  LIB3431-021-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                   489
E value
                   2.0e-54
Match length
                  131
% identity
                   81
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir__A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
Seq. No.
                  399073
                  LIB3431-021-P1-K1-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  35
E value
                   6.0e-10
Match length
                  35
% identity
                  100
NCBI Description
                  Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  399074
Seq. ID
                  LIB3431-021-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q3800878
BLAST score
                  543
E value
                  1.0e-55
Match length
                  150
% identity
```

(AF096281) threonine dehydratase/deaminase [Arabidopsis



thaliana]

```
Seq. No.
Seq. ID
                   LIB3431-021-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   404
E value
                   3.0e-42
Match length
                   117
                   83
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   399076
Seq. No.
Seq. ID
                   LIB3431-021-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g4585882
                   459
BLAST score
E value
                   4.0e-46
                   97
Match length
% identity
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   399077
Seq. ID
                   LIB3431-021-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g4581114
BLAST score
                   295
E value
                   1.0e-26
Match length
                   63
% identity
NCBI Description
                   (AC005825) putative HesB-like protein; required for
                   efficient nitrogen fixation in Cyanobacteria [Arabidopsis
                   thaliana]
Seq. No.
                   399078
Seq. ID
                   LIB3431-021-P1-K1-G8
Method
                   BLASTX -
NCBI GI
                   g5881940
BLAST score
                   259
E value
                   2.0e-22
Match length
                   143
% identity
NCBI Description
                   (AL117387) putative secreted protein [Streptomyces
                   coelicolor A3(2)]
                   399079
Seq. No.
Seq. ID
                   LIB3431-021-P1-K1-H1
Method ·
                   BLASTN
NCBI GI
                   g11957
BLAST score
                   198
E value
                   1.0e-107
Match length
                   202
```

```
% identity
NCBI Description Rice complete chloroplast genome
                   399080
Seq. No.
Seq. ID
                   LIB3431-021-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   q4973254
BLAST score
                   446
E value
                   3.0e-44
Match length
                   103
% identity
                   (AF144386) thioredoxin f2 [Arabidopsis thaliana]
NCBI Description
                   399081
Seq. No.
                   LIB3431-021-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g320617
BLAST score
                   509
                   8.0e-52
E value
Match length
                   97
                   99
% identity
NCBI Description
                   chlorophyll a/b-binding protein II precursor - rice
                   >qi 227612 prf 1707316B chlorophyll a/b binding protein 2
                   [Oryza sativa]
                   399082 -
Seq. No.
Seq. ID
                   LIB3431-021-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   g2501190
BLAST score
                   655
E value
                   8.0e-69
                   136
Match length
                   92
% identity
                   THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
NCBI Description
                   >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                   [Zea mays]
                   399083
Seq. No.
Seq. ID
                   LIB3431-021-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g3914603
BLAST score
                   607
                   3.0e-63
E value
Match length
                   117
% identity
                   100
                   RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                   CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                   activase [Oryza sativa]
                   399084
Seq. No.
Seq. ID
                   LIB3431-021-P1-K1-H5
                   BLASTX
Method
NCBI GI
                   g1352468
BLAST score
                   296
E value
                   8.0e-27
```

```
Match length
                  67
                  81
% identity
                  BETA-FRUCTOFURANOSIDASE 1 PRECURSOR (SUCROSE-6-PHOSPHATE
NCBI Description
                  HYDROLASE 1) (INVERTASE 1) >gi 1122439 (U16123) invertase
                  [Zea mays]
Seq. No.
                  399085
Seq. ID
                  LIB3431-021-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q131225
BLAST score
                  570
                  8.0e-59
E value
                  124
Match length
                  90
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  399086
Seq. ID
                  LIB3431-021-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  425
E value
                  8.0e-42
Match length
                  121
% identity
                  68
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
Seq. No.
                  399087
Seq. ID
                  LIB3431-021-P1-N1-A10
Method
                  BLASTX
NCBI GI
                  q6103011
                  220
BLAST score
                  6.0e-18
E value
Match length
                  58
                  72
% identity
NCBI Description
                  (X84225) precursor of photosystem II subunit (22KDa)
                  [Nicotiana tabacum]
                  399088
Seq. No.
                  LIB3431-021-P1-N1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1350742
BLAST score
                  159
                  1.0e-10
E value
                  43
Match length
% identity
                  58
                  PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi 1086831 (U41264)
NCBI Description
                  coded for by C. elegans cDNA yk64g10.5; coded for by C.
                  elegans cDNA yk51f3.5; coded for by C. elegans cDNA
                  yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for
                  by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA
```

yk64g1

NCBI GI

```
399089
Seq. No.
                  LIB3431-021-P1-N1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6016678
                  221
BLAST score
                  7.0e-18
E value
Match length
                  58
% identity
                   (AC009991) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  399090
Seq. ID
                  LIB3431-021-P1-N1-A4
Method
                  BLASTX
NCBI GI
                  q6016678
BLAST score
                  186
                   1.0e-13
E value
Match length
                  63
% identity
                   54
                   (AC009991) unknown protein [Arabidopsis thaliana]
NCBI Description
                   399091
Seq. No.
                  LIB3431-021-P1-N1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q482311
                   404
BLAST score
E value
                   3.0e-39
Match length
                  85
% identity
                   95
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                   399092
Seq. No.
                  LIB3431-021-P1-N1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1632831
BLAST score
                   257
E value
                   4.0e-22
                   67
Match length
                   76
% identity
                   (Z49698) orf [Ricinus communis]
NCBI Description
                   399093
Seq. No.
                  LIB3431-021-P1-N1-B11
Seq. ID
Method
                   BLASTX
                   g671740
NCBI GI
BLAST score
                   415
E value
                   1.0e-40
                   76
Match length
                   99
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   399094
Seq. No.
                  LIB3431-021-P1-N1-B12
Seq. ID
Method
                  BLASTN
```

g2306980

Method

BLASTX

```
BLAST score
                    59
                    2.0e-24
E value
Match length
                    79
                    94
% identity
                    Oryza sativa photosystem I antenna protein (Lhca) mRNA,
NCBI Description
                    complete cds
                   399095
Seq. No.
Seq. ID
                    LIB3431-021-P1-N1-B2
Method
                    BLASTX
NCBI GI
                    g464986
BLAST score
                    341
E value
                    6.0e-32
Match length
                    67
                    93
% identity
                    UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                    LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                    >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana
                    >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                    enzyme homolog [Arabidopsis thaliana] >gi 349211 (L00639)
                    ubiquitin conjugating enzyme [Arabidopsis thaliana]
                    >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
enzyme E2 [Arabidopsis thaliana]
                    >gi 4455355 emb CAB36765.1 (AL035524) ubiquitin-protein
                    ligase UBC9 [Arabidopsis thaliana]
                    399096
Seq. No.
Seq. ID
                    LIB3431-021-P1-N1-B4
Method
                    BLASTX
NCBI GI
                    g131225
BLAST score
                    301
E value
                    3.0e-27
Match length
                    73
% identity
                    78
NCBI Description
                    PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                    V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I
                    hydrophobic protein [Hordeum vulgare]
Seq. No.
                    399097
Seq. ID
                    LIB3431-021-P1-N1-B6
Method
                    BLASTX
NCBI GI
                    g115794
BLAST score
                    411
E value
                    4.0e-40
Match length
                    87
% identity
NCBI Description
                    CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
                    III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato
                    >gi_19277_emb_CAA42818_ (X60275) LHCII type III
                    [Lycopersicon esculentum]
Seq. No.
                    399098
                    LIB3431-021-P1-N1-B7
Seq. ID
```

```
NCBI GI
                  g115794
BLAST score
                  546
E value
                  6.0e-56
Match length
                  111
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
                  III CAB-13) >gi 72748 pir CDTO33 chlorophyll a/b-binding
                  protein type III precursor (cab-13) - tomato
                  >qi 19277 emb CAA42818 (X60275) LHCII type III
                  [Lycopersicon esculentum]
Seq. No.
                  399099
Seq. ID
                  LIB3431-021-P1-N1-B8
Method
                  BLASTN
NCBI GI
                  q20181
BLAST score
                  188
E value
                  1.0e-101
Match length
                  196
% identity
                  99 -
NCBI Description Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
Seq. No.
                  399100
Seq. ID
                  LIB3431-021-P1-N1-C12
Method
                  BLASTX
NCBI GI
                  g129916
BLAST score
                  240
E value
                  4.0e-20
                  79
Match length
                  70
% identity
                  PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911 pir TVWTGY
NCBI Description
                  phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat
                  >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase
                  (AA 1 - 401) [Triticum aestivum]
Seq. No.
                  399101
Seq. ID
                  LIB3431-021-P1-N1-C2
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  237
                  8.0e-20
E value
Match length
                  44
                  100
% identity
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  399102
Seq. No.
Seq. ID
                  LIB3431-021-P1-N1-C3
Method
                  BLASTX
NCBI GI
                  q693920
                  347
BLAST score
E value
                  1.0e-32
Match length
                  66
% identity
                  100
NCBI Description
                  (U21113) chlorophyll a/b binding protein [Solanum
                  tuberosum]
```

```
399103
Seq. No.
Seq. ID
                   LIB3431-021-P1-N1-C4
Method
                   BLASTX
NCBI GI
                   g3885882
BLAST score
                   266
E value
                   4.0e-23
Match length
                   58
% identity
                   (AF093629) inorganic pyrophosphatase [Oryza sativa]
NCBI Description
                   399104
Seq. No.
Seq. ID
                   LIB3431-021-P1-N1-C5
Method
                   BLASTX
NCBI GI
                   g417260
                   313
BLAST score
                   1.0e-28
E value
                   78
Match length
% identity
                   76
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                   lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                   light-regulated gene [Oryza sativa]
Seq. No.
                   399105
Seq. ID
                   LIB3431-021-P1-N1-C8
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   507
E value
                   2.0e-51
Match length
                   99
                   95
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   399106
Seq. No.
                   LIB3431-021-P1-N1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4336608
BLAST score
                   243
E value
                   1.0e-20
Match length
                   61
% identity
NCBI Description
                   (AF099111) sigma factor; Sig2 [Zea mays]
                   399107
Seq. No.
                   LIB3431-021-P1-N1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3885886
BLAST score
                   221
E value
                   7.0e-18
```

Match length

```
Match length
                  39
                  100
% identity
                  (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
NCBI Description
                  399108
Seq. No.
Seq. ID
                  LIB3431-021-P1-N1-D4
Method
                  BLASTX
NCBI GI
                  g21839
BLAST score
                  355
                  1.0e-33
E value
                  74
Match length
                  95
% identity
                  (X57952) phosphoribulokinase [Triticum aestivum]
NCBI Description
                  399109
Seq. No.
Seq. ID
                  LIB3431-021-P1-N1-D5
Method
                  BLASTX
NCBI GI
                  g2494320
                  252
BLAST score
                  2.0e-21
E value
Match length
                  58
                  78
% identity
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)
NCBI Description
                  >gi 1806575_emb_CAA67868_ (X99517) Eukaryotic initiation
                  factor-5 [Zea mays]
                  399110
Seq. No.
                  LIB3431-021-P1-N1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g482311
BLAST score
                  508
                  1.0e-51
E value
                  99
Match length
% identity
                  100
NCBI Description
                  photosystem II oxygen-evolving complex protein 1 - rice
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                  399111
Seq. No.
Seq. ID
                  LIB3431-021-P1-N1-D7
Method
                  BLASTX
NCBI GI
                  g1346109
BLAST score
                  286
E value
                  1.0e-25
                  55
Match length
% identity
                  98
NCBI Description
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
                  PROTEIN (GPB-LR) (RWD) >gi 540535_dbj_BAA07404_ (D38231)
                  RWD [Oryza sativa]
Seq. No.
                  399112
Seq. ID
                  LIB3431-021-P1-N1-D8
Method
                  BLASTX
NCBI GI
                  g131225
                  257
BLAST score
E value
                  2.0e-22
```

Match length

```
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  399113
                  LIB3431-021-P1-N1-D9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q438246
BLAST score
                  56
                  1.0e-22
E value
Match length
                  92
                  90
% identity
                  S.tuberosum mRNA for glycine hydroxymethyltransferase
NCBI Description
Seq. No.
                  399114
Seq. ID
                  LIB3431-021-P1-N1-E10
Method
                  BLASTN
NCBI GI
                  g1835730
BLAST score
                  144
E value
                  2.0e-75
Match length
                  156
% identity
                  98
NCBI Description
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
                  complete cds
Seq. No.
                  399115
Seq. ID
                  LIB3431-021-P1-N1-E11
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  233
E value
                  3.0e-19
Match length
                  44
% identity
                  98
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  399116
Seq. ID
                  LIB3431-021-P1-N1-E12
Method
                  BLASTX
NCBI GI
                  g3738261
BLAST score
                  368
E value
                  4.0e-35
Match length
                  83
% identity
NCBI Description
                  (AB018412) chloroplast phosphoglycerate kinase [Populus
                  nigra]
Seq. No.
                  399117
Seq. ID
                  LIB3431-021-P1-N1-E4
Method
                  BLASTX
NCBI GI
                  q1835731
BLAST score
                  252
E value
                  1.0e-21
```

E value

3.0e-25

```
% identity
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  399118
Seq. No.
Seq. ID
                  LIB3431-021-P1-N1-E8
Method
                  BLASTX
NCBI GI
                  g132166
BLAST score
                  159
E value
                  8.0e-11
Match length
                  31
                  87
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                  >gi 81660 pir S04048 ribulose-bisphosphate carboxylase
                  activase precursor - Arabidopsis thaliana
                  >gi 16471 emb CAA32429 (X14212) rubisco activase (AA 1 -
                  473) [Arabidopsis thaliana]
                  399119
Seq. No.
Seq. ID
                  LIB3431-021-P1-N1-F1
Method
                  BLASTN
NCBI GI
                  q3789951
BLAST score
                  77
E value
                  4.0e-35
Match length
                  161
                  87
% identity
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  399120
Seq. No.
                  LIB3431-021-P1-N1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g551047
BLAST score
                  222
E value
                  4.0e-18
Match length
                  43
% identity
NCBI Description
                 (X79277) type II LHCI [Lolium temulentum]
Seq. No.
                  399121
                  LIB3431-021-P1-N1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  200
E value
                  2.0e-15
Match length
                  39
                  97
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  399122
                  LIB3431-021-P1-N1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2688822
BLAST score
                  284
```

```
98
Match length
% identity
                   63
NCBI Description
                   (U93272) pyrophosphate-dependent phosphofructo-1-kinase
                   [Prunus armeniaca]
Seq. No.
                   399123
Seq. ID
                  LIB3431-021-P1-N1-F6
Method
                  BLASTX
NCBI GI
                  q2570515
BLAST score
                   196
E value
                   6.0e-15
Match length
                   41
% identity
NCBI Description
                   (AF022740) glycolate oxidase [Oryza sativa]
Seq. No.
                  399124
Seq. ID
                  LIB3431-021-P1-N1-F7
Method
                  BLASTX
NCBI GI
                  q3789954
BLAST score
                  390
                  1.0e-37
E value
Match length
                  72
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  399125
Seq. No.
                  LIB3431-021-P1-N1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  173
                  2.0e-12
E value
Match length
                  49
% identity
                  71
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                  399126
                  LIB3431-021-P1-N1-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20262
BLAST score
                  105
E value
                  3.0e-52
Match length
                  169
% identity
                  91
NCBI Description O.sativa light-induced mRNA
                  399127
Seq. No.
Seq. ID
                  LIB3431-021-P1-N1-G3
Method
                  BLASTX
NCBI GI
                  q3800878
BLAST score
                  206
E value
                  4.0e-16
Match length
                  58
% identity
NCBI Description
                  (AF096281) threonine dehydratase/deaminase [Arabidopsis
```

thaliana]

Seq. ID

```
Seq. No.
                  399128
Seq. ID
                  LIB3431-021-P1-N1-G4
Method
                  BLASTX
NCBI GI
                  g421916
BLAST score
                  243
E value
                  1.0e-20
Match length
                  45.
                  100
% identity
                  chlorophyll a/b-binding protein - English ivy (fragment)
NCBI Description
                  >gi_12582_emb_CAA48410_ (X68333) light harvesting
                  chlorophyll a /b binding protein [Hedera helix]
Seq. No.
                  399129
Seq. ID
                  LIB3431-021-P1-N1-G5
Method
                  BLASTX
NCBI GI
                  g115813
BLAST score
                  229
E value
                  7.0e-19
Match length
                  54
                  83
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                  399130
                  LIB3431-021-P1-N1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1698548
BLAST score
                  254
E value
                  1.0e-21
Match length
                  68
                  69
% identity
NCBI Description (U58971) calmodulin-binding protein [Nicotiana tabacum]
Seq. No.
                  399131
Seq. ID
                  LIB3431-021-P1-N1-G7
Method-
                  BLASTX
NCBI GI
                  g2582822
BLAST score
                  268
E value
                  2.0e-23
Match length
                  75
% identity
                  (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
NCBI Description
                  Protein of 32kDa) [Solanum tuberosum]
Seq. No.
                  399132
Seq. ID
                  LIB3431-021-P1-N1-H2
Method
                  BLASTN
NCBI GI
                  g3868755
BLAST score
                  98
E value
                  4.0e-48
Match length
                  134
% identity
                  93
NCBI Description Oryza sativa CatC gene for catalase, complete cds
Seq. No.
                  399133
```

LIB3431-021-P1-N1-H3

E value

2.0e-15

```
BLASTX
Method
NCBI GI
                   g2501190
BLAST score
                   240
                   4.0e-20
E value
Match length
                   68
                   75
% identity
NCBI Description
                   THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
                   >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
                   - maize >gi 596080 (U17351) thiamine biosynthetic enzyme
                   [Zea mays]
                   399134
Seq. No.
Seq. ID
                   LIB3431-021-P1-N1-H6
Method
                   BLASTX
NCBI GI
                   g131176
BLAST score
                   161
E value
                   4.0e-11
Match length
                   32
                   97
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                   >gi 72683 pir F1BH4 photosystem I chain IV precursor -
                   barley >gi 19087 emb CAA68782 (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi 226163 prf 1413233A
                   10.8kD photosystem I protein [Hordeum vulgare var.
                   distichum]
                   399135
Seq. No.
Seq. ID
                   LIB3431-021-P1-N1-H7
Method
                   BLASTX
NCBI GI
                   g131225
BLAST score
                   304
                   1.0e-27
E value
Match length
                   75
% identity
                   77
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                   precursor - barley >gi 167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
Seq. No.
                   399136
                   LIB3431-021-P1-N1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5738542
BLAST score
                   234
E value
                   1.0e-19
Match length
                   56
% identity
                   (AJ245867) photosystem I subunit XI precursor [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   399137
Seq. ID
                   LIB3431-021-P1-N1-H9
Method
                   BLASTX
NCBI GI
                   g115813
BLAST score
                   200
```

Match length 51 76 % identity CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III NCBI Description CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum] Seq. No. 399138 Seq. ID LIB3431-022-P1-K1-A1 Method BLASTX NCBI GI g2407281 BLAST score 632 E value 4.0e-66 Match length 121 98 % identity (AF017363) ribulose 1,5-bisphosphate carboxylase small NCBI Description subunit [Oryza sativa] 399139 Seq. No. LIB3431-022-P1-K1-A12 Seq. ID BLASTX Method NCBI GI q3212865 BLAST score 409 6.0e-40 E value Match length 145 % identity 56 (AC004005) unknown protein [Arabidopsis thaliana] NCBI Description Seq. No. 399140 LIB3431-022-P1-K1-A3 Seq. ID Method BLASTX NCBI GI g5640111 BLAST score 296 1.0e-26 E value Match length 97 % identity NCBI Description (AJ243875) RAD23 protein [Lycopersicon esculentum] Seq. No. 399141 LIB3431-022-P1-K1-A4 Seq. ID Method BLASTN NCBI GI g3885891 BLAST score 44 E value 1.0e-15 Match length 109

95

% identity NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)

mRNA, complete cds

Seq. No. 399142

LIB3431-022-P1-K1-A5 Seq. ID

Method BLASTX NCBI GI g132105 BLAST score 637 E value 1.0e-66 Match length 137 % identity 88

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

```
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
```

```
399143
Seq. No.
Seq. ID
                  LIB3431-022-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g1173347
                  736
BLAST score
                  3.0e-78
E value
                  148
Match length
                  96
% identity
NCBI Description
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi 14265 emb CAA46507
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  399144
                  EIB3431-022-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  544
                  9.0e-56
E value
                  142
Match length
                  75
% identity
                  (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
Seq. No.
                  399145
Seq. ID
                  LIB3431-022-P1-K1-A9
                  BLASTX
Method
NCBI GI
                  q2245086
                  373
BLAST score
E value
                  1.0e-35
                  104
Match length
% identity
                   68
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  399146
Seq. No.
Seq. ID
                  LIB3431-022-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g132105
                  609
BLAST score
E value
                  2.0e-63
                  131
Match length
% identity
                  88
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
```

(D00643) small subunit of ribulose-1,5-bisphosphate

```
sativa] >gi_226375 prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  399147
Seq. No.
Seq. ID
                  LIB3431-022-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g3929924
BLAST score
                  298
                   6.0e-27
E value
Match length
                   56
% identity
                   100
                   (AB020502) catalase [Oryza sativa]
NCBI Description
                  399148
Seq. No.
Seq. ID
                  LIB3431-022-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  g218209
BLAST score
                   159
E válue
                   5.0e-84
Match length
                   303
                   97
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS2106
                   399149
Seq. No.
Seq. ID
                  LIB3431-022-P1-K1-B3
Method
                  BLASTX
NCBI GI
                   g4982498
BLAST score
                   333
E value
                   5.0e-31
Match length
                  83
% identity
                   76
NCBI Description
                   (AC000107) F17F8.4 [Arabidopsis thaliana]
                  399150
Seq. No.
                  LIB3431-022-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789952
BLAST score
                   557
E value
                   2.0e-57
Match length
                  114
% identity
                   96
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                  sativa]
                  399151
Seq. No.
                  LIB3431-022-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  304
E value
                  1.0e-27
```

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

76

76

NCBI Description (Z72488) CP12 [Nicotiana tabacum]

Match length

% identity

```
Seq. No.
                   399152
Seq. ID
                   LIB3431-022-P1-K1-B9
                   BLASTX
Method
NCBI GI
                   g5802244
BLAST score
                   282
E value
                   5.0e-25
Match length
                   62
% identity
                   84
                   (AF169022) seed maturation protein PM37 [Glycine max]
NCBI Description
                   399153
Seq. No.
Seq. ID
                   LIB3431-022-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   g6006363
BLAST score
                   245
                   1.0e-20
E value
Match length
                   45
% identity
                   100
                   (AP000559) ESTs AU078183(C62904), C73912(E21020) correspond
NCBI Description
                   to a region of the predicted gene.; Similar to water stress
                   inducible protein (U74296) [Oryza sativa]
Seq. No.
                   399154
Seq. ID
                   LIB3431-022-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q1661160
BLAST score
                   437
E value
                   3.0e-43
Match length
                   97
% identity
                   84
                   (U74295) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   399155
Seq. ID
                   LIB3431-022-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g3273243
BLAST score
                   365
E value
                   7.0e-35
Match length
                   117
% identity
                   61
                   (AB004660) NLS receptor [Oryza sativa]
NCBI Description
                   >gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza
                   sativa]
Seq. No.
                   399156
Seq. ID
                   LIB3431-022-P1-K1-C5
Method
                   BLASTN
NCBI GI
                   q6015437
BLAST score
                   35
E value
                   5.0e-10
Match length
                   35
% identity
                   100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   399157
Seq. ID
                   LIB3431-022-P1-K1-C6
```

E value

2.0e-24

```
Method
                   BLASTX
                   g5295988
NCBI GI
BLAST score
                   656
                   7.0e-69
E value
                   148
Match length
                   90
% identity
NCBI Description
                   (AB003327) MADS box-like protein [Oryza sativa]
                   399158
Seq. No.
Seq. ID
                   LIB3431-022-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   g6006363
                   370
BLAST score
                   2.0e-35
E value
Match length
                   71
                   100
% identity
                   (AP000559) ESTs AU078183(C62904), C73912(E21020) correspond
NCBI Description
                   to a region of the predicted gene.; Similar to water stress
                   inducible protein (U74296) [Oryza sativa]
                   399159
Seq. No.
                   LIB3431-022-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4512613
BLAST score
                   295
E value
                   1.0e-26
Match length
                   66
% identity
                   80
                   (AC004793) F28K20.12 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   399160
                   LIB3431-022-P1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4371296
BLAST score
                   307
E value
                   5.0e-28
Match length
                   134
% identity
                   (AC006260) putative receptor protein kinase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   399161
                   LIB3431-022-P1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g448445
BLAST score
                   263
E value
                   8.0e-23
Match length
                   72
% identity
                   69
                  CFO ATP synthase:SUBUNIT=9 [Spinacia oleracea]
NCBI Description
                   399162
Seq. No.
                   LIB3431-022-P1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3935175
BLAST score
                   277
```

E value

3.0e-49

```
Match length
                   84
                   67
% identity
NCBI Description
                   (AC004557) F17L21.18 [Arabidopsis thaliana]
                   399163
Seq. No.
Seq. ID
                   LIB3431-022-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   q3789954
BLAST score
                   661
                   2.0e-69
E value
                   125
Match length
                   98
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   satival
                   399164
Seq. No.
Seq. ID
                   LIB3431-022-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   593
                   2.0e-61
E value
Match length
                   130
                   87
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   399165
                   LIB3431-022-P1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4099148
BLAST score
                   582
E value
                   3.0e-60
Match length
                   147
% identity
                   82
                   (U84268) YLP [Hordeum vulgare]
NCBI Description
Seq. No.
                   399166
Seq. ID
                   LIB3431-022-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   g2293288
BLAST score
                   175
E value
                   2.0e-12
Match length
                   152
% identity
                   33
                   (AF008220) YtcB [Bacillus subtilis]
NCBI Description
                   >qi 2635571 emb CAB15065 (Z99119) similar to NDP-sugar
                   epimerase [Bacillus subtilis]
Seq. No.
                   399167
                   LIB3431-022-P1-K1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5106775
BLAST score
                   488
```

BLAST score

```
Match length
                   96
% identity
                   98
                   (AF067732) ribosomal protein S12 [Hordeum vulgare]
NCBI Description
                   399168
Seq. No.
Seq. ID
                   LIB3431-022-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
                   9.0e-20
E value
Match length
                   44
                   100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   399169
Seq. No.
                   LIB3431-022-P1-K1-E10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g6063542
BLAST score
                   259
E value
                   2.0e-22
                   47
Match length
                   100
% identity
                   (AP000615) EST C74302(E30840) corresponds to a region of
NCBI Description
                   the predicted gene.; similar to glyceraldehyde-3-phosphate
                   dehydrogenase. (M64118) [Oryza sativa]
                   399170
Seq. No.
                   LIB3431-022-P1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4469021
BLAST score
                   312
E value
                   1.0e-28
Match length
                   85
% identity
                   71
                  (AL035602) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   399171
Seq. ID
                   LIB3431-022-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   592
E value
                   2.0e-61
Match length
                   134
% identity
                   88
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   399172
                   LIB3431-022-P1-K1-E2
Seq. ID
Method
                   BLASTX
                   q1835731
NCBI GI
```

```
5.0e-56
E value
Match length
                  103
% identity
                  100
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  399173
Seq. No.
                  LIB3431-022-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q81601
BLAST score
                  159
                  1.0e-10
E value
Match length
                  43
                  70
% identity
NCBI Description
                  chaperonin 60 beta - Arabidopsis thaliana
Seq. No.
                  399174
Seq. ID
                  LIB3431-022-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  q3789954
BLAST score
                  546
                  5.0e-56
E value
Match length
                  106
% identity
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
Seq. No.
                  399175
                  LIB3431-022-P1-K1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1245938
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
                  heart atrium, mRNA, 2998 nt]
                  399176
Seq. No.
Seq. ID
                  LIB3431-022-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g1661160
BLAST score
                  636
E value
                  1.0e-66
Match length
                  142
% identity
                  87
NCBI Description (U74295) chlorophyll a/b binding protein [Oryza sativa]
                  399177
Seq. No.
Seq. ID
                  LIB3431-022-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g4557093
BLAST score
                  215
E value
                  3.0e-17
Match length
                  65
% identity
```

NCBI Description (AF001136) zinc finger protein [Pinus radiata]

```
399178
Seq. No.
                  LIB3431-022-P1-K1-E9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3075487
BLAST score
                  322
                  0.0e+00
E value
                  322.
Match length
% identity
                  100
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  399179
Seq. ID
                  LIB3431-022-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2493494
BLAST score
                  547
E value
                  4.0e-56
Match length
                  112
                  89
% identity
                  SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2)
NCBI Description
                  >gi 619351 bbs 153537 CP-MII.2=serine carboxypeptidase
                  [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436
                  aa] >gi 6102957 emb CAB59202.1 (X78878) serine carboxylase
                  II-2 [Hordeum vulgare]
                  399180
Seq. No.
Seq. ID
                  LIB3431-022-P1-K1-F11
                  BLASTX
Method
NCBI GI
                  g115787
BLAST score
                  584
                  2.0e-60
E value
                  133
Match length
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  399181
Seq. ID
                  LIB3431-022-P1-K1-F12
                  BLASTX
Method
NCBI GI
                  g3618310
BLAST score
                  473
E value
                  2.0e-47
Match length
                  123
% identity
                  (AB001883) zinc finger protein [Oryza sativa]
NCBI Description
                  399182
Seq. No.
Seq. ID
                  LIB3431-022-P1-K1-F2
                  BLASTX
Method
NCBI GI
                  g710626
                  188
BLAST score
                  5.0e-14
E value
Match length
                  45
```

69

% identity

```
NCBI Description (D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941
                  (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                  thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
                  thaliana]
Seq. No.
                  399183
                  LIB3431-022-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5541681
BLAST score
                  327
E value
                  2.0e-30
Match length
                  124
                  56
% identity
                  (AL096859) putative protein [Arabidopsis thaliana]
NCBI Description
                  399184
Seq. No.
Seq. ID
                  LIB3431-022-P1-K1-F4
                  BLASTX
Method
NCBI GI
                  g5230790
BLAST score
                  162
                  6.0e-11
E value
Match length
                  46
                  70
% identity
NCBI Description
                  (AF107027) histone H1 WH1A.4 [Triticum aestivum]
Seq. No.
                  399185
Seq. ID
                  LIB3431-022-P1-K1-F5
                  BLASTX
Method
NCBI GI
                  g6016736
BLAST score
                  253
E value
                  1.0e-21
                  86
Match length
% identity
                  (AC009325) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  399186
                  LIB3431-022-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  237
E value
                  9.0e-20
Match length
                  44
% identity
                  100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  399187
Seq. No.
Seq. ID
                  LIB3431-022-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  q320618
BLAST score
                  576
E value
                  2.0e-59
Match length
                  125
                  87
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
```

```
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   399188
Seq. No.
Seq. ID
                   LIB3431-022-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   g5295954
BLAST score
                   363
                   2.0e-34
E value
Match length
                   72
% identity
                   97
                   (AB026295) hypothetical protein [Oryza sativa]
NCBI Description
                   399189
Seq. No.
Seq. ID
                   LIB3431-022-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   622
E value
                   7.0e-65
Match length
                   135
                   87
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   399190
Seq. No.
Seq. ID
                   LIB3431-022-P1-K1-G12
Method
                   BLASTN
NCBI GI
                   g2062705
BLAST score
                   35
                   5.0e-10
E value
Match length
                   35
% identity
                   100
NCBI Description
                   Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                   399191
Seq. ID
                   LIB3431-022-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g120657
BLAST score
                   528
E value
                   6.0e-54
                   132
Match length
% identity
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
                   CHLOROPLAST >gi_66024_pir__DEZMG3
                   glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                   maize >gi 168479 (M18976) glyceraldehyde-3-phosphate
                   dehydrogenase [Zea mays] >gi 763035 emb CAA33455 (X15408)
                   qlyceraldehyde-3-phosphate dehydrogenase [Zea mays]
                   399192
Seq. No.
                   LIB3431-022-P1-K1-G5
Seq. ID
Method
```

BLASTX

Seq. ID

```
g629775
NCBI GI
BLAST score
                   740
                   1.0e-78
E value
                   149
Match length
                   92
% identity
NCBI Description beta-ketoacyl-ACP synthase - barley (fragment)
Seq. No.
                   399193
Seq. ID
                   LIB3431-022-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   614
E value
                   6.0e-64
Match length
                   132
% identity
                   88
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094 pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   399194
Seq. No.
Seq. ID
                   LIB3431-022-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g5816998
BLAST score
                   276
E value
                   2.0e-24
Match length
                   121
% identity
                   47
NCBI Description
                   (AL110123) putative protein [Arabidopsis thaliana]
Seq. No.
                   399195
Seq. ID
                   LIB3431-022-P1-K1-G9
Method
                   BLASTN
NCBI GI
                   q4959460
BLAST score
                   37
E value
                   3.0e-11
Match length
                   37
% identity
                   100
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
                   399196
Seq. No.
Seq. ID
                   LIB3431-022-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g2213600
BLAST score
                   364
E value
                   1.0e-34
Match length
                   131
% identity
NCBI Description
                  (AC000348) T7N9.20 [Arabidopsis thaliana]
                   399197
Seq. No.
```

LIB3431-022-P1-K1-H11

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```
BLASTX
Method
NCBI GI
                   g1171978
BLAST score
                   418
E value
                   4.0e-45
Match length
                   128
% identity
                   63
NCBI Description
                   POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2)
                   (PABP 2) >gi_304109 (L19418) poly(A)-binding protein
                   [Arabidopsis thaliana] >gi 2911051 emb_CAA17561_ (AL021961)
                   poly(A)-binding protein [Arabidopsis thaliana]
Seq. No.
                   399198
Seq. ID
                   LIB3431-022-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   g3345477
BLAST score
                   317
E value
                   3.0e-29
Match length
                   115
                   57
% identity
                  (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                   399199
Seq. No.
Seq. ID
                   LIB3431-022-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   q1707998
BLAST score
                   417
E value
                   6.0e-41
Match length
                   118
                   73
% identity
NCBI Description
                   SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi 481944 pir S40218 glycine
                   hydroxymethyltransferase (EC 2.1.2.1) - potato
                  >gi_438247_emb_CAA81082_ (Z25863) glycine
hydroxymethyltransferase [Solanum tuberosum]
Seq. No.
                   399200
Seq. ID
                   LIB3431-022-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g3184559
BLAST score
                   289
E value
                   7.0e-26
Match length
                   128
                   50
% identity
                   (AF052290) putative c-type cytochrome biogenesis protein
NCBI Description
                   [Synechococcus PCC7002]
                   399201
Seq. No.
Seq. ID
                   LIB3431-022-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   g3510256
BLAST score
                   180
                   3.0e-13
E value
Match length
                   41
% identity
```

NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]

Method

BLASTN

```
399202
Seq. No.
Seq. ID
                   LIB3431-022-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   8.0e-20
Match length
                   44
% identity
                   100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi 6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                   399203
Seq. No.
                  LIB3431-022-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3126854
BLAST score
                   730
E value
                   1.0e-77
Match length
                   139
                   99
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   399204
Seq. No.
Seq. ID
                  LIB3431-022-P1-N1-A1
Method
                  BLASTX
NCBI GI
                   q671740
                   202
BLAST score
E value
                   1.0e-15
Match length
                   51
% identity
                   80
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   399205
Seq. No.
Seq. ID
                  LIB3431-022-P1-N1-A4
Method
                  BLASTX
NCBI GI
                  q3885892
BLAST score
                  235
                   1.0e-19
E value
Match length
                   47
% identity
                   98
NCBI Description
                   (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
                  399206
Seq. No.
Seq. ID
                  LIB3431-022-P1-N1-A5
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  197
                   3.0e-15
E value
                  37
Match length
% identity
                  100
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
                  399207
Seq. No.
                  LIB3431-022-P1-N1-A6
Seq. ID
```

```
g14264
NCBI GI
BLAST score
                   51
E value
                   1.0e-19
Match length
                   115
% identity
                   86
NCBI Description T.aestivum gene for sedoheptulose-1,7-bisphoshatase
                   399208
Seq. No.
Seq. ID
                   LIB3431-022-P1-N1-A7
Method
                   BLASTX
NCBI GI
                   q3345477
BLAST score
                   183
E value
                   2.0e-13
Match length
                   33
                   100
% identity
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                   399209
Seq. ID
                   LIB3431-022-P1-N1-A9
                   BLASTX
Method
NCBI GI
                   g2245086
BLAST score
                   224
                   3.0e-18
E value
Match length
                   65
% identity
                   66
NCBI Description (Z97343) hypothetical protein [Arabidopsis thaliana]
                   399210
Seq. No.
Seq. ID
                   LIB3431-022-P1-N1-B1
                   BLASTX
Method
NCBI GI
                   g132105
BLAST score
                   364
E value
                   1.0e-34
Match length
                   73
% identity
                   95
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   399211
Seq. ID
                   LIB3431-022-P1-N1-B10
                   BLASTX
                   q3929924
```

```
      Seq. ID
      LIB3431-022-P1-N1-B10

      Method
      BLASTX

      NCBI GI
      g3929924

      BLAST score
      221

      E value
      5.0e-18

      Match length
      43

      % identity
      98

      NCBI Description
      (AB020502) catalase [Oryza sativa]

      Seq. No.
      399212

      Seq. ID
      LIB3431-022-P1-N1-B12
```

```
BLASTN
Method
NCBI GI
                   g3075487
BLAST score
                   42
E value
                   3.0e-14
                   82
Match length
                   88
% identity
NCBI Description
                   Oryza sativa chlorophyll a/b-binding protein (RCABP69)
                   mRNA, complete cds
                   399213
Seq. No.
Seq. ID
                   LIB3431-022-P1-N1-B2
                   BLASTN
Method
NCBI GI
                   q218209
BLAST score
                   159
E value
                   5.0e-84
Match length
                   304
                   97
% identity
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS2106
Seq. No.
                   399214
Seq. ID
                   LIB3431-022-P1-N1-B3
Method
                   BLASTX
NCBI GI
                   q4982498
BLAST score
                   187
E value
                   5.0e-14
                   59
Match length
% identity
                   59
NCBI Description
                   (AC000107) F17F8.4 [Arabidopsis thaliana]
Seq. No.
                   399215
                   LIB3431-022-P1-N1-B5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3789951
BLAST score
                   168
E value
                   2.0e-89
Match length
                   374
% identity
                   93
                   Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
Seq. No.
                   399216
                   LIB3431-022-P1-N1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   402
E value
                   4.0e-39
Match length
                   73
                   100
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
```

carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)

```
carboxylase S [Oryza sativa]
                  399217
Seq. No.
Seq. ID
                  LIB3431-022-P1-N1-B9
Method
                  BLASTX
NCBI GI
                  g1125691
BLAST score
                  180
                  4.0e-13
E value
                  62
Match length
                  65
% identity
                  (X94301) DnaJ protein [Solanum tuberosum]
NCBI Description
Seq. No.
                  399218
Seq. ID
                  LIB3431-022-P1-N1-C1
Method
                  BLASTX
NCBI GI
                  g4929312
BLAST score
                  328
E value
                  2.0e-30
Match length
                  112
                  63
% identity
                  (AF145045) TATC [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  399219
Seq. ID
                  LIB3431-022-P1-N1-C10
Method
                  BLASTN
                  g6006355
NCBI GI
BLAST score
                  384
                  0.0e+00
E value
                  388
Match length
                  100
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
NCBI Description
Seq. No.
                  399220
                  LIB3431-022-P1-N1-C12
Seq. ID
Method
                  BLASTX -
NCBI GI
                  q3036951
BLAST score
                  431
E value
                  1.0e-42
Match length
                  81
                  100
% identity
                   (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
```

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >qi 226375 prf 1508256A ribulose bisphosphate

 Seq. No.
 399221

 Seq. ID
 LIB3431-022-P1-N1-C2

 Method
 BLASTX

 NCBI GI
 g2072555

 RLAST score
 237

NCBI GI g20/2555
BLAST score 237
E value 9.0e-20
Match length 44
% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

[Nicotiana sylvestris]

Seq. No.

```
399222
Seq. No.
                   LIB3431-022-P1-N1-C6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g5295987
BLAST score
                   362
E value
                   0.0e + 00
Match length
                   435
% identity
                   95
                   Oryza sativa mRNA for MADS box-like protein, complete cds,
NCBI Description
                   clone:S10304
                   399223
Seq. No.
Seq. ID
                   LIB3431-022-P1-N1-C7
                   BLASTN
Method
                   g6006355
NCBI GI
                   249
BLAST score
                   1.0e-138
E value
Match length
                   310
                   95
% identity
                   Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
NCBI Description
                   399224
Seq. No.
                   LIB3431-022-P1-N1-C8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4512613
BLAST score
                   305
E value
                   7.0e-28
                   67
Match length
% identity
                   82
NCBI Description
                   (AC004793) F28K20.12 [Arabidopsis thaliana]
Seq. No.
                   399225
Seq. ID
                   LIB3431-022-P1-N1-D12
Method
                   BLASTX
NCBI GI
                   g3789954
BLAST score
                   361
E value
                   3.0e - 34
                   67
Match length
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   399226
Seq. No.
Seq. ID
                   LIB3431-022-P1-N1-D4
Method
                   BLASTX
NCBI GI
                   g115787
                   396
BLAST score
E value
                   2.0e-38
                   75
Match length
                   100
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
```

Seq. ID

```
LIB3431-022-P1-N1-D5
Seq. ID
Method
                  BLASTX
                  g3334409
NCBI GI
BLAST score
                  204
E value
                  5.0e-16
Match length
                  52
% identity
                  79
                  VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT)
NCBI Description
                  >gi 2129765_pir__S71261 V-type proton-ATPase - Arabidopsis
                  thaliana >gi_1143394_emb_CAA63086_ (X92117) V-type
                  proton-ATPase [Arabidopsis thaliana]
                  399228
Seq. No.
Seq. ID
                  LIB3431-022-P1-N1-D7
                  BLASTX
Method
NCBI GI
                  g5106775
BLAST score
                  342
                  4.0e-32
E value
Match length
                  71
% identity
                  92
NCBI Description (AF067732) ribosomal protein S12 [Hordeum vulgare]
                  399229
Seq. No.
Seq. ID
                  LIB3431-022-P1-N1-D8
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  226
                  2.0e-18
E value
Match length
                  46
                  91
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  399230
Seq. No.
Seq. ID
                  LIB3431-022-P1-N1-E11
Method
                  BLASTX
NCBI GI
                  q4469021
BLAST score
                  310
E value
                  2.0e-28
Match length
                  72
                  81
% identity -
NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]
                  399231
Seq. No.
Seq. ID
                  LIB3431-022-P1-N1-E12
Method
                  BLASTX
NCBI GI
                  g3036946
                  277
BLAST score
                  2.0e-24
E value
Match length
                  52
% identity
                  100
                  (AB012637) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
Seq. No.
                  399232
```

LIB3431-022-P1-N1-E2

BLAST score

```
Method
                   BLASTX
NCBI GI
                   g1835731
BLAST score
                   283
                   3.0e-25
E value
                   67
Match length
                   82
% identity
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                   399233
Seq. No.
Seq. ID
                   LIB3431-022-P1-N1-E4
Method
                   BLASTX
NCBI GI
                   q3789954
BLAST score
                   357
                   7.0e-34
E value
Match length
                   66
                   100
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   399234
Seq. No.
Seq. ID
                   LIB3431-022-P1-N1-E5
Method
                   BLASTX
NCBI GI
                   g3789954
BLAST score
                   163
E value
                   3.0e-11
Match length
                   54
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   399235
Seq. No.
Seq. ID
                   LIB3431-022-P1-N1-E7
Method
                   BLASTX
NCBI GI
                   q4512125
BLAST score
                   178
E value
                   5.0e-13
Match length
                   32
% identity
                   100
                   (AF133340) putative chlorophyll a/b-binding protein
NCBI Description
                   [Phalaenopsis sp. 'KCbutterfly']
Seq. No.
                   399236
Seq. ID
                   LIB3431-022-P1-N1-E8
Method
                   BLASTN
NCBI GI
                   g20181
BLAST score
                   100
E value
                   7.0e-49
Match length
                   176
% identity
                   89
NCBI Description
                  Rice cab2R gene for light harvesting chlorophyll
                   a/b-binding protein
Seq. No.
                   399237
Seq. ID
                   LIB3431-022-P1-N1-E9
Method
                   BLASTN
NCBI GI
                   q3075487
```

NCBI GI

BLAST score

.g3036951

```
1.0e-153
E value
Match length
                  279
% identity
                  100
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
                  mRNA, complete cds
Seq. No.
                  399238
Seq. ID
                  LIB3431-022-P1-N1-F10
Method
                  BLASTX
NCBI GI
                  q2493494
BLAST score
                  199
E value
                  3.0e-15
Match length
                  48
                  81
% identity
                  SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2)
NCBI Description
                  >gi 619351 bbs 153537 CP-MII.2=serine carboxypeptidase
                  [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436
                  aa] >gi_6102957_emb_CAB59202.1_ (X78878) serine carboxylase
                  II-2 [Hordeum vulgare]
Seq. No.
                  399239
Seq. ID
                  LIB3431-022-P1-N1-F11
Method
                  BLASTX
NCBI GI
                  q3036942
BLAST score
                  251
E value
                  2.0e-21
Match length
                  47
                  100
% identity
                   (AB012636) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                  399240
Seq. No.
Seq. ID
                  LIB3431-022-P1-N1-F12
Method
                  BLASTX
NCBI GI
                  q3618310
BLAST score
                  366
E value
                  6.0e-35
Match length
                  77
                  92
% identity
NCBI Description
                  (AB001883) zinc finger protein [Oryza sativa]
Seq. No.
                  399241
Seq. ID
                  LIB3431-022-P1-N1-F6
                  BLASTN
Method
NCBI GI
                  q6103440
BLAST score
                  45
E value
                  3.0e-16
                  85
Match length
% identity
                  Oryza sativa metallothionein-like protein (ML2) mRNA,
NCBI Description
                  complete cds
                  399242
Seq. No.
Seq. ID
                  LIB3431-022-P1-N1-F8
                  BLASTX
Method
```

Match length

```
2.0e-24
E value
Match length
                  54
                   98
% identity
                   (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                  399243
Seq. No.
                  LIB3431-022-P1-N1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5295936
BLAST score
                  310
                   1.0e-174
E value
                   411
Match length
% identity
                   94
                  Oryza sativa genomic DNA, chromosome 6, clone:P0681F10,
NCBI Description
                   complete sequence
Seq. No.
                   399244
Seq. ID
                  LIB3431-022-P1-N1-G10
Method
                  BLASTX
NCBI GI
                  g3928150
BLAST score
                   412
E value
                   3.0e-40
Match length
                   110
% identity
                   72
                   (AJ131049) hypothetical protein [Cicer arietinum]
NCBI Description
                   399245
Seq. No.
                  LIB3431-022-P1-N1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120661
BLAST score
                   178
E value
                   6.0e-13
Match length
                   32
                   100
% identity
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
                   PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
                   dehydrogenase A-subunit precursor [Nicotiana tabacum]
Seq. No.
                   399246
Seq. ID
                   LIB3431-022-P1-N1-G6
Method
                   BLASTX
NCBI GI
                   q347451
BLAST score
                   263
E value
                   7.0e-23
Match length
                   51
% identity
                   100
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   399247
Seq. ID
                   LIB3431-022-P1-N1-H11
Method
                   BLASTX
NCBI GI
                   g2213871
BLAST score
                   195
E value
                   7.0e-15
```

```
% identity
NCBI Description
                   (AF003126) poly(A)-binding protein [Mesembryanthemum
                   crystallinum]
                   399248
Seq. No.
Seq. ID
                   LIB3431-022-P1-N1-H12
                   BLASTX
Method
NCBI GI
                   g3345477
                   156
BLAST score
                   2.0e-10
E value
                   30
Match length
                   97
% identity
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
                   399249
Seq. No.
Seq. ID
                   LIB3431-022-P1-N1-H2
                   BLASTX
Method
NCBI GI
                   g1707998
BLAST score
                   153
                   5.0e-10
E value
Match length
                   29
% identity
                   100
                   SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi 481944 pir S40218 glycine
                   hydroxymethyltransferase (EC 2.1.2.1) - potato
                  >gi_438247_emb_CAA81082_ (Z25863) glycine
hydroxymethyltransferase [Solanum tuberosum]
Seq. No.
                   399250
Seq. ID
                   LIB3431-022-P1-N1-H6
                   BLASTX
Method
NCBI GI
                   g3510256
BLAST score
                   167
E value
                   1.0e-11
Match length
                   41
                   73
% identity
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
                   399251
Seq. No.
                   LIB3431-022-P1-N1-H7
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2072554
BLAST score
                   310
                   1.0e-174
E value
Match length
                   322
% identity
                   99
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   cds
                   399252
Seq. No.
Seq. ID
                   LIB3431-022-P1-N1-H8
Method
                   BLASTX
NCBI GI
                   g115802
                   190
BLAST score
                   2.0e-14
E value
```

35

Match length

Seq. ID

Method

% identity CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I NCBI Description CAB-36) (LHCP) >gi_100311_pir___\$21827 chlorophyll a/b-binding protein $(cab-\overline{3}6)$ - common tobacco >gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding protein [Nicotiana tabacum] 399253 Seq. No. ~ LIB3431-023-P1-K1-A1 Seq. ID Method BLASTX NCBI GI g5430769 BLAST score 349 6.0e-33 E value Match length 130 55 % identity (AC007504) Similar to somatic embryogenesis receptor-like NCBI Description kinase [Arabidopsis thaliana] 399254 Seq. No. LIB3431-023-P1-K1-A11 Seq. ID . Method BLASTX NCBI GI g1657621 BLAST score 212 E value 8.0e-17 109 Match length 54 % identity (U72505) G6p [Arabidopsis thaliana] >gi 3068711 (AF049236) NCBI Description putative acyl-coA dehydrogenase [Arabidopsis thaliana] >gi 5478795 dbj BAA82478.1_ (AB017643) Short-chain acyl CoA oxidase [Arabidopsis thaliana] 399255 Seq. No. Seq. ID LIB3431-023-P1-K1-A3 Method BLASTX NCBI GI q1907270 BLAST score 485 E value 7.0e-49 Match length 122 74 % identity NCBI Description (X96761) sulphate transporter protein [Sporobolus stapfianus] Seq. No. 399256 LIB3431-023-P1-K1-A4 Seq. ID Method BLASTX NCBI GI q5734618 BLAST score 244 7.0e-27 E value 154 Match length % identity (AP000391) Similar to Arabidopsis thaliana chromosome II NCBI Description BAC F5H14 genomic sequence; unknown protein (AC006234) [Oryza sativa] 399257 Seq. No.

51039

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LIB3431-023-P1-K1-A5

BLASTX

Seq. No.

```
NCBI GI
                  q1173327
BLAST score
                  227
                  1.0e-18
E value
                  107 ·
Match length
% identity
                  50
NCBI Description
                  U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A')
                  >gi_322619_pir__S30580 U2 snRNP protein A' - Arabidopsis
                  thaliana >gi 17669 emb CAA48890 (X69137) U2 small nuclear
                  ribonucleoprotein A' [Arabidopsis thaliana]
Seq. No.
                  399258
                  LIB3431-023-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548605
BLAST score
                  519
E value
                  1.0e-57
Match length
                  132
                  91
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
                  399259
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-A8
                  BLASTN
Method
NCBI GI
                  g2586088
BLAST score
                  35
E value
                  5.0e-10
Match length
                  43
% identity
                  Oryza longistaminata receptor kinase-like protein, family
NCBI Description
                  member A2, pseudogene sequence
                  399260
Seq. No.
                  LIB3431-023-P1-K1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1052960
BLAST score
                  400
E value
                  7.0e-39
                  90
Match length
% identity
NCBI Description (U37437) PNIL34 [Ipomoea nil]
Seq. No.
                  399261
                  LIB3431-023-P1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g6006848
BLAST score
                  252
E value
                  2.0e-21
Match length
                  133
% identity
                  (AC009540) unknown protein, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
```

```
LIB3431-023-P1-K1-B10
Seq. ID
Method
                  BLASTN
                  g20153
NCBI GI
BLAST score
                  157
E value
                   8.0e-83
Match length
                  157
% identity
                  100
                  O.sativa random single-copy DNA fragment 12RG143R
NCBI Description
                  399263
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q3913425
                  323
BLAST score
                  7.0e-30
E value
Match length
                  76
                  79
% identity
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                  HELICASE >gi_2275203 (AC002337) RNA helicase isolog
               - [Arabidopsis thaliana]
                  399264
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q2407281
BLAST score
                  705
E value
                   1.0e-74
Match length
                  132
% identity
                   99
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
Seq. No.
                  399265
Seq. ID
                  LIB3431-023-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q6016732
BLAST score
                  203
E value
                  2.0e-18
Match length
                  86
% identity
                   (AC009325) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 6091719 gb AAF03431.1 AC010797 7 (AC010797)
                  hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  399266
Seq. ID
                  LIB3431-023-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  q3885887
BLAST score
                  419
                  0.0e + 00
E value
Match length
                  442
% identity
                  99
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                  complete cds
                  399267
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-B6
```

```
Method
                   BLASTX
NCBI GI
                   q2147484
BLAST score
                   592
                   2.0e-61
E value
Match length
                   137
% identity
                   81
                  homeotic protein - Phalaenopsis sp >gi_1173622 (U34743)
NCBI Description
                   homeobox protein [Phalaenopsis sp. 'hybrid SM9108']
                   399268
Seq. No.
Seq. ID
                   LIB3431-023-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g2660676
BLAST score
                   614
E value
                   5.0e-64
Match length
                   134
% identity
                   81
                  (AC002342) Dreg-2 like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   399269
Seq. ID
                   LIB3431-023-P1-K1-C1
                   BLASTX
Method
NCBI GI
                   q6006848
BLAST score
                   405
E value
                   2.0e-45
Match length
                   141
                   67
% identity
                   (AC009540) unknown protein, 5' partial [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   399270
Seq. ID
                   LIB3431-023-P1-K1-C11
Method
                   BLASTN
NCBI GI
                   g2306980
BLAST score
                   53
E value
                   7.0e-21
Match length
                   85
% identity
                   91
                   Oryza sativa photosystem I antenna protein (Lhca) mRNA,
NCBI Description
                   complete cds
                   399271
Seq. No.
Seq. ID
                   LIB3431-023-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   607
E value
                   4.0e-63
Match length
                   132
                   87
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
```

sativa] >gi 226375 prf 1508256A ribulose bisphosphate

BLAST score

376

carboxylase S [Oryza sativa]

```
399272
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g461550
BLAST score
                  578
E value
                  1.0e-59
Match length
                  150
                  71
% identity
                  ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR
NCBI Description
                  >qi 81635 pir B39732 H+-transporting ATP synthase (EC
                  3.6.1.34) gamma-1 chain precursor, chloroplast -
                  Arabidopsis thaliana >gi 166632 (M61741) ATP synthase
                  gamma-subunit [Arabidopsis thaliana]
                  >gi_5732056_gb_AAD48955.1_AF149414_4 (AF149414) Arabidopsis
                  thaliana APC1-ATP synthase gamma chain 1 (GB:M61741);
                  contains similarity to Pfam PF00231 -ATP synthase;
                  score=658.6, E=3.1e-194n n+1
                  399273
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  550
                  2.0e-56
E value
Match length
                  121
% identity
                  88
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
Seq. No.
                  399274
                  LIB3431-023-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  9.0e-20
Match length
                  44
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  399275
                  LIB3431-023-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4995089
BLAST score
                  544
E value
                  4.0e-68
Match length
                  152
% identity
NCBI Description
                  (AJ242712) malate dehydrogenase 1 [Brassica napus]
Seq. No.
                  399276
                  LIB3431-023-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3643608
```

```
5.0e-36
E value
Match length
                   95
                   75
% identity
                   (AC005395) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4874312_gb_AAD31374.1_AC006053_16 (AC006053)
                  hypothetical protein [Arabidopsis thaliana]
                  399277
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g4803952
BLAST score
                  284
E value
                  3.0e-25
Match length
                  69
% identity
                  (AC006202) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  399278
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-C9
                  BLASTX
Method
                  q4455350
NCBI GI
                  322
BLAST score
E value
                  1.0e-29
                  79
Match length
% identity
                  81
                  (AL035524) putative protein [Arabidopsis thaliana]
NCBI Description
                  399279
Seq. No.
                  LIB3431-023-P1-K1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2052383
BLAST score
                  403
E value
                  3.0e-39
                  86
Match length
% identity
                  80
NCBI Description
                  (U66345) calreticulin [Arabidopsis thaliana]
                  399280
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g3885892
BLAST score
                  440
E value
                  1.0e-43
Match length
                  83
                  100
% identity
NCBI Description
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
                  399281
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q2072555
                  237
BLAST score
E value
                  9.0e-20
Match length
                  44
                  100
% identity
NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
```

protein [Oryza sativa] 399282 Seq. No. Seq. ID LIB3431-023-P1-K1-D2 Method BLASTX NCBI GI g5816996 406 BLAST score E value 1.0e-39 85 Match length % identity 91 (AL110123) ribosomal protein L32-like protein [Arabidopsis NCBI Description thaliana] 399283 Seq. No. LIB3431-023-P1-K1-D3 Seq. ID Method BLASTX NCBI GI g132105 BLAST score 560 E value 1.0e-57 Match length 122 86 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa] 399284 Seq. No. LIB3431-023-P1-K1-D5 Seq. ID Method BLASTX NCBI GI g5816996 BLAST score 282 E value 5.0e-25 . . Match length 61 % identity (AL110123) ribosomal protein L32-like protein [Arabidopsis NCBI Description thaliana] 399285 Seq. No. LIB3431-023-P1-K1-D8 Seq. ID Method BLASTX NCBI GI g4914457 392 BLAST score 6.0e-38 E value 122 Match length % identity (AL050400) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 399286 LIB3431-023-P1-K1-E1 Seq. ID Method BLASTX

q3929924

620

NCBI GI BLAST score

NCBI GI

```
E value
                   4.0e-74
Match length
                   135
                   99
% identity
NCBI Description
                   (AB020502) catalase [Oryza sativa]
                   399287
Seq. No.
Seq. ID
                   LIB3431-023-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g3789954
BLAST score
                   778
                   3.0e-83
E value
Match length
                   145
                   100
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   399288
Seq. No.
Seq. ID
                   LIB3431-023-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   q517500
BLAST score
                   270
                   7.0e-24
E value
                   66
Match length
                   82
% identity
NCBI Description
                   (M87435) precursor of the oxygen evolving complex 17 kDa
                   protein [Zea mays] >gi_444338_prf__1906386A photosystem II
                   OE17 protein [Pisum sativum]
                   399289
Seq. No.
Seq. ID
                   LIB3431-023-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   g100849
BLAST score
                   365
E value
                   8.0e-49
Match length
                   128
% identity
                   acetolactate synthase (EC 4.1.3.18) (clone pSOG108) - maize
NCBI Description
                   >gi 22139 emb CAA45116 (X63553) acetohydroxyacid synthase
                   [Zea mays]
Seq. No.
                   399290
                   LIB3431-023-P1-K1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131225
BLAST score
                   316
E value
                   1.0e-56
Match length
                   122
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                   precursor - barley >gi_167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
Seq. No.
                   399291
Seq. ID
                   LIB3431-023-P1-K1-E7
Method
                   BLASTN
```

q6015437

NCBI GI

g320618

```
39
BLAST score
                   2.0e-12
E value
Match length
                  39
                   100
% identity
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
                   399292
Seq. No.
Seq. ID
                   LIB3431-023-P1-K1-E8
Method
                  BLASTX
                   g5922612
NCBI GI
                   226
BLAST score
                   2.0e-18
E value
                   136
Match length
% identity
                   59
                   (APO00492) EST AU078118(E3904) corresponds to a region of
NCBI Description
                   the predicted gene.; similar to Arabidopsis thaliana BAC
                   IG002P16; No definition line found. (AF007270) [Oryza
                   sativa]
                   399293
Seq. No.
                   LIB3431-023-P1-K1-E9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3023159
BLAST score
                   37
E value
                   3.0e-11
Match length
                   53
                   92
% identity
                   Zantedeschia aethiopica geranylgeranyl reductase mRNA,
NCBI Description
                   partial cds
Seq. No.
                   399294
                   LIB3431-023-P1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4033838
BLAST score
                   505
E value
                   3.0e-51
Match length
                   150
% identity
                   (Y18550) sigma-like factor [Arabidopsis thaliana]
NCBI Description
                   >gi 4972299 dbj BAA78109.1_ (AB021120) RNA polymerase sigma
                   subunit SigE [Arabidopsis thaliana]
                   399295
Seq. No.
                   LIB3431-023-P1-K1-F11
Seq. ID
Method
                   BLASTX
                   g1304215
NCBI GI
BLAST score
                   362
E value
                   2.0e-34
Match length
                   110
% identity
                   42
                   (D84392) precursor of rice 22 kDa protein of photosystem II
NCBI Description
                   (PSII-S) [Oryza sativa]
                   399296
Seq. No.
                   LIB3431-023-P1-K1-F12
Seq. ID
Method
                   BLASTX
```

```
BLAST score
                  435
E value
                  2.0e-70
Match length
                  133
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza satīva]
Seq. No.
                  399297
Seq. ID
                  LIB3431-023-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                  348
E value
                  8.0e-33
Match length
                  118
                  87
% identity
NCBI Description
                 (AF022738) chlorophyll a-b binding protein [Oryza sativa]
                  399298
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q547712
BLAST score
                  510
E value
                  9.0e-52
Match length
                  103
                  98
% identity
                  EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)
NCBI Description
                  >gi 542153 pir S38358 translation initiation factor eIF-4A
                  - \overline{rice} > gi_303\overline{84}4_{dbj_BAA02152_} (D12627) eukaryotic
                  initiation factor 4A [Oryza sativa]
                  399299
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-F7
                  BLASTX
Method
NCBI GI
                  g2407281
BLAST score
                  784
E value
                  7.0e-84
Match length
                  148
                  99
% identity
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  399300
Seq. ID
                  LIB3431-023-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  664
E value
                  7.0e-70
                  130
Match length
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
```

[Oryza sativa]

```
399301
Seq. No.
                  LIB3431-023-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501190
BLAST score
                  591
E value
                  3.0e-61
Match length
                  140
                  84
% identity
NCBI Description
                  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
                  >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
                  - maize >gi 596080 (U17351) thiamine biosynthetic enzyme
                  [Zea mays]
                  399302
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  9.0e-20
Match length
                  44
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  399303
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-G3
Method
                  BLASTX
                  g4079798
NCBI GI
                  558
BLAST score
                  2.0e-57
E value
                  143
Match length
% identity
                  78
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
                  399304
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g66298
BLAST score
                  347
                  9.0e-36
E value
                  87
Match length
                  84
% identity
NCBI Description
                  catalase (EC 1.11.1.6) - rice >gi_20192_emb_CAA43814_
                   (X61626) catalase [Oryza sativa]
                  399305
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-G7
Method
                  BLASTX
                  g4972093
NCBI GI
                  263
BLAST score
                  9.0e-23
E value
                  116
Match length
                  47
% identity
NCBI Description (AL078468) putative protein [Arabidopsis thaliana]
```

Method.

BLASTX

```
399306
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g3789954
BLAST score
                  639
                  6.0e-67
E value
                  119
Match length
% identity
NCBI Description
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                  sativa]
                  399307
Seq. No.
                  LIB3431-023-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  582
                  3.0e-60
E value
Match length
                  125
                  87
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  399308
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g120510
                  380
BLAST score
                  2.0e-36
E value
Match length
                  86
% identity
                  FERRITIN 2 PRECURSOR >gi_82688 pir S24057 ferritin
NCBI Description
                  precursor (clone FM2) - maize >gi 22278_emb_CAA43664_
                  (X61392) ferritin [Zea mays]
                  399309
Seq. No.
                  LIB3431-023-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  263
                  2.0e-28
E value
Match length
                  62
% identity
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  399310
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-H12
```

```
g1835731
NCBI GI
BLAST score
                  283
                   3.0e-25
E value
Match length
                  64
% identity
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  399311
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g226263
BLAST score
                  177
                  3.0e-13
E value
                  78
Match length
                  53
% identity
NCBI Description chlorophyll a/b binding protein [Glycine max]
                  399312
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g871931
                  356
BLAST score
                  7.0e-34
E value
Match length
                  72
                  99
% identity
                  (D30763) ferredoxin [Oryza sativa]
NCBI Description
                  399313
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g4850400
BLAST score
                  145
E value
                  2.0e-19
Match length
                  93
% identity
                   68
                   (AC007357) Similar to gb M86917 oxysterol-binding protein
NCBI Description
                  from Homo sapiens. [Arabidopsis thaliana]
Seq. No.
                  399314
Seq. ID
                  LIB3431-023-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g5123939
BLAST score
                  242
                  5.0e-33
E value
                  102
Match length
% identity
                  73
NCBI Description
                   (AL079349) putative protein [Arabidopsis thaliana]
                  399315
Seq. No.
                  LIB3431-023-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82080
BLAST score
                  494
                  7.0e-50
E value
                  136
Match length
```

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato

69

% identity

```
399316
Seq. No.
Seq. ID
                  LIB3431-023-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g3914425
BLAST score
                  600
                  2.0e-62
E value
                  143
Match length
                  77
% identity
NCBI Description
                  PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
                  CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
                  >gi 2511596 emb CAA74029.1 (Y13695) multicatalytic
                  endopeptidase complex, proteasome precursor, beta subunit
                  [Arabidopsis thaliana] >gi 3421117 (AF043536) 20S
                  proteasome beta subunit PBE1 [Arabidopsis thaliana]
                  >gi 4850389 gb AAD31059.1 AC007357 8 (AC007357) Identical
                  to gb Y13695 multicatalytic endopeptidase complex,
                  proteasome precursor, beta subunit (prce) from Arabidopsis
                  thaliana. ESTs gb_Y09360, gb_F13852, gb_T20555, gb_T44620,
                  gb AI099779 and gb AA5861
                  399317
Seq. No.
Seq. ID
                  LIB3431-023-P1-N1-A11
                  BLASTX
Method
NCBI GI
                  g1657621
BLAST score
                  146
                  4.0e-09
E value
Match length
                  36
% identity
                  (U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236)
NCBI Description
                  putative acyl-coA dehydrogenase [Arabidopsis thaliana]
                  >gi 5478795 dbj BAA82478.1 (AB017643) Short-chain acyl CoA
                  oxidase [Arabidopsis thaliana]
                  399318
Seq. No.
                  LIB3431-023-P1-N1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5803242
BLAST score
                  228
                  1.0e-125
E value
                  365
Match length
                  99
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
NCBI Description
Seq. No.
                  399319
Seq. ID
                  LIB3431-023-P1-N1-A4
Method
                  BLASTX
NCBI GI
                  g5734618
BLAST score
                  154
E value
                  4.0e-10
                  93
Match length
% identity
                  (AP000391) Similar to Arabidopsis thaliana chromosome II
NCBI Description
                  BAC F5H14 genomic sequence; unknown protein (AC006234)
```

>gi 226872 prf 1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

[Oryza sativa]

E value

Match length

% identity

7.0e-56

99

```
Seq. No.
                   399320
Seq. ID
                   LIB3431-023-P1-N1-A6
Method
                   BLASTN
NCBI GI
                   q304219
BLAST score
                   36
E value
                   5.0e-11
Match length
                   68
% identity
NCBI Description
                   Hordeum vulgare chloroplast photosystem I PSK-I subunit
                   mRNA, complete cds
                   399321
Seq. No.
                   LIB3431-023-P1-N1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g347451
BLAST score
                   207
E value
                   3.0e-16
Match length
                   39
                  · 100
% identity
NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                   sativa]
Seq. No.
                   399322
Seq. ID
                   LIB3431-023-P1-N1-B5
Method
                   BLASTN
NCBI GI
                   g3885887
BLAST score
                   164.
E value
                   4.0e-87
Match length
                   272
% identity
NCBI Description
                   Oryza sativa high mobility group protein (HMG) mRNA,
                   complete cds
                   399323
Seq. No.
                   LIB3431-023-P1-N1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1076724
BLAST score
                   263
                   7.0e-23
E value
                   56
Match length
% identity
NCBI Description
                   LHCI-680, photosystem I antenna protein - barley
                   >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                   antenna protei\overline{n} [Hordeu\overline{m} vulgare]
                   399324
Seq. No.
                   LIB3431-023-P1-N1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g671740
BLAST score
                   546
```

100 (X84730) ribulose-bisphosphate carboxylase [synthetic NCBI Description construct]

```
399325
Seq. No.
Seq. ID
                  LIB3431-023-P1-N1-C2
                  BLASTX
Method
NCBI GI
                  g231610
BLAST score
                  215
                  3.0e-17
E value
Match length
                  65
% identity
                  74
                  ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 67880 pir PWNTG H+-transporting ATP synthase (EC
                  3.6.1.34) gamma chain precursor, chloroplast - common
                  tobacco >gi 19785 emb CAA45152 (X63606) ATP synthase
                  (gamma subunit) [Nicotiana tabacum]
                  399326
Seq. No.
                  LIB3431-023-P1-N1-C3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g606816
BLAST score
                  301
E value
                  1.0e-169
                  321
Match length
% identity
                  98
                  Oryza sativa chloroplast carbonic anhydrase mRNA, complete
NCBI Description
                  399327
Seq. No.
Seq. ID
                  LIB3431-023-P1-N1-C4
Method
                  BLASTN
NCBI GI
                  q2072554
BLAST score
                  403
E value
                  0.0e + 00
                  403
Match length
                  100
% identity
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                  399328
Seq. No.
Seq. ID
                  LIB3431-023-P1-N1-C5
Method
                  BLASTX
NCBI GI
                  g3183079
BLAST score
                  629
E value
                  1.0e-65
                  147
Match length
% identity
                  82
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
NCBI Description
                  >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate
                  dehydrogenase [Oryza sativa]
                  399329
Seq. No.
                  LIB3431-023-P1-N1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g731707
BLAST score
                  204
E value
                  2.0e-22
Match length
                  116
% identity
                  47
NCBI Description SET1 PROTEIN >gi 626647 pir S48961 hypothetical protein
```

Method

BLASTX

```
399330
Seq. No.
Seq. ID
                  LIB3431-023-P1-N1-D11
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  405
                  0.0e+00
E value
Match length
                  405
                  100
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  cds
                  399331
Seq. No.
                  LIB3431-023-P1-N1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g671740
BLAST score
                  388
                  3.0e-37
E value
Match length
                  115
% identity
                  53
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                  399332
                  LIB3431-023-P1-N1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5816996
BLAST score
                  333
E value
                  6.0e-31
Match length
                  86
% identity
                  79
                  (AL110123) ribosomal protein L32-like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  399333
                  LIB3431-023-P1-N1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  402
E value
                  4.0e-39
Match length
                  73
% identity
                  100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  399334
Seq. ID
                  LIB3431-023-P1-N1-D5
```

YHR119w - yeast (Saccharomyces cerevisiae) >gi 529135

(U00059) Set1p [Saccharomyces cerevisiae]

E value

2.0e-28

```
NCBI GI
                  g3885519
                  164
BLAST score
                   2.0e-11
E value
                   35
Match length
% identity
                   (AF084204) similar to ribosomal protein L32 [Medicago
NCBI Description
                  sativa]
                   399335
Seq. No.
                  LIB3431-023-P1-N1-D9
Seq. ID
                  BLASTX
Method
                   g1070408
NCBI GI
BLAST score
                   148
                   2.0e-09
E value
                  27
Match length
                   100
% identity
                  ferredoxin [2Fe-2S] I - rice
NCBI Description
                   399336
Seq. No.
                   LIB3431-023-P1-N1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3929924
BLAST score
                   292
E value
                   3.0e-26
                   56
Match length
                   98
% identity
                   (AB020502) catalase [Oryza sativa]
NCBI Description
                   399337
Seq. No.
                   LIB3431-023-P1-N1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3789954
BLAST score
                   384
                   5.0e-37
E value
Match length
                   71
                  100
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   399338
Seq. No.
Seq. ID
                   LIB3431-023-P1-N1-E3
                   BLASTX
Method
                   g100849
NCBI GI
BLAST score
                   367
E value
                   4.0e-35
                   85
Match length
                   86
% identity
                   acetolactate synthase (EC 4.1.3.18) (clone pSOG108) - maize
NCBI Description
                   >gi_22139_emb_CAA45116_ (X63553) acetohydroxyacid synthase
                   [Zea mays]
                   399339
Seq. No.
Seq. ID
                   LIB3431-023-P1-N1-E5
                   BLASTX
Method
NCBI GI
                   g131225
BLAST score
                   311
```

```
89
Match length
% identity
                   69
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                   precursor - barley >gi_167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
Seq. No.
                   399340
Seq. ID
                   LIB3431-023-P1-N1-F10
Method
                   BLASTX
NCBI GI
                   q4033838
BLAST score
                   251
E value
                   2.0e-21
Match length
                   60
                   80
% identity
                   (Y18550) sigma-like factor [Arabidopsis thaliana]
NCBI Description
                   >gi 4972299 dbj BAA78109.1 (AB021120) RNA polymerase sigma
                   subunit SigE [Arabidopsis thaliana]
                   399341
Seq. No.
                   LIB3431-023-P1-N1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g6103011
BLAST score
                   352
E value
                   2.0e-33
                   75
Match length
% identity
                   47
                   (X84225) precursor of photosystem II subunit (22KDa)
NCBI Description
                   [Nicotiana tabacum]
                   399342
Seq. No.
                   LIB3431-023-P1-N1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q289920
BLAST score
                   300
E value
                   3.0e-27
                   57
Match length
% identity
                   100
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   399343
Seq. No.
                   LIB3431-023-P1-N1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g118170
BLAST score
                   307
E value
                   6.0e-28
                   59
Match length
                   100
% identity
                   CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I)
NCBI Description
                   >gi_82491_pir__A28464 oryzacystatin - rice >gi_169784
(J03469) oryzacystatin [Oryza sativa] >gi_169807 (M29259)
                   oryzastatin [Oryza sativa] >gi_259137 bbs 120195 (S49967)
                   oryzacystatin=cysteine protease inhibitor [Oryza=rice,
                   Peptide, 102 aa] [Oryza] >gi_1280613 (U54702) oryzacystatin
```

[Oryza sativa]

Method

BLASTX

```
Seq. No.
                   399344
Seq. ID
                   LIB3431-023-P1-N1-F5
Method
                   BLASTX
NCBI GI
                   g115794
BLAST score
                   467
                   9.0e-47
E value
                   94
Match length
% identity
                   91
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
                   III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato
                   >gi_19277_emb_CAA42818_ (X60275) LHCII type III
                   [Lycopersicon esculentum]
Seq. No.
                   399345
Seq. ID
                   LIB3431-023-P1-N1-F6
Method
                   BLASTX
NCBI GI
                   q547712
BLAST score
                   219
E value
                   1.0e-17
Match length
                   43
                   100
% identity
NCBI Description
                   EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)
                   >gi_542153_pir__S38358 translation initiation factor eIF-4A
                   - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic
                   initiation factor 4A [Oryza sativa]
                   399346
Seq. No.
Seq. ID
                   LIB3431-023-P1-N1-F7
Method
                   BLASTX
NCBI GI
                   q347451
BLAST score
                   169
                   8.0e-12
E value
                   32
Match length
                   100
% identity
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                   sativa]
                   399347
Seq. No.
Seq. ID
                   LIB3431-023-P1-N1-F9
Method
                   BLASTX
NCBI GI
                   q134034
BLAST score
                   238
                   6.0e-20
E value
Match length
                   66
% identity
NCBI Description
                   30S RIBOSOMAL PROTEIN S30, CHLOROPLAST PRECURSOR (CS-S5)
                   (CS5) (S22) (RIBOSOMAL PROTEIN 1) (PSRP-1)
                   >gi_279640_pir__R3SPS5 ribosomal protein CS-S22 precursor,
                   chloroplast - spinach >gi_12316_emb_CAA41960_ (X59270)
                   chloroplast ribosomal protein S22 [Spinacia oleracea]
                   >gi_18031_emb_CAA33403_ (X15344) spinach S22 r-protein
                   [Spinacia oleracea]
                   399348
Seq. No.
                   LIB3431-023-P1-N1-G10
Seq. ID
```

NCBI GI

g132105

```
g421916
NCBI GI
                  199
BLAST score
                  2.0e-15
E value
                  37
Match length
                  100
% identity
                  chlorophyll a/b-binding protein - English ivy (fragment)
NCBI Description
                  >gi_12582_emb_CAA48410_ (X68333) light harvesting
                  chlorophyll a /b binding protein [Hedera helix]
Seq. No.
                  399349
                  LIB3431-023-P1-N1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2072555
BLAST score
                  237
                  9.0e-20
E value
Match length
                  44
                  100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  399350
Seq. ID
                  LIB3431-023-P1-N1-G5
Method
                  BLASTX
NCBI GI
                  q2130069
BLAST score
                  192
E value
                  2.0e-14
Match length
                  39
                  95
% identity
NCBI Description
                  catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  399351
Seq. ID
                  LIB3431-023-P1-N1-G7
Method
                  BLASTX
NCBI GI
                  q4972093
BLAST score
                  236
                  1.0e-19
E value ·
Match length
                  59
                   76
% identity
NCBI Description
                  (AL078468) putative protein [Arabidopsis thaliana]
                  399352
Seq. No.
                  LIB3431-023-P1-N1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3789954
BLAST score
                  329
E value
                  1.0e-30
Match length
                  62
% identity
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  399353
Seq. No.
                  LIB3431-023-P1-N1-G9
Seq. ID
Method
                  BLASTX
```

Seq. ID

```
BLAST score
                   507
                   2.0e-51
E value
Match length
                   93
% identity
                   99
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >qi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >qi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  399354
Seq. ID
                  LIB3431-023-P1-N1-H10
Method
                  BLASTN
NCBI GI
                  g455510
BLAST score
                  100
E value
                  8.0e-49
Match length
                  104
% identity
                  99
NCBI Description Rice mRNA for ferritin, partial sequence
Seq. No.
                  399355
Seq. ID
                  LIB3431-023-P1-N1-H11
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  226
E value
                  1.0e-124
Match length
                  338
% identity
                  92
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                  399356
Seq. No.
Seq. ID
                  LIB3431-023-P1-N1-H12
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  284
E value
                  2.0e-25
Match length
                  71
% identity
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                  399357
Seq. ID
                  LIB3431-023-P1-N1-H4
Method
                  BLASTX
NCBI GI
                  g871931
BLAST score
                  204
E value
                  7.0e-16
Match length
                  38
% identity
NCBI Description
                  (D30763) ferredoxin [Oryza sativa]
Seq. No.
                  399358
```

LIB3431-023-P1-N1-H8

```
BLASTX
Method
NCBI GI
                   g115813
                   220
BLAST score
                   8.0e-18
E value
Match length
                   53
% identity
                   81
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                   CAB-8) >gi 19182_emb_CAA33330_ (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
                   399359
Seq. No.
                   LIB3431-023-P1-N1-H9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3914430
BLAST score
                   241
                   3.0e-20
E value
                   75
Match length
                   60
% identity
NCBI Description
                   PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
                   CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
                   >gi 2285800 dbj BAA21650 (D78172) 26S proteasome beta
                   subunit [Spinacia oleracea]
                   399360
Seq. No.
Seq. ID
                   LIB3431-024-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   q5902390
BLAST score
                   218
E value
                   1.0e-17
Match length
                   109
% identity
NCBI Description
                   (AC008148) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   399361
Seq. ID
                   LIB3431-024-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   q135535
BLAST score
                   377
E value
                   2.0e-36
Match length
                   93
                   81
% identity
                   T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
NCBI Description
                   (CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide
                   Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_
(D11351) t-complex polypeptide 1 homologue [Arabidopsis
                   thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT
                   alpha/TCP-1 [Arabidopsis thaliana]
Seq. No.
                   399362
Seq. ID
                   LIB3431-024-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   q3885894
BLAST score
                   565
E value
                   4.0e-58
Match length
                   139
% identity
NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
```

Match length

119

```
Seq. No.
                  399363
Seq. ID
                  LIB3431-024-P1-K1-A4
Method
                  BLASTN
NCBI GI
                  g487319
BLAST score
                  47
E value
                  3.0e-17
Match length
                  47
                  100
% identity
NCBI Description Rice mRNA EN66, partial sequence
Seq. No.
                  399364
Seq. ID
                  LIB3431-024-P1-K1-A7
                  BLASTX
Method
NCBI GI
                  g5902390
BLAST score
                  174
E value
                  2.0e-12
Match length
                  119
                  40
% identity
                  (AC008148) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  399365
Seq. No.
Seq. ID
                  LIB3431-024-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  673
                  6.0e-71
E value
                  125
Match length
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
Seq. No.
                  399366
                  LIB3431-024-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  530
                  4.0e-54
E value
Match length
                  96
% identity
                  100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  399367
                  LIB3431-024-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g729478
BLAST score
                  343
E value
                  3.0e-32
```

Seq. ID

```
% identity
NCBI Description
                  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
                  >gi 442481 dbj BAA04616 (D17790) ferredoxin-NADP+
                  reductase [Oryza sativa] >gi 6069649 dbj BAA85425.1
                  (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
                  a region of the predicted gene.; similar to
                  ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
                  399368
Seq. No.
Seq. ID
                  LIB3431-024-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q1707998
BLAST score
                  227
E value
                  1.0e-18
Match length
                  83
                  59
% identity
                  SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi_481944_pir__S40218 glycine
                  hydroxymethyltransferase (EC 2.1.2.1) - potato
                  >gi 438247 emb CAA81082_ (Z25863) glycine
                  hydroxymethyltransferase [Solanum tuberośum]
Seq. No.
                  399369
Seq. ID
                  LIB3431-024-P1-K1-B12
Method
                  BLASTX
                  g167097
NCBI GI
BLAST score
                  279
E value
                  3.0e-37
Match length
                  95
                  83
% identity
                   (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                  [Hordeum vulgare]
Seq. No.
                  399370
Seq. ID
                  LIB3431-024-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  q20262
BLAST score
                  139
E value
                  2.0e-72
Match length
                  159
                  97
% identity
NCBI Description O.sativa light-induced mRNA
Seq. No.
                  399371
Seq. ID
                  LIB3431-024-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q3789954
BLAST score
                  623
E value
                  4.0e-65
Match length
                  115
% identity
                  100
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
Seq. No.
                  399372
```

LIB3431-024-P1-K1-B5



```
BLASTX
Method
                  g131225
NCBI GI
                  350
BLAST score
                  3.0e-33
E value
                  76
Match length
                  89
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  399373
                  LIB3431-024-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  237
                  6.0e-20
E value
Match length
                  44
                  100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >qi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  399374
                  LIB3431-024-P1-K1-B7
Seq. ID
Method
                  BLASTX-
NCBI GI
                  g1835731
BLAST score
                  479
E value
                   4.0e-48
Match length
                  102
                  89
% identity
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                  399375
Seq. ID
                  LIB3431-024-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  531
E value
                  2.0e-54
Match length
                  101
                  100
% identity
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                  399376
Seq. ID
                  LIB3431-024-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g4512616
BLAST score
                  497
                  3.0e-50
E value
Match length
                  120
% identity
                   (AC004793) Contains similarity to qi 1653332 extragenic
NCBI Description
                  suppressor (SuhB) from Synechocystis sp. gb D90912 and is a
                  member of the Inositol monophophatase family PF 00459. EST
```

Seq. No. 399377

gb AA597395 comes from this gene. [Arabidopsis tha

Seq. ID

```
LIB3431-024-P1-K1-C10
Seq. ID
Method
                  BLASTX
                  g2407279
NCBI GI
BLAST score
                  315
                  7.0e-29
E value
Match length
                  63
                  97
% identity
                  (AF017362) aldolase [Oryza sativa]
NCBI Description
                  399378
Seq. No.
                  LIB3431-024-P1-K1-C11
Seq. ID
                  BLASTX
Method
                  g320618
NCBI GI
BLAST score
                  458
                  9.0e-46
E value
Match length
                  106
                  83
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi 218172 dbj BAA00536 (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >qi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                  399379
Seq. No.
                  LIB3431-024-P1-K1-C12
Seq. ID
Method
                  BLASTX
                  g1835731
NCBI GI
BLAST score
                  322
E value
                  9.0e-30
                  72
Match length
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                  399380
                  LIB3431-024-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4938486
BLAST score
                  327
E value
                  1.0e-30
Match length
                  78
% identity
                   (AL078464) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  399381
Seq. ID
                  LIB3431-024-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g482445
                  604
BLAST score
E value
                  6.0e-63
Match length
                  121
                  95
% identity
                  chlorophyll a/b-binding protein precursor - swollen
NCBI Description
                  duckweed >gi_168296 (M29334) light-harvesting chlorophyll
                  a/b protein precursor [Lemna gibba]
Seq. No.
                  399382
```

LIB3431-024-P1-K1-C6

Seq. ID

```
Method
                  BLASTX
                  q4884866
NCBI GI
                  275
BLAST score
                  2.0e-24
E value
Match length
                  96
                  57
% identity
                   (AF133531) water channel protein MipI [Mesembryanthemum
NCBI Description
                  crystallinum]
                  399383
Seq. No.
                  LIB3431-024-P1-K1-C7
Seq. ID
Method
                  BLASTX
                  g3402713
NCBI GI
                  248
BLAST score
E value
                  5.0e-21
Match length
                  64
                  72
% identity
                  (AC004261) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  399384
                  LIB3431-024-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
                  9.0e-20
E value
Match length
                  44
                  100
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >qi 6103441 qb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  399385
Seq. ID
                  LIB3431-024-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  g20181
BLAST score
                  58
                  5.0e-24
E value
Match length
                  62
                  98
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
Seq. No.
                  399386
                  LIB3431-024-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913641
BLAST score
                  483
                   6.0e-49
E value
Match length
                  95
% identity
                  FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi 3041777 dbj BAA25423 (AB007194)
                  fructose-1,6-bisphosphatase [Oryza sativa]
Seq. No.
                  399387
                  LIB3431-024-P1-K1-D10
```

Method

BLASTX

```
Method
                  BLASTX
                  q4689380
NCBI GI
BLAST score
                  620
                  9.0e-65
E value
                  125
Match length
% identity
                   (AF139465) LHCII type III chlorophyll a/b binding protein
NCBI Description
                   [Vigna radiata]
                  399388
Seq. No.
                  LIB3431-024-P1-K1-D12
Seq. ID
Method
                  BLASTX
                  g320618
NCBI GI
BLAST score
                   463
E value
                   2.0e-46
Match length
                  106
% identity
                  83
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                  399389
                  LIB3431-024-P1-K1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2306980
BLAST score
                  150
E value
                  7.0e-79
Match length
                   174
% identity
                   97
                  Oryza sativa photosystem I antenna protein (Lhca) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   399390
                  LIB3431-024-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g871931
BLAST score
                   361
E value
                   1.0e-36
Match length
                   85
% identity
                   (D30763) ferredoxin [Oryza sativa]
NCBI Description
Seq. No.
                   399391
                  LIB3431-024-P1-K1-D4
Seq. ID
Method
                  BLASTN
NCBI GI
                   g6015437
                   35
BLAST score
E value
                   4.0e-10
                   35
Match length
                   100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   399392
                  LIB3431-024-P1-K1-D6
Seq. ID
```

Method

BLASTX

```
NCBI GI
                  g2342719
BLAST score
                  324
E value
                  6.0e-30
                  139
Match length
% identity
                  50
                  (AC002341) SF16 protein isolog [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  399393
                  LIB3431-024-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4585882
BLAST score
                  399
E value
                  7.0e-39
Match length
                  127
                  62
% identity
NCBI Description
                   (AC005850) PSI type III chlorophyll a/b-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                  399394
Seq. ID
                  LIB3431-024-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  547
E value
                  3.0e-56
                  108
Match length
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
Seq. No.
                  399395
                  LIB3431-024-P1-K1-E10
Seq. ID
                  BLASTX
Method
                  q133936
NCBI GI
BLAST score
                   685
E value
                  3.0e-72
Match length
                  132
                  100
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi 70867 pir R3RZ3
NCBI Description
                  ribosomal protein S3 - rice chloroplast
                  >qi 12025 emb CAA33934 (X15901) ribosomal protein S3
                   [Oryza sativa] >gi_226646_prf__1603356BW ribosomal protein
                  S3 [Oryza sativa]
                  399396
Seq. No.
                  LIB3431-024-P1-K1-E12
Seq. ID
Method
                  BLASTX
                  g2130069
NCBI GI
BLAST score
                  749
                  8.0e-80
E value
Match length
                  135
% identity
                  99
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]
Seq. No.
                  399397
Seq. ID
                  LIB3431-024-P1-K1-E2
```

```
NCBI GI
                  g2827516
                  264
BLAST score
E value
                   5.0e-23
Match length
                  89
                  55
% identity
                   (AL021633) DNA topoisomerase like-protein [Arabidopsis
NCBI Description
                  thaliana]
                   399398
Seq. No.
Seq. ID
                  LIB3431-024-P1-K1-E3
Method
                  BLASTN
NCBI GI
                   g20181
BLAST score
                   109
                   4.0e-54
E value
                   113
Match length
                   99
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                   a/b-binding protein
                   399399
Seq. No.
                   LIB3431-024-P1-K1-E4
Seq. ID
                   BLASTX
Method
                   g1835731
NCBI GI
BLAST score
                   412
                   2.0e-40
E value
                                                                        .
Match length
                   81
% identity
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                   399400
                   LIB3431-024-P1-K1-E7
Seq. ID
                   BLASTN
Method
                   q6015437
NCBI GI
                   35
BLAST score
                   6.0e-10
E value
                   35
Match length
                   100
% identity
                   Homo sapiens PEX1 mRNA, complete cds
NCBI Description
                   399401
Seq. No.
                   LIB3431-024-P1-K1-E8
Seq. ID
                   BLASTX
Method
                   q320617
NCBI GI
                   471
BLAST score
                   2.0e-48
E value
Match length
                   122
% identity
                   chlorophyll a/b-binding protein II precursor - rice
NCBI Description
                   >gi 227612 prf 1707316B chlorophyll a/b binding protein 2
                   [Oryza sativa]
                   399402
Seq. No.
                   LIB3431-024-P1-K1-F1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2072555
                   237
BLAST score
```

9.0e-20

E value

```
Match length
                  44
                  100
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >qi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  399403
                  LIB3431-024-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  606
                   4.0e-63
E value
Match length
                  114
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  399404
                  LIB3431-024-P1-K1-F2
Seq. ID
Method
                  BLASTX
                  q5360230
NCBI GI
                  500
BLAST score
                   5.0e-51
E value
Match length
                  88
% identity
NCBI Description
                  (AB015287) Ran [Oryza sativa]
                  399405
Seq. No.
                  LIB3431-024-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g462195
                   309
BLAST score
                   3.0e-28
E value
                  74
Match length
                   81
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi_100682_pir__S21636 GOS2 protein - rice
                  >qi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                  >gi 3789950 (AF094774) translation initiation factor [Oryza
                  satīva]
Seq. No.
                  399406
                  LIB3431-024-P1-K1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4582436
BLAST score
                  388
                  1.0e-37
E value
Match length
                  94
% identity
                   (AC007196) unknown protein [Arabidopsis thaliana]
NCBI Description
                   399407
Seq. No.
                  LIB3431-024-P1-K1-F5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g6015437
                  36
BLAST score
                  1.0e-10
E value
```

36

Match length

Seq. ID

```
100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  399408
Seq. No.
Seq. ID
                  LIB3431-024-P1-K1-F7
                  BLASTX
Method
                  g4929312
NCBI GI
                  233
BLAST score
                  8.0e-29
E value
Match length
                  123
% identity
                  59
NCBI Description (AF145045) TATC [Arabidopsis thaliana]
Seq. No.
                  399409
                  LIB3431-024-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2564253
BLAST score
                  361
                  2.0e-34
E value
Match length
                  83
                  81
% identity
                  (Z99996) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase
NCBI Description
                  [Hordeum vulgare]
Seq. No.
                  399410
                  LIB3431-024-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2245062
BLAST score
                  418
                  5.0e-41
E value
                  104
Match length
                  77
% identity
NCBI Description (Z97342) hypothetical protein [Arabidopsis thaliana]
                  399411
Seq. No.
                  LIB3431-024-P1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2190543
BLAST score
                  145
                  3.0e-09
E value
Match length
                  98
% identity
                  (AC001229) EST gb N37484 comes from this gene. [Arabidopsis
NCBI Description
                  thaliana]
                  399412
Seq. No.
                  LIB3431-024-P1-K1-G10
Seq. ID
                  BLASTX
Method
                  g4883530
NCBI GI
BLAST score
                  235
                  1.0e-19
E value
Match length
                  110
% identity
                  48
                  (AF123266) remorin 2 [Lycopersicon esculentum]
NCBI Description
Seq. No.
                  399413
```

LIB3431-024-P1-K1-G12

```
Method
                  BLASTX
NCBI GI
                  g5902158
BLAST score
                  246
                  6.0e-21
E value
Match length
                  75
                  56
% identity
                  zinc finger protein 183 (RING finger, C3HC4 type)
NCBI Description
                  >gi 3123165_sp 015541_Z183 HUMAN ZINC FINGER PROTEIN 183
                  >qi 2274982 emb CAA66907 (X98253) ZNF183 [Homo sapiens]
                  >gi 2341022 (AC002477) zinc-finger protein [Homo sapiens]
Seq. No.
                  399414
                  LIB3431-024-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  237
                  6.0e-20
E value
Match length
                  44
% identity
                  100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  399415
                  LIB3431-024-P1-K1-G4
Seq. ID
                  BLASTX
Method
                  q115787
NCBI GI
BLAST score
                  380
E value
                  1.0e-36
Match length
                  92
                  85
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461 pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  399416
Seq. No.
                  LIB3431-024-P1-K1-G6
Seq. ID
Method
                  BLASTX
                  q1657859
NCBI GI
BLAST score
                  155
                  2.0e-10
E value
                  60
Match length
                  55
% identity
                  (U73218) chlorophyll a/b-binding protein WCAB precursor
NCBI Description
                  [Triticum aestivum]
                  399417
Seq. No.
Seq. ID
                  LIB3431-024-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q3386621
                  554
BLAST score
                  6.0e-57
E value
Match length
                  147
% identity
                  (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
```

E value

8.0e-20

```
Seq. No.
                  399418
Seq. ID
                  LIB3431-024-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q4538947
BLAST score
                  166
                  1.0e-11
E value
Match length
                  61
                  54
% identity
                  (AL049483) putative mitochondrial carrier protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  399419
Seq. ID
                  LIB3431-024-P1-K1-G9
                  BLASTX
Method
                  q132105
NCBI GI
BLAST score
                  289
                  4.0e-26
E value
Match length
                  76
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208 dbj BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  399420
Seq. No.
                  LIB3431-024-P1-K1-H1
Seq. ID
Method
                  BLASTX
                  q3885886
NCBI GI
BLAST score
                  327
                  8.0e-31
E value
                  65
Match length
% identity
                  (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
NCBI Description
Seq. No.
                  399421
Seq. ID
                  LIB3431-024-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q1931644
                  250
BLAST score
                  3.0e-21
E value
                  105
Match length
% identity
                  (U95973) membrane protein PTM1 precursor isolog
NCBI Description
                  [Arabidopsis thaliana]
                  399422
Seq. No.
                  LIB3431-024-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2072555
                  237
BLAST score
```

```
Match length
                  44
                  100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  399423
                  LIB3431-024-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                   6.0e-20
Match length
                   44
                  100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >qi 6103441 qb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  399424
                  LIB3431-024-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  189
E value
                   3.0e-14
Match length
                   49
% identity
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                   399425
Seq. ID
                  LIB3431-024-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q1498315
BLAST score
                   250
                  7.0e-25
E value
Match length
                   121
% identity
                   (U56419) IAP100 [Pisum sativum]
NCBI Description
                   399426
Seq. No.
Seq. ID
                  LIB3431-024-P1-K1-H5
Method
                  BLASTX
NCBI GI
                   q1617197
BLAST score
                   290
                   6.0e-26
E value
                  76
Match length
% identity
                   (Z72488) CP12 [Nicotiana tabacum]
NCBI Description
                   399427
Seq. No.
                  LIB3431-024-P1-K1-H6
Seq. ID
Method
                  BLASTN
                   q3821780
NCBI GI
                   34
BLAST score
E value
                   9.0e-10
Match length
                   34
                   100
% identity
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
```

```
399428
Seq. No.
                  LIB3431-024-P1-K1-H8
Seq. ID
                  BLASTX
Method
                  q3288821
NCBI GI
                  490
BLAST score
                  2.0e-49
E value
                  129
Match length
                  75
% identity
                 (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                  transaminase [Arabidopsis thaliana]
                  >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
                  alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
                  399429
Seq. No.
                  LIB3431-024-P1-N1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3345477
                  212
BLAST score
                  7.0e-17
E value
                  40
Match length
                  97
% identity
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
                  399430
Seq. No.
                  LIB3431-024-P1-N1-A3
Seq. ID
                  BLASTN
Method
                  g3885893
NCBI GI
BLAST score
                  99
                  3.0e-48
E value
Match length
                  131
% identity
NCBI Description Oryza sativa photosystem-1 H subunit GOS5 (PSI-H) mRNA,
                  complete cds
                  399431
Seq. No.
                  LIB3431-024-P1-N1-A9
Seq. ID
                  BLASTX
Method
                  g132105
NCBI GI
BLAST score
                  288
                  4.0e-26
E value
Match length
                  57
                  95
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   399432
                  LIB3431-024-P1-N1-B10
Seq. ID
```

BLASTX

q729478

Method NCBI GI

100

```
BLAST score
                   370
                   2.0e-35
E value
Match length
                   73
                   92
% identity
                   FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                   >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1
                   (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
                   a region of the predicted gene.; similar to
                   ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
                   399433
Seq. No.
                   LIB3431-024-P1-N1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132166
BLAST score
                   156
                   2.0e-10
E value
Match length
                   31
                   84
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                   CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                   >gi 81660 pir S04048 ribulose-bisphosphate carboxylase
                   activase precursor - Arabidopsis thaliana
                   >gi 16471 emb CAA32429 (X14212) rubisco activase (AA 1 -
                   473) [Arabidopsis thaliana]
                   399434
Seq. No.
Seq. ID
                   LIB3431-024-P1-N1-B2
Method
                   BLASTX
                   q417260
NCBI GI
BLAST score
                   268
                   2.0e-23
E value
                   69
Match length
% identity
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003_pir__S33632
NCBI Description
                   lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                   light-regulated gene [Oryza sativa]
Seq. No.
                   399435
                   LIB3431-024-P1-N1-B4
Seq. ID
Method
                   BLASTX
                   g3789954
NCBI GI
BLAST score
                   335
                   3.0e-31
E value
Match length
                   62
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
Seq. No.
                   399436
Seq. ID
                   LIB3431-024-P1-N1-B5
Method
                   BLASTX
NCBI GI
                   g131225
BLAST score
                   196
                   5.0e-15
E value
Match length
                   51
```

73

% identity

NCBI GI

```
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi 100605 pir_ A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  399437
                  LIB3431-024-P1-N1-B6
Seq. ID
Method
                  BLASTX
                  g2072555
NCBI GI
BLAST score
                  196
                  5.0e-15
E value
Match length
                  37
                  100
% identity
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  399438
                  LIB3431-024-P1-N1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131225
BLAST score
                  216
E value
                  2.0e-17
Match length
                  56
                  73
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein
                  precursor - barley >qi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  399439
                  LIB3431-024-P1-N1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1835731
BLAST score
                  590
E value
                  4.0e-61
Match length
                  126
% identity
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                  399440
Seq. ID
                  LIB3431-024-P1-N1-C1
Method
                  BLASTX
NCBI GI
                  q4512616
BLAST score
                  334
E value
                  3.0e-31
Match length
                  80
% identity
NCBI Description
                  (AC004793) Contains similarity to gi 1653332 extragenic
                  suppressor (SuhB) from Synechocystis sp. gb D90912 and is a
                  member of the Inositol monophophatase family PF 00459. EST
                  gb AA597395 comes from this gene. [Arabidopsis tha
Seq. No.
                  399441
Seq. ID
                  LIB3431-024-P1-N1-C10
Method
                  BLASTX
```

g2407279

```
BLAST score
                  216
                  2.0e-17
E value
Match length
                  44
% identity
                  100
NCBI Description (AF017362) aldolase [Oryza sativa]
                  399442
Seq. No.
Seq. ID
                  LIB3431-024-P1-N1-C11
Method ·
                  BLASTX
NCBI GI
                  q3036946
BLAST score
                  319
                  2.0e-29
E value
Match length
                  61
% identity
                   (AB012637) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                  399443
Seq. No.
Seq. ID
                  LIB3431-024-P1-N1-C12
Method
                  BLASTX
                  q1835731
NCBI GI
                  188
BLAST score
                  3.0e-14
E value
Match length
                  48
                  77
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                  399444
Seq. No.
Seq. ID
                  LIB3431-024-P1-N1-C3
Method
                  BLASTX
NCBI GI
                  g3036942
BLAST score
                  243
                  1.0e-20
E value
Match length
                  45
                  100
% identity
                   (AB012636) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                  399445
Seq. No.
Seq. ID
                  LIB3431-024-P1-N1-C8
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  246
                  1.0e-136
E value
Match length
                  282
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  cds
                  399446
Seq. No.
Seq. ID
                  LIB3431-024-P1-N1-D1
Method
                  BLASTX
NCBI GI
                  g3913641
BLAST score
                  211
                  4.0e-17
E value
Match length
                  41
```

100

% identity

```
NCBI Description FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                  (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi 3041777 dbj_BAA25423_ (AB007194)
                  fructose-1,6-bisphosphatase [Oryza sativa]
                  399447
Seq. No.
                  LIB3431-024-P1-N1-D10
Seq. ID
                  BLASTX
Method
                  g479406
NCBI GI
                  396
BLAST score
                  2.0e-38
E value
Match length
                  78
                  95
% identity
                  chlorophyll a/b-binding protein - garden pea
NCBI Description
                  >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding
                  protein [Pisum sativum]
Seq. No.
                  399448
                  LIB3431-024-P1-N1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3510256
BLAST score
                  194
E value
                  7.0e-15
Match length
                  48
                  67
% identity
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]
                  399449
Seq. No.
Seq. ID
                  LIB3431-024-P1-N1-D12
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  432
                  1.0e-42
E value
Match length
                  82
% identity
                  100
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  399450
                  LIB3431-024-P1-N1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q551047
BLAST score
                  268
                  2.0e-23
E value
Match length
                  52
                  96
% identity
                  (X79277) type II LHCI [Lolium temulentum]
NCBI Description
                  399451
Seq. No.
                  LIB3431-024-P1-N1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2305114
BLAST score
                  291
                  1.0e-163
E value
```

NCBI Description

```
Match length
                  334
                  97
% identity
NCBI Description
                  Oryza sativa ferredoxin mRNA, complete cds
                  399452
Seq. No.
                  LIB3431-024-P1-N1-D4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  35
                  4.0e-10
E value
Match length
                  35
% identity
                  100
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
Seq. No.
                  399453
Seq. ID
                  LIB3431-024-P1-N1-D9
Method
                  BLASTX
NCBI GI
                  q115813
BLAST score
                  233
                  2.0e-19
E value
Match length
                  53
                  85
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >qi 19182 emb CAA33330 (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  399454
Seq. No.
                  LIB3431-024-P1-N1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q347451
BLAST score
                  224
                  3.0e-18
E value
                   46
Match length
% identity
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa]
                  399455
Seq. No.
                  LIB3431-024-P1-N1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2130069
BLAST score
                  194
                   9.0e-15
E value
                  39
Match length
% identity
                  95
NCBI Description
                  catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
                  399456
Seq. No.
                  LIB3431-024-P1-N1-E3
Seq. ID
Method
                  BLASTN
                  q20181
NCBI GI
BLAST score
                  106
E value
                  2.0e-52
Match length
                  113
% identity ~
                  Rice cab2R gene for light harvesting chlorophyll
```

a/b-binding protein

```
399457
Seq. No.
Seq. ID
                  LIB3431-024-P1-N1-E4
Method
                  BLASTX
                  q1835731
NCBI GI
                  297
BLAST score
E value
                  7.0e-27
                  67
Match length
% identity
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  399458
Seq. No.
                  LIB3431-024-P1-N1-E8
Seq. ID
Method
                  BLASTX
                  g3126854
NCBI GI
                  240
BLAST score
E value
                  3.0e-20
Match length
                  65
% identity
                  74
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  399459
Seq. No.
Seq. ID
                  LIB3431-024-P1-N1-F1
                  BLASTN
Method
NCBI GI
                  q2072554
                  388
BLAST score
                  0.0e+00
E value
                  388
Match length
                  100
% identity
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                  cds
                  399460
Seq. No.
Seq. ID
                  LIB3431-024-P1-N1-F10
Method
                  BLASTX
NCBI GI
                  g3126854
                  261
BLAST score
                  1.0e-22
E value
                  52
Match length
                  94
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  399461
Seq. No.
                  LIB3431-024-P1-N1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q6069643
BLAST score
                  51
E value
                  1.0e-19
                  79
Match length
                  91
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0514G12
Seq. No.
                  399462
                  LIB3431-024-P1-N1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5360229
```

Match length

NCBI Description

% identity

65

52

```
BLAST score
                   394
                   0.0e + 00
E value
                   419
Match length
                   98
% identity
                   Oryza sativa mRNA for Ran, complete cds
NCBI Description
Seq. No.
                   399463
                   LIB3431-024-P1-N1-F3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3789949
BLAST score
                   83
                   1.0e-38
E value
                   95
Match length
                   97
% identity
                   Oryza sativa translation initiation factor (GOS2) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   399464
                   LIB3431-024-P1-N1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4582436
BLAST score
                   162
E value
                   7.0e-11
Match length
                   77
% identity
                   47
                   (AC007196) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   399465
Seq. ID
                   LIB3431-024-P1-N1-F7
Method
                   BLASTX
NCBI GI
                   g4929312
BLAST score
                   203
E value
                   7.0e-16
Match length
                   70
% identity
                   63
                   (AF145045) TATC [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   399466
Seq. ID
                   LIB3431-024-P1-N1-G10
Method
                   BLASTX
NCBI GI
                   g4731573
BLAST score
                   201
E value
                   1.0e-15
Match length
                   48
                   77
% identity
NCBI Description
                   (AF123265) remorin 1 [Lycopersicon esculentum]
Seq. No.
                   399467
                   LIB3431-024-P1-N1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5262156
BLAST score
                   226
E value
                   2.0e-18
```

(AL080237) putative protein [Arabidopsis thaliana]

```
Seq. No.
                  399468
                  LIB3431-024-P1-N1-G2
Seq. ID
Method ·
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  227
                  1.0e-18
E value
Match length
                  44
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  399469
Seq. No.
                  LIB3431-024-P1-N1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115784
BLAST score
                  182
E value
                  2.0e-13
Match length
                  33
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I (CAB)
NCBI Description
                  (LHCP) >gi 167525 (M16058) chlorophyll a/b-binding protein
                  [Cucumis sativus]
Seq. No.
                  399470
Seq. ID
                  LIB3431-024-P1-N1-G5
Method
                  BLASTX
NCBI GI
                  q167097
BLAST score
                  151
E value
                  5.0e-17
Match length
                  52
% identity
                  (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                  [Hordeum vulgare]
Seq. No.
                  399471
Seq. ID
                  LIB3431-024-P1-N1-G6
Method
                  BLASTX
NCBI GI
                  g115784
BLAST score
                  150
E value
                  1.0e-09
Match length
                  33
                  85
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I (CAB)
                  (LHCP) >gi 167525 (M16058) chlorophyll a/b-binding protein
                  [Cucumis sativus]
Seq. No.
                  399472
Seq. ID
                  LIB3431-024-P1-N1-G9
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  320
E value
                  1.0e-29
Match length
                  61
% identity
                  98
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
```

```
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

399473
LIB3431-024-P1-N1-H1
BLASTX
```

Seq. ID LIB3431-024-P
Method BLASTX
NCBI GI g3885886
BLAST score 317
E value 3.0e-29
Match length 56
% identity 98

Seq. No.

NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]

 Seq. No.
 399474

 Seq. ID
 LIB3431-024-P1-N1-H12

 Method
 BLASTX

 NCBI GI
 g2072555

 BLAST score
 237

 E value
 9.0e-20

 Match longth
 44

Match length 44 % identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 399475

Seq. ID LIB3431-024-P1-N1-H2

Method BLASTN
NCBI GI g2072554
BLAST score 293
E value 1.0e-164
Match length 301
% identity 99

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 399476

Seq. ID LIB3431-024-P1-N1-H3

Method BLASTX
NCBI GI g1835731
BLAST score 189
E value 3.0e-14
Match length 49
% identity 78

NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.

Seq. ID LIB3431-024-P1-N1-H5

399477

Method BLASTX
NCBI GI g1617197
BLAST score 180
E value 3.0e-13

```
Match length
                  36
                  92
% identity
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
                  399478
Seq. No.
                  LIB3431-024-P1-N1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454458
BLAST score
                  208
                  2.0e-16
E value
Match length
                  69
% identity
                  62
                  (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  399479
Seq. ID
                  LIB3431-024-P1-N1-H8
Method
                  BLASTX
NCBI GI
                  q226263
BLAST score
                  155
                  3.0e-10
E value
Match length
                  31
                  94
% identity
                  chlorophyll a/b binding protein [Glycine max]
NCBI Description
Seq. No.
                  399480
                  LIB3431-025-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4325041
BLAST score
                  573
E value
                   5.0e-59
Match length
                  128
% identity
                   (AF117339) FtsH-like protein Pftf precursor [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                  399481
Seq. ID
                  LIB3431-025-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  330
E value
                  0.0e+00
Match length
                  330
                  100
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  399482
Seq. No.
                  LIB3431-025-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5702231
BLAST score
                  161
E value
                  9.0e-11
Match length
                  44
% identity
                   (AF145386) hypersensitive reaction associated Ca2+-binding
NCBI Description
```

protein [Phaseolus vulgaris]

```
Seq. No.
                  399483
                  LIB3431-025-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2501491
BLAST score
                  182
                  1.0e-13
E value
Match length
                  90
% identity
                  FLAVONOL 3-O-GLUCOSYLTRANSFERASE 1 (UDP-GLUCOSE FLAVONOID
NCBI Description
                  3-O-GLUCOSYLTRANSFERASE 1) >gi 542014_pir__S41950
                  UTP-glucose glucosyltransferase - cassava
                  >gi 453246 emb CAA54609 (X77459) UTP-glucose
                  glucosyltransferase [Manihot esculenta]
                  399484
Seq. No.
Seq. ID
                  LIB3431-025-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  433
                  1.0e-42
E value
Match length
                  79
% identity
                  99
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                  399485
Seq. ID
                  LIB3431-025-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q1362184
BLAST score
                  447
                  4.0e-44
E value
Match length
                  91
% identity
                  100
NCBI Description
                  histone H2B-8 - wheat >gi 531058 dbj BAA07157 (D37943)
                  protein H2B-8 [Triticum aestivum]
                  399486
Seq. No.
                  LIB3431-025-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076800
BLAST score
                  681
                  1.0e-71
E value
Match length
                  148
% identity
NCBI Description
                  L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
                  maize >qi 600116 emb CAA84406 (Z34934) cytosolic ascorbate
                  peroxidase [Zea mays] >gi 1096503 prf 2111423A ascorbate
                  peroxidase [Zea mays]
Seq. No.
                  399487
                  LIB3431-025-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3868756
BLAST score
                  842
                  2.0e-90
E value
Match length
                  154
```

100

% identity

```
NCBI Description (D86611) catalase [Oryza sativa]
Seq. No.
                  399488
                  LIB3431-025-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4753659
BLAST score
                  199
E value
                  3.0e-15
Match length
                  117
% identity
                  (AL049751) putative protein [Arabidopsis thaliana]
NCBI Description
                  399489
Seq. No.
                  LIB3431-025-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4104220
BLAST score
                  656
E value
                  1.0e-68
Match length
                  184
                  73
% identity
                  (AF033538) caffeic acid O-methyltransferase; LPOMT1 [Lolium
NCBI Description
                  perenne]
Seq. No.
                  399490
Seq. ID
                  LIB3431-025-P1-K1-C10
Method
                  BLASTX
                  g2245136
NCBI GI
BLAST score
                  786
E value
                  6.0e-84
Match length
                  216
                  69
% identity
                  (Z97344) trehalose-6-phosphate synthase like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  399491
                  LIB3431-025-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q629829
BLAST score
                  896
E value
                  8.0e-97
Match length
                  215
% identity
                  79
                  protochlorophyllide reductase (EC 1.3.1.33) - wheat
NCBI Description
                  >qi 510677 emb CAA54042 (X76532) protochlorophyilide
                  reductase [Triticum aestivum]
                  399492
Seq. No.
                  LIB3431-025-P1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  35
                  5.0e-10
E value
Match length
                  35
% identity
                  100
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
```

399493

Seq. No.

```
Seq. ID
                  LIB3431-025-P1-K1-C9
                  BLASTX
Method
                  g517500
NCBI GI
BLAST score
                  281
                  8.0e-25
E value
                  156
Match length
% identity
                  44
                  (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
Seq. No.
                  399494
                  LIB3431-025-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1353352
BLAST score
                  238
                  1.0e-37
E value
Match length
                  130
% identity
                  72
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
Seq. No.
                  399495
                  LIB3431-025-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2245136
BLAST score
                  416
E value
                  1.0e-40
Match length
                  176
% identity
                   (297344) trehalose-6-phosphate synthase like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  399496
Seq. ID
                  LIB3431-025-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g129233
BLAST score
                  615
E value
                  7.0e-64
Match length
                  118
                  97
% identity
NCBI Description
                  ORYZAIN GAMMA CHAIN PRECURSOR >gi 67646 pir KHRZOG oryzain
                   (EC 3.4.22.-) gamma precursor - rice
                  >gi 218185 dbj BAA14404 (D90408) oryzain gamma precursor
                   [Oryza sativa]
Seq. No.
                  399497
Seq. ID
                  LIB3431-025-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q1076725
BLAST score
                  419
E value
                  6.0e-41
Match length
                  92
% identity
NCBI Description
                  NADPH dehydrogenase (EC 1.6.99.1) - barley
                  >qi 683476 emb CAA59228 (X84738) NADPH dehydrogenase
```

[Hordeum vulgare]

```
399498
Seq. No.
                  LIB3431-025-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2055273
BLAST score
                  1024
                  1.0e-112
E value
Match length
                  236
                  83
% identity
NCBI Description
                  (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]
                  399499
Seq. No.
                  LIB3431-025-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555 ·
BLAST score
                  237
E value
                  1.0e-19
                  44
Match length
                  100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  399500
Seq. No.
                  LIB3431-025-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                  459
E value
                  1.0e-57
                  165
Match length
                  74
% identity
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
                  399501
Seq. No.
                  LIB3431-025-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2582822
BLAST score
                  606
E value
                  7.0e-63
                  168
Match length
% identity
                   (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
NCBI Description
                  Protein of 32kDa) [Solanum tuberosum]
                  399502
Seq. No.
                  LIB3431-025-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g462195
BLAST score
                  524
                  4.0e-53
E value
                  115
Match length
% identity
                  89
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi 100682 pir S21636 GOS2 protein - rice
                  >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                  >gi_3789950 (AF094774) translation initiation factor [Oryza
```

```
sativa]
                  399503
Seq. No.
                  LIB3431-025-P1-K1-E6
Seq. ID
Method
                  BLASTX
                  g2425101
NCBI GI
BLAST score
                  798
E value
                  3.0e-85
                  215
Match length
                  64
% identity
                  (AF019743) cationic peroxidase [Oryza sativa]
NCBI Description
                  399504
Seq. No.
                  LIB3431-025-P1-K1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1841354
BLAST score
                  66
                  2.0e-29
E value
                  66
Match length
                  100
% identity
                  Oryza sativa mitochondrial DNA for cytochrome c oxidase
NCBI Description
                  subunit Vb precursor, complete cds
                  399505
Seq. No.
                  LIB3431-025-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3913239
BLAST score
                  406
                  2.0e-39
E value
Match length
                  146
                  58
% identity
                  PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP
NCBI Description
                  SYNTHASE) >gi_2612941 (AF024512) CLA1 transketolase-like
                  protein [Oryza sativa]
                  399506
Seq. No.
                  LIB3431-025-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1084455
                  503
BLAST score
                  8.0e-51
E value
                  118
Match length
                  81
% identity
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
                  399507
Seq. No.
                  LIB3431-025-P1-K1-F11
Seq. ID
Method
                  BLASTX
                  g1777961
NCBI GI
                  958
BLAST score
                  1.0e-104
E value
                  233
Match length
% identity
                  (U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum
NCBI Description
```

vulgare]

Method

BLASTX

```
Seq. No.
                  399508
Seq. ID
                  LIB3431-025-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q400803
BLAST score
                  509
                  3.0e-64
E value
                  154
Match length
                  82
% identity
                  2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE
NCBI Description
                  (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I)
                  >gi_283033_pir__A42807 phosphoglycerate mutase (EC
                  5.4.2.1), 2, 3-bisphosphoglycerate-independent - maize
                  >gi 168588 (M80912) 2,3-bisphosphoglycerate-independent
                  phosphoglycerate mutase [Zea mays]
Seq. No.
                  399509
Seq. ID
                  LIB3431-025-P1-K1-F2
Method
                  BLASTX
                  q132105
NCBI GI
                  423
BLAST score
                  2.0e-41
E value
Match length
                  81
% identity
                  96
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >qi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  399510
Seq. ID
                  LIB3431-025-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g4467098
BLAST score
                  324
E value
                  1.0e-29
Match length
                  136
% identity
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  399511
Seq. ID
                  LIB3431-025-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g6093671
BLAST score
                  388
E value
                  2.0e-37
Match length
                  122
% identity
                  61
NCBI Description
                  CATIONIC PEROXIDASE 1 PRECURSOR >qi 1491776 (M37636)
                  cationic peroxidase [Arachis hypogaea]
Seq. No.
                  399512
Seq. ID
                  LIB3431-025-P1-K1-F6
```

```
g1617197
NCBI GI
BLAST score
                  304
E value
                  2.0e-27
                  76
Match length
                  76
% identity
                  (Z72488) CP12 [Nicotiana tabacum]
NCBI Description
                  399513
Seq. No.
                  LIB3431-025-P1-K1-F7
Seq. ID
Method
                  BLASTX
                  g4938484
NCBI GI
BLAST score
                  326
                  6.0e-30
E value
                  205
Match length
% identity
                  45
                   (AL078464) transcription factor-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  399514
Seq. No.
                  LIB3431-025-P1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1706260
                  355
BLAST score
                  2.0e-33
E value
                  68
Match length
                  94
% identity
NCBI Description
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597
                  cysteine proteinase 1 precursor - maize
                  >gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea
                  mays]
                  399515
Seq. No.
Seq. ID
                  LIB3431-025-P1-K1-F9
Method
                  BLASTX
                  g5815410
NCBI GI
BLAST score
                  828
                  4.0e-94
E value
Match length
                  209
% identity
                  83
                  (AF177392) blast and wounding induced mitogen-activated
NCBI Description
                  protein kinase [Oryza sativa]
                  399516
Seq. No.
                  LIB3431-025-P1-K1-G10
Seq. ID
Method
                  BLASTX
                  g1653953
NCBI GI
                  212
BLAST score
                  6.0e-17
E value
                  130
Match length
% identity
                   (D90917) hypothetical protein [Synechocystis sp.]
NCBI Description
                  399517
Seq. No.
                  LIB3431-025-P1-K1-G9
Seq. ID
Method
                  BLASTX
                  g3789954
NCBI GI
```

1065

BLAST score

NCBI GI

```
E value
                  1.0e-116
Match length
                  199
                  100
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  399518
Seq. No.
                  ·LIB3431-025-P1-K1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1737492
BLAST score
                  626
                  4.0e-65
E value
                  177
Match length
                  71
% identity
                  (U81318) poly(A)-binding protein [Triticum aestivum]
NCBI Description
                  399519
Seq. No.
                  LIB3431-025-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3913641
                  1185
BLAST score
                  1.0e-130
E value
Match length
                  227
                  100
% identity
                  FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi 3041777 dbj_BAA25423_ (AB007194)
                  fructose-1,6-bisphosphatase [Oryza sativa]
                  399520
Seq. No.
Seq. ID
                  LIB3431-025-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q4678280
                  259
BLAST score
                  5.0e-22
E value
                  152
Match length
                  36
% identity
NCBI Description
                  (AL049660) zinc finger-like protein [Arabidopsis thaliana]
Seq. No.
                  399521
                  LIB3431-025-P1-K1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g115787
BLAST score
                  544
                  1.0e-107
E value
Match length
                  224
                  91
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                  399522
                  LIB3431-025-P1-K1-H9
Seq. ID
Method
                  BLASTX
```

q3036951

```
BLAST score
                   611
E value
                   2.0e-63
Match length
                   117
                   98
% identity
NCBI Description
                   (AB012639) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
                   399523
Seq. No.
                  LIB3431-025-P1-N1-A1
Seq. ID
Method
                  BLASTX
                   g3885882
NCBI GI
BLAST score
                   275
                   3.0e-24
E value
Match length
                   55
% identity
                   98
                   (AF093629) inorganic pyrophosphatase [Oryza sativa]
NCBI Description
Seq. No.
                   399524
                  LIB3431-025-P1-N1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3808101
BLAST score
                   303
E value
                   1.0e-27
Match length
                  73
% identity
                  88
                   (AJ012165) chloroplast protease [Capsicum annuum]
NCBI Description
Seq. No.
                   399525
Seq. ID
                  LIB3431-025-P1-N1-A12
Method
                  BLASTN
NCBI GI
                   g2072554
BLAST score
                   330
                   0.0e+00
E value
Match length
                   330
% identity
                   100
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
Seq. No.
                   399526
Seq. ID
                  LIB3431-025-P1-N1-A5
Method
                  BLASTN
NCBI GI
                  g395929
BLAST score
                  82
E value
                   5.0e-38
Match length
                  145
% identity
                  90
NCBI Description
                  O.sativa retrotransposon Tos1-1
                  399527
Seq. No.
Seq. ID
                  LIB3431-025-P1-N1-A7
Method
                  BLASTX
NCBI GI
                  q693920
BLAST score
                  340
E value
                   6.0e-32
Match length
                   68
% identity
                   (U21113) chlorophyll a/b binding protein [Solanum
NCBI Description
```

tuberosum] 399528 Seq. No. Seq. ID LIB3431-025-P1-N1-A9 Method BLASTX g4877984 NCBI GI BLAST score 274 E value 4.0e-24

% identity (AF145755) THA4 [Zea mays] NCBI Description

399529 Seq. No.

Match length

LIB3431-025-P1-N1-B1 Seq. ID

61

90

Method BLASTN NCBI GI g5091597 BLAST score 132 6.0e-68 E value 219 Match length 26 % identity

Oryza sativa chromosome 1 BAC 10A19I, complete sequence NCBI Description

399530 Seq. No.

LIB3431-025-P1-N1-B10 Seq. ID

Method BLASTX NCBI GI g2499966 BLAST score 249 E value 3.0e-21 Match length 66 77 % identity

PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E NCBI Description

A) >gi 632722 bbs 151001 (S72356) photosystem I subunit PSI-E [Nicotiana sylvestris, leaves, Peptide Chloroplast,

141 aa] [Nicotiana sylvestris]

399531 Seq. No.

LIB3431-025-P1-N1-B11 Seq. ID

BLASTX Method NCBI GI g671740 BLAST score 295 1.0e-26 E value Match length 57 98 % identity

NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic

construct]

399532 Seq. No.

LIB3431-025-P1-N1-B2 Seq. ID

BLASTX Method NCBI GI g1362184 342 BLAST score 4.0e-32 E value Match length 71 100 % identity

histone H2B-8 - wheat >gi 531058 dbj BAA07157 (D37943) NCBI Description

protein H2B-8 [Triticum aestivum]

Match length

99

```
399533
Seq. No.
                   LIB3431-025-P1-N1-B3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q433216
BLAST score
                   211
E value
                   1.0e-115
Match length
                   232
% identity
NCBI Description
                   Rice mRNA for ascorbate peroxidase (gene name SS622),
                   partial cds
                   399534
Seq. No.
Seq. ID
                   LIB3431-025-P1-N1-B8
Method
                   BLASTX
                   g1617197
NCBI GI
                   300
BLAST score
                   3.0e-27
E value
                   71
Match length
                   77
% identity
                   (Z72488) CP12 [Nicotiana tabacum]
NCBI Description
                   399535
Seq. No.
                   LIB3431-025-P1-N1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g729135
                   267
BLAST score
                   2.0e-23
E value
Match length
                   55
% identity
                   89
                   CAFFEIC ACID 3-O-METHYLTRANSFERASE
NCBI Description
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                   3-O-METHYLTRANSFERASE) (COMT) >gi 283034 pir S28612
                   catechol O-methyltransferase (EC 2.1.1.6) - maize
                   >gi 168532 (M73235) O-methyltransferase [Zea mays]
                   399536
Seq. No.
                   LIB3431-025-P1-N1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g129707
BLAST score
                   405
                   2.0e-39
E value
                   97
Match length
% identity
                   84
                   PROTOCHLOROPHYLLIDE REDUCTASE (PCR)
NCBI Description
                   (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE)
                   >gi 100550 pir S08406 protochlorophyllide reductase (EC
                   1.3.1.33) - oat (fragment) >gi 829253 emb CAA34913
                   (X17067) protochlorophyllide reductase (314 AA) [Avena
                   sativa]
Seq. No.
                   399537
                   LIB3431-025-P1-N1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   523
                   3.0e-53
E value
```

```
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  399538
Seq. No.
                  LIB3431-025-P1-N1-C6
Seq. ID
                  BLASTX
Method
                  g2072555
NCBI GI
BLAST score
                  228
                  1.0e-18
E value
Match length
                  42
                  100
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  399539
Seq. No.
                  LIB3431-025-P1-N1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3914466
                  395
BLAST score
                  2.0e-38
E value
Match length
                  72
                  99
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi 2981214 (AF052429) photosystem I complex PsaN
                  subunit precursor [Zea mays]
Seq. No.
                  399540
                  LIB3431-025-P1-N1-C9
Seq. ID
                  BLASTX
Method
                  q517500
NCBI GI
                  374
BLAST score
                  7.0e-36
E value
                  90
Match length
                  81
% identity
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi 444338_prf__1906386A photosystem II
                  OE17 protein [Pisum sativum]
Seq. No.
                  399541
Seq. ID
                  LIB3431-025-P1-N1-D1
                  BLASTX
Method
                  g1353352
NCBI GI
                  227
BLAST score
E value
                  1.0e-18
                  59
Match length
                  75
% identity
                   (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
                  399542
Seq. No.
                  LIB3431-025-P1-N1-D10
Seq. ID
Method
                  BLASTX
                  q3126854
NCBI GI
                  392
BLAST score
                  5.0e-38
E value
```

74

Match length

```
100
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  399543
Seq. No.
                  LIB3431-025-P1-N1-D11
Seq. ID
Method
                  BLASTX
                  g5091556
NCBI GI
BLAST score
                  194
                   9.0e-15
E value
                  55
Match length
                  58
% identity
                   (AC007067) T10024.25 [Arabidopsis thaliana]
NCBI Description
                  399544
Seq. No.
                  LIB3431-025-P1-N1-D12
Seq. ID
Method
                  BLASTX
                  q1841466
NCBI GI
BLAST score
                  182
                   2.0e-13
E value
                  32
Match length
                  94
% identity
                   (Y11003) putative pre-pro-cysteine proteinase [Nicotiana
NCBI Description
                  tabacum]
                                                 399545
Seq. No.
                  LIB3431-025-P1-N1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4587990
BLAST score
                  250
                   2.0e-21
E value
Match length
                  88
% identity
                   (AF085279) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   399546
Seq. No.
                  LIB3431-025-P1-N1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2598151
BLAST score
                  222
E value
                   5.0e-18
Match length
                   43
% identity
                   (AF027350) NADPH:protochlorophyllide oxidoreductase porB
NCBI Description
                   [Pinus taeda]
Seq. No.
                  399547
Seq. ID
                  LIB3431-025-P1-N1-D7
Method
                  BLASTX
NCBI GI
                  g417260
BLAST score
                  300
E value
                   3.0e-27
Match length
                  76
                  75
% identity
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                  lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
```

light-regulated gene [Oryza sativa]

```
Seq. No.
                  399548
                  LIB3431-025-P1-N1-D9
Seq. ID
Method
                  BLASTX
                  g2072555
NCBI GI
BLAST score
                  237
                  9.0e-20
E value
Match length
                  44
% identity
                  100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  399549
                  LIB3431-025-P1-N1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  240
                  3.0e-20
E value
Match length
                  47
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                  399550
                  LIB3431-025-P1-N1-E2
Seq. ID
Method
                  BLASTX
                  q167097
NCBI GI
BLAST score
                  151
E value
                  1.0e-20
Match length
                  61
% identity
                  87
                  (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                  [Hordeum vulgare]
Seq. No.
                  399551
                  LIB3431-025-P1-N1-E3
Seq. ID
Method
                  BLASTX
                  g4567263
NCBI GI
                  282
BLAST score
E value
                  5.0e-25
                  70
Match length
% identity
NCBI Description
                  (AC006841) putative cell division inhibitor [Arabidopsis
                  thaliana]
                  399552
Seq. No.
                  LIB3431-025-P1-N1-E5
Seq. ID
Method
                  BLASTX
                  q462195
NCBI GI
                  372
BLAST score
E value
                  1.0e-35
                  72
Match length
                  100
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi 100682 pir _S21636 GOS2 protein - rice
                  >qi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                  >gi 3789950 (AF094774) translation initiation factor [Oryza
```

Seq. No.

399558

399553 Seq. No. LIB3431-025-P1-N1-E6 Seq. ID Method BLASTN NCBI GI g5777612 BLAST score 407 0.0e+00 E value Match length 418 99 % identity Oryza sativa chromosome 4 BAC q3037-207F1 complete genome NCBI Description 399554 Seq. No. LIB3431-025-P1-N1-E7 Seq. ID Method BLASTN NCBI GI g1841354 66 BLAST score E value 2.0e-29 Match length 66 % identity 100 Oryza sativa mitochondrial DNA for cytochrome c oxidase NCBI Description subunit Vb precursor, complete cds Seq. No. 399555 LIB3431-025-P1-N1-E8 Seq. ID Method BLASTX NCBI GI q3036951 BLAST score 427 E value 4.0e-42 Match length 80 100 % identity (AB012639) light harvesting chlorophyll a/b-binding protein NCBI Description [Nicotiana sylvestris] Seq. No. 399556 LIB3431-025-P1-N1-E9 Seq. ID Method BLASTX NCBI GI q3913239 BLAST score 256 E value 4.0e-40 Match length 132 % identity 75 NCBI Description PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) >gi 2612941 (AF024512) CLA1 transketolase-like protein [Oryza sativa] Seq. No. 399557 LIB3431-025-P1-N1-F10 Seq. ID Method BLASTN NCBI GI q600766 BLAST score 296 E value 1.0e-166 Match length 364 % identity NCBI Description Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds

sativa]

Method

BLASTN

```
Seq. ID
                  LIB3431-025-P1-N1-F11
Method
                  BLASTX
NCBI GI
                  g1777961
BLAST score
                   342
                   4.0e-32
E value
Match length
                  114
% identity
                   61
                   (U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum
NCBI Description
                   vulgare]
                   399559
Seq. No.
Seq. ID
                   LIB3431-025-P1-N1-F2
Method
                  BLASTX
NCBI GI
                   q347451
BLAST score
                   236
E value
                   1.0e-19
Match length
                   47
% identity
                   98
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   399560
Seq. ID
                  LIB3431-025-P1-N1-F5
Method
                  BLASTX
                  q520568
NCBI GI
BLAST score
                   262
                   1.0e-22
E value
                   87
Match length
% identity
                   63
NCBI Description
                   (U12314) peroxidase [Cenchrus ciliaris].
                   399561
Seq. No.
                   LIB3431-025-P1-N1-F6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1617197
BLAST score
                   287
                   1.0e-25
E value
Match length
                   71
                   73
% identity
NCBI Description
                  (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                   399562
                   LIB3431-025-P1-N1-F8
Seq. ID
                   BLASTX
Method
                   a2118130
NCBI GI
BLAST score
                   255
                   7.0e-22
E value
Match length
                   47
                   94
% identity
                  cysteine proteinase (EC 3.4.22.-), glucose
NCBI Description
                   starvation-induced - maize (fragment)
                   >gi_559532_emb_CAA57675 (X82185) cysteine proteinase [Zea
                   mays]
Seq. No.
                   399563
Seq. ID
                   LIB3431-025-P1-N1-F9
```

BLAST score

229

```
NCBI GI
                  g5815409
BLAST score
                  420
                  0.0e + 00
E value
Match length
                  449
% identity
                  98
                  Oryza sativa blast and wounding induced mitogen-activated
NCBI Description
                  protein kinase (BWMK1) mRNA, complete cds
Seq. No.
                  399564
Seq. ID
                  LIB3431-025-P1-N1-G10
Method
                  BLASTX
NCBI GI
                  g1653953
BLAST score
                  190
                  3.0e-14
E value
                  91
Match length
% identity
                  (D90917) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                  399565
                  LIB3431-025-P1-N1-G11
Seq. ID
Method
                  BLASTX
                  q2130073
NCBI GI
                  308
BLAST score
E value
                  4.0e-28
Match length
                  60
                  100
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
NCBI Description
                  cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase
                  C-1 [Oryza sativa] >gi 790970 dbj BAA08830 (D50301)
                  aldolase C-1 [Oryza sativa]
                  399566
Seq. No.
                  LIB3431-025-P1-N1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g786177
BLAST score
                  55
                  4.0e-22
E value
Match length
                  130
                  86
% identity
NCBI Description Rice DNA for aldolase C-1, complete cds
                  399567
Seq. No.
Seq. ID
                  LIB3431-025-P1-N1-G3
Method
                  BLASTX
NCBI GI
                  g2708745
BLAST score
                  197
E value
                  3.0e-15
                  48
Match length
                  81
% identity
                   (AC003952) putative calcium-dependent ser/thr protein
NCBI Description
                  kinase [Arabidopsis thaliana]
                  399568
Seq. No.
Seq. ID
                  LIB3431-025-P1-N1-G5
                  BLASTX
Method
NCBI GI
                  q21839
```

```
E value
                  7.0e-19
Match length
                  47
% identity
                  96
                  (X57952) phosphoribulokinase [Triticum aestivum]
NCBI Description
                  399569
Seq. No.
                  LIB3431-025-P1-N1-G9
Seq. ID
Method
                  BLASTX
                  g3789954
NCBI GI
                  354
BLAST score
                  2.0e-33
E value
Match length
                  66
% identity
                  98
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  399570
Seq. No.
Seq. ID
                  LIB3431-025-P1-N1-H10
Method
                  BLASTX
NCBI GI
                  q1737492
BLAST score
                  280
E value
                  6.0e-25
Match length
                  70
% identity
                  (U81318) poly(A)-binding protein [Triticum aestivum]
NCBI Description
                  399571
Seq. No.
                  LIB3431-025-P1-N1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q517500
BLAST score
                  296
                  8.0e-27
E value
Match length
                  94
% identity
NCBI Description
                   (M87435) precursor of the oxygen evolving complex 17 kDa
                  protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
                  399572
Seq. No.
Seq. ID
                  LIB3431-025-P1-N1-H2
                  BLASTX
Method
NCBI GI
                  q1651922
BLAST score
                  176
                  1.0e-12
E value
                  59
Match length
% identity
                  (D90901) hypothetical protein [Synechocystis sp.]
NCBI Description
                  399573
Seq. No.
                  LIB3431-025-P1-N1-H3
Seq. ID
Method
                  BLASTX
                  g3913641
NCBI GI
BLAST score
                  529
E value
                  5.0e-54
Match length
                  100
% identity
NCBI Description
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
```

Method

BLASTX

```
(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi 3041777 dbj BAA25423_ (AB007194)
                  fructose-1,6-bisphosphatase [Oryza sativa]
                  399574
Seq. No.
                  LIB3431-025-P1-N1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g129707
BLAST score
                  419
                  4.0e-41
E value
                  95
Match length
% identity
                  86
                  PROTOCHLOROPHYLLIDE REDUCTASE (PCR)
NCBI Description
                  (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE)
                  >gi 100550 pir S08406 protochlorophyllide reductase (EC
                  1.3.1.33) - oat (fragment) >gi 829253_emb CAA34913
                  (X17067) protochlorophyllide reductase (314 AA) [Avena
                  sativa]
                  399575
Seq. No.
Seq. ID
                  LIB3431-025-P1-N1-H7
Method
                  BLASTX
NCBI GI
                  g4512125
BLAST score
                  243
                  1.0e-20
E value
                  45
Match length
                  100
% identity
                  (AF133340) putative chlorophyll a/b-binding protein
NCBI Description
                  [Phalaenopsis sp. 'KCbutterfly']
Seq. No.
                  399576
                  LIB3431-025-P1-N1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q267120
BLAST score
                  284
                  2.0e-25
E value
Match length
                  71
% identity
NCBI Description
                  THIOREDOXIN F-TYPE, CHLOROPLAST PRECURSOR (TRX-F)
                  >qi 100070 pir S20929 thioredoxin f precursor - garden pea
                  >gi_20907_emb_CAA45098_ (X63537) thioredoxin F [Pisum
                  sativum] >gi 1388086 (U35830) thioredoxin f [Pisum sativum]
                  399577
Seq. No.
Seq. ID
                  LIB3431-025-P1-N1-H9
Method
                  BLASTX
NCBI GI
                  g3036951
BLAST score
                  450
                  9.0e-45
E value
Match length
                  85
% identity
                  100
                  (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
Seq. No.
                  399578
Seq. ID
                  LIB3431-026-P1-K1-A1
```

BLAST score

371

```
q2570511
NCBI GI
BLAST score
                   213
                   3.0e-17
E value
Match length
                   79
                   59
% identity
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                   399579
Seq. No.
Seq. ID
                   LIB3431-026-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   q170131
BLAST score
                   278
E value
                   9.0e-25
                   87
Match length
                   66
% identity
                   (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
NCBI Description
                   399580
Seq. No.
                   LIB3431-026-P1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3345477
BLAST score
                   434
                   6.0e-43
E value
                   129
Match length
                   66
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description `
                   399581
Seq. No.
                   LIB3431-026-P1-K1-A12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g115787
BLAST score
                   475
                   1.0e-47
E value
                   112
Match length
                   86
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   399582
Seq. No.
Seq. ID
                   LIB3431-026-P1-K1-A2
                   BLASTX
Method
                   g2407281
NCBI GI
BLAST score
                   658
E value
                   4.0e-69
Match length
                   125
                   98
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq. No.
                   399583
                   LIB3431-026-P1-K1-A3
Seq. ID
Method
                   BLASTX
                   g1352461
NCBI GI
```

Seq. No.

399588

```
8.0e-39
E value
Match length
                  98
                  77
% identity
                  IN2-2 PROTEIN
NCBI Description
                  399584
Seq. No.
                  LIB3431-026-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  672
E value
                  7.0e-71
                  124
Match length
                  100
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  399585
Seq. ID `
                  LIB3431-026-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q3345477
BLAST score
                  269
E value
                  1.0e-23
Match length
                  98
                  58
% identity
NCBI Description
                  (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                  399586
Seq. ID
                  LIB3431-026-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q4538920
BLAST score
                  150
E value
                  1.0e-09
Match length
                  57
% identity
NCBI Description
                  (AL049483) nitrogen fixation like protein [Arabidopsis
                  thaliana]
Seq. No.
                  399587
Seq. ID
                  LIB3431-026-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  q218209
BLAST score
                  34
E value
                  1.0e-09
Match length
                  78
                  87
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
```

```
Seq. ID
                  LIB3431-026-P1-K1-A8
                  BLASTX
Method
NCBI GI
                  g132105
BLAST score
                  614
                  6.0e-64
E value
Match length
                  132
% identity
                  88
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  399589
                  LIB3431-026-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q871931
BLAST score
                  420
E value
                  3.0e-41
Match length
                  116
                  74
% identity
NCBI Description (D30763) ferredoxin [Oryza sativa]
                  399590
Seq. No.
Seq. ID
                  LIB3431-026-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q5360230
BLAST score
                  631
                  6.0e-66
E value
Match length
                  120
% identity
                  97
NCBI Description (AB015287) Ran [Oryza sativa]
                  399591
Seq. No.
Seq. ID
                  LIB3431-026-P1-K1-B10
Method
                  BLASTX
                  q1617197
NCBI GI
BLAST score
                  297
                  9.0e-27
E value
                  76
Match length
% identity
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
                  399592
Seq. No.
                  LIB3431-026-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006881
BLAST score
                  356
                  9.0e-34
E value
Match length
                  105
% identity
```

NCBI Description (Z99707) putative protein [Arabidopsis thaliana]

```
Seq. No.
                  399593
                  LIB3431-026-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4588906
                  409
BLAST score
                  5.0e-40
E value
                  90
Match length
% identity :
                  87
                  (AF118149) ribosomal protein S7 [Secale cereale]
NCBI Description
                  399594
Seq. No.
Seq. ID
                  LIB3431-026-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q5478797
BLAST score
                  822
E value
                  3.0e-88
                  159
Match length
                  94
% identity
                  (AB021310) chlorophyll b synthase [Oryza sativa]
NCBI Description
Seq. No.
                  399595
                  LIB3431-026-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173347
BLAST score
                  322
                  9.0e-43
E value
Match length
                  108
% identity
NCBI Description
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >qi 100803 pir S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >qi 14265 emb CAA46507
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  399596
Seq. ID
                  LIB3431-026-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q1835731
BLAST score
                  387
                  2.0e-37
E value
Match length
                  85
                  87
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                  399597
Seq. ID
                  LIB3431-026-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  451
E value
                  4.0e-45
Match length
                  86
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                  399598
Seq. ID
                  LIB3431-026-P1-K1-B6
```

```
Method
                  BLASTX
NCBI GI
                  g3868756
BLAST score
                  494
                  3.0e-50
E value
Match length
                  88
% identity
                  100
                  (D86611) catalase [Oryza sativa]
NCBI Description
Seq. No.
                  399599
                  LIB3431-026-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  237
                  9.0e-20
E value
Match length
                  44
% identity
                  100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >qi 6103441 qb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  399600
                  LIB3431-026-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5668640
BLAST score
                  515
E value
                  2.0e-52
Match length
                  148
% identity
NCBI Description
                  (AL109619) putative protein [Arabidopsis thaliana]
Seq. No.
                  399601
                  LIB3431-026-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  713
E value
                  2.0e-75
Match length
                  131
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >qi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  399602
Seq. No.
                  LIB3431-026-P1-K1-C4
Seq. ID
Method
                  BLASTX
                  g125580
NCBI GI
BLAST score
                  498
E value
                  2.0e-50
Match length
                  116
% identity
NCBI Description
                  PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
```

```
2.7.1.19) - wheat >gi 5924030 emb CAB56544.1 (X51608)
                  phosphoribulokinase [Triticum aestivum]
                  399603
Seq. No.
Seq. ID
                  LIB3431-026-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g2072727
BLAST score
                  670
                  2.0e-70
E value
                  131
Match length
% identity
                  98
                  (Y12595) Fd-GOGAT protein [Oryza sativa]
NCBI Description
Seq. No.
                  399604
Seq. ID
                  LIB3431-026-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  529
                  4.0e-54
E value
Match length
                  121
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >qi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  399605
Seq. ID
                  LIB3431-026-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  q3345477
BLAST score
                  544
E value
                  1.0e-55
Match length
                  149
% identity
NCBI Description
                  (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                  399606
Seq. ID
                  LIB3431-026-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q4490332
BLAST score
                  424
E value
                  1.0e-41
Match length
                  140
% identity
NCBI Description
                  (AL035656) putative protein [Arabidopsis thaliana]
Seq. No.
                  399607
Seq. ID
                  LIB3431-026-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q1362066
BLAST score
                  392
E value
                  6.0e - 38
Match length
                  90
% identity
```

(PRK) >gi 100839 pir S15743 phosphoribulokinase (EC

NCBI Description small GTP-binding protein - garden pea

Match length

124

```
[Pisum sativum]
Seq. No.
                  399608
Seq. ID
                  LIB3431-026-P1-K1-D10
Method
                  BLASTX
                  q115787
NCBI GI
BLAST score
                  489
                  2.0e-49
E value
                  113
Match length
                  87
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461_pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                  399609
Seq. No.
Seq. ID
                  LIB3431-026-P1-K1-D11
Method
                  BLASTX
                  g2688839
NCBI GI
                  531
BLAST score
                  3.0e-54
E value
                  136
Match length
                  69
% identity
                   (AF003347) ATP phosphoribosyltransferase [Thlaspi
NCBI Description
                  goesingense]
                  399610
Seq. No.
                  LIB3431-026-P1-K1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3176690
BLAST score
                   639
                   6.0e-67
E value
                   129
Match length
                   91
% identity
                   (AC003671) Similar to ubiquitin ligase gb_D63905 from S.
NCBI Description
                   cerevisiae. EST gb R65295 comes from this gene.
                   [Arabidopsis thaliana]
                   399611
Seq. No.
                  LIB3431-026-P1-K1-D4
Seq. ID
Method
                   BLASTX
                   g3004565
NCBI GI
                   289
BLAST score
E value
                   8.0e-29
Match length
                   80
% identity
                   (AC003673) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   399612
Seq. No.
                   LIB3431-026-P1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g320618
                   558
BLAST score
                   2.0e-57
E value
```

>qi 871510 emb CAA90080 (Z49900) small GTP-binding protein

NCBI Description

```
% identity
                  85
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  399613
                  LIB3431-026-P1-K1-D6
Seq. ID
Method
                  BLASTX
                  g733458
NCBI GI
BLAST score
                  145
                  4.0e-09
E value
                  77
Match length
                  51
% identity
                   (U23190) chlorophyll a/b-binding apoprotein CP24 precursor
NCBI Description
                   [Zea mays]
Seq. No.
                  399614
                  LIB3431-026-P1-K1-D8
Seq. ID
                  BLASTX
Method
                  g170131
NCBI GI
                  391
BLAST score
E value
                  8.0e-38
                  116
Match length
% identity
                   (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
NCBI Description
                   399615
Seq. No.
Seq. ID
                  LIB3431-026-P1-K1-D9
                  BLASTX
Method
                  q2570511
NCBI GI
                   561
BLAST score
                   8.0e-58
E value
Match length
                   107
% identity
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                   399616
Seq. No.
Seq. ID
                   LIB3431-026-P1-K1-E10
                   BLASTX
Method
NCBI GI
                   q2673913
                   244
BLAST score
                   1.0e-20
E value
                   66
Match length
% identity
                   (AC002561) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   399617
Seq. No.
Seq. ID
                   LIB3431-026-P1-K1-E11
Method
                   BLASTX
                   g2055273
NCBI GI
                   611
BLAST score
E value
                   1.0e-63
Match length
                   135
% identity
                   (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]
```

Seq. No.

399623

```
399618
Seq. No.
                  LIB3431-026-P1-K1-E12
Seq. ID
                  BLASTX
Method
                  q733454
NCBI GI
                   548
BLAST score
E value
                   3.0e-56
                  126
Match length
% identity
                  83
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                   399619
Seq. No.
                  LIB3431-026-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3345477
BLAST score
                   598
E value
                   5.0e-62
Match length
                   120
                   95
% identity
NCBI Description
                   (AB016283) carbonic anhydrase [Oryza sativa]
                   399620
Seq. No.
Seq. ID
                  LIB3431-026-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q1617197
BLAST score
                   304
                   1.0e-27
E value
Match length
                  76
% identity
NCBI Description
                   (Z72488) CP12 [Nicotiana tabacum]
                   399621
Seq. No.
                  LIB3431-026-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3288821
BLAST score
                   528
E value
                   6.0e-54
Match length
                   137
% identity
                   (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                  transaminase [Arabidopsis thaliana]
                  >gi 4733989 gb AAD28669.1 AC007209 5 (AC007209)
                  alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
Seq. No.
                   399622
                  LIB3431-026-P1-K1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2688824
BLAST score
                   146
E value
                   4.0e-09
                  76
Match length
                   45
% identity
NCBI Description
                   (U93273) putative auxin-repressed protein [Prunus
                  armeniaca]
```

```
LIB3431-026-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115796
BLAST score
                  848
E value
                  2.0e-91
                  159
Match length
                  98
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB) (LHCP) >gi 218174 dbj BAA00537 (D00642) type II
                  light-harvesting chlorophyll a/b-binding protein [Oryza
                  sativa]
Seq. No.
                  399624
                  LIB3431-026-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131388
BLAST score
                  257
                  3.0e-22
E value
Match length
                  102
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408)
                  33kDa oxygen evolving protein of photosystem II [Triticum
                  aestivum]
                  399625
Seq. No.
Seq. ID
                  LIB3431-026-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  632
                  3.0e-66
E value
Match length
                  116
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  399626
Seq. No.
Seq. ID
                  LIB3431-026-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  567
                  2.0e-58
E value
Match length
                  122
                  87
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >qi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4.\overline{1}.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
```

carboxylase S [Oryza sativa]

Method

BLASTX

```
Seq. No.
                  399627
                  LIB3431-026-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q733454
BLAST score
                  431
                  1.0e-42
E value
Match length
                  103
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                  399628
Seq. No.
Seq. ID
                  LIB3431-026-P1-K1-F8
                  BLASTX
Method
NCBI GI
                  g3859597
BLAST score
                  275
E value
                  3.0e-24
                  96
Match length
% identity
                  54
                  (AF104919) No definition line found [Arabidopsis thaliana]
NCBI Description
                  399629
Seq. No.
                  LIB3431-026-P1-K1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1619603
                                                                             ....
BLAST score
                  316
                  1.0e-178
E value
Match length
                  335
                  99
% identity
NCBI Description
                  O.sativa mRNA for lipid transfer protein
                  >gi_1667589_gb_U77295_OSU77295 Oryza sativa lipid transfer
                  protein (LTP) mRNA, complete cds
                  399630
Seq. No.
Seq. ID
                  LIB3431-026-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q3242708
BLAST score
                  414
E value
                  2.0e-40
Match length
                  144
% identity
                  56
                  (AC003040) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  399631
Seq. ID
                  LIB3431-026-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g2624326
BLAST score
                  245
                  8.0e-21
E value
Match length
                  56
% identity
                  86
                  (AJ002893) OsGRP1 [Oryza sativa]
NCBI Description
                  399632
Seq. No.
                  LIB3431-026-P1-K1-G2
Seq. ID
```

Seq. No. Seq. ID

```
NCBI GI
                  g2306981
BLAST score
                  143
                  4.0e-09
E value
Match length
                  23
% identity
                  100
                  (AF010321) photosystem I antenna protein [Oryza sativa]
NCBI Description
Seq. No.
                  399633
                  LIB3431-026-P1-K1-G3
Seq. ID
                  BLASTX
Method
                  q1617206
NCBI GI
BLAST score
                  158
E value
                  1.0e-10
                  47
Match length
                  64
% identity
                  (Z72489) CP12 [Pisum sativum]
NCBI Description
Seq. No.
                  399634
Seq. ID
                  LIB3431-026-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g3885888
BLAST score
                  357
E value
                  8.0e-34
                  115
Match length
                  68
% identity
                  (AF093632) high mobility group protein [Oryza śativa]
NCBI Description
                  399635
Seq. No.
                  LIB3431-026-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131192
                  441
BLAST score
                  1.0e-43
E value
                  128
Match length
                  70
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi 100606 pir S20937
                  photosystem I chain V precursor - barley
                  >gi_19091_emb_CAA42727_ (X60158) photosystem I polypeptide
                  PSI-G precursor [Hordeum vulgare]
                  399636
Seq. No.
Seq. ID
                  LIB3431-026-P1-K1-G7
                  BLASTX
Method
NCBI GI
                  g115787
                  668
BLAST score
                  2.0e-70
E value
                  134
Match length
                  96
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  399637
```

LIB3431-026-P1-K1-G8

```
BLASTX
Method
NCBI GI
                   q129915
BLAST score
                   492
E value
                   8.0e-50
Match length
                   104
% identity
                   PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
NCBI Description
                   >qi 66912 pir TVWTGC phosphoglycerate kinase (EC 2.7.2.3)
                   precursor, chloroplast - wheat >gi 21833 emb CAA33303
                   (X15233) phosphoglycerate kinase (ĀA 1 - 480) [Triticum
                   aestivum] >gi 3293043 emb CAA51931 (X73528)
                   phosphoglycerate kinase [Triticum aestivum]
                   399638
Seq. No.
                   LIB3431-026-P1-K1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q131176
                   299
BLAST score
E value
                   5.0e-27
Match length
                   58
                   98
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                   >gi_72683_pir__F1BH4 photosystem I chain IV precursor -
                   barley >gi 19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi 226163_prf_ 1413233A
                   10.8kD photosystem I protein [Hordeum vulgare var.
                   distichum]
                   399639
Seq. No.
Seq. ID
                   LIB3431-026-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   g3292814
BLAST score
                   298
                   7.0e-27
E value
Match length
                   80
                  , 68
% identity
NCBI Description
                   (AL031018) putative protein [Arabidopsis thaliana]
                   399640
Seq. No.
Seq. ID
                   LIB3431-026-P1-K1-H3
                   BLASTX
Method
                   g3411227
NCBI GI
BLAST score
                   402
                   3.0e-39
E value
                   84
Match length
                   90
% identity
                   (AF078874) NBS-LRR type disease resistance protein 02
NCBI Description
                   [Avena sativa]
                   399641
Seq. No.
                   LIB3431-026-P1-K1-H4
Seq. ID
                   BLASTX
Method
                   g3913018
NCBI GI
BLAST score
                   694
E value
                   2.0e-73
```

140

Match length

```
% identity
                  100
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  399642
Seq. No.
Seq. ID
                  LIB3431-026-P1-K1-H5
Method
                  BLASTX
                  q5007084
NCBI GI
BLAST score
                  383
                  3.0e-37
E value
Match length
                  90
                  80
% identity
                   (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
Seq. No.
                  399643
Seq. ID
                  LIB3431-026-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q3176725
BLAST score
                  200
                  2.0e-15
E value
                  98
Match length
% identity
                   (AC002392) unknown protein [Arabidopsis thaliana]
NCBI Description
                  399644
Seq. No.
                  LIB3431-026-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2754849
                  248
BLAST score
                  5.0e-21
E value
                  55
Match length
% identity
NCBI Description
                   (AF039000) putative serine-glyoxylate aminotransferase
                   [Fritillaria agrestis]
                  399645
Seq. No.
                  LIB3431-026-P1-K1-H9
Seq. ID
Method
                  BLASTX
                  q1617197
NCBI GI
BLAST score
                  304
                  1.0e-27
E value
                  76
Match length
                  76
% identity
NCBI Description
                  (Z72488) CP12 [Nicotiana tabacum]
                  399646
Seq. No.
                  LIB3431-026-P1-N1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3777599
BLAST score
                  44
E value
                  2.0e-15
Match length
                  155
% identity
                  88
NCBI Description
                  Oryza sativa clone LS101 50S ribosomal protein L5 (rpl5)
                  mRNA, nuclear gene encoding chloroplast protein, partial
```

Method

NCBI GI

E value

BLAST score

BLASTX

240 4.0e-20

g2462750

```
399647
Seq. No.
                  LIB3431-026-P1-N1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g134034
BLAST score
                  220
                  8.0e-18
E value
Match length
                  61
% identity
                  67
                  30S RIBOSOMAL PROTEIN S30, CHLOROPLAST PRECURSOR (CS-S5)
NCBI Description
                  (CS5) (S22) (RIBOSOMAL PROTEIN 1) (PSRP-1)
                  >gi 279640_pir__R3SPS5 ribosomal protein CS-S22 precursor,
                  chloroplast - spinach >gi_12316_emb_CAA41960_ (X59270)
                  chloroplast ribosomal protein S22 [Spinacia oleracea]
                  >gi 18031 emb CAA33403 (X15344) spinach S22 r-protein
                  [Spinacia oleracea]
                  399648
Seq. No.
                  LIB3431-026-P1-N1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  226
                  2.0e-18
E value
Match length
                  42
% identity
                  100
                  (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
Seq. No.
                  399649
                  LIB3431-026-P1-N1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g421916
BLAST score
                  167
E value
                  1.0e-11
Match length
                  30
                  100
% identity
                  chlorophyll a/b-binding protein - English ivy (fragment)
NCBI Description
                  >qi 12582 emb CAA48410 (X68333) light harvesting
                  chlorophyll a /b binding protein [Hedera helix]
Seq. No.
                  399650
                  LIB3431-026-P1-N1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  345
E value
                  2.0e-32
Match length
                  65
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                  399651
Seq. ID
                  LIB3431-026-P1-N1-A3
```

cds

```
Match length
                  65
% identity
                  69
                  (AC002292) Highly similar to auxin-induced protein
NCBI Description
                  (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                  399652
Seq. ID
                  LIB3431-026-P1-N1-A4
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  277
                  2.0e-24
E value
Match length
                  53
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  399653
                  LIB3431-026-P1-N1-A5
Seq. ID
Method
                  BLASTX
                  q3345477
NCBI GI
                  210
BLAST score
E value
                  1.0e-16
Match length
                  40
                  97
% identity
                  (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
Seq. No.
                  399654
Seq. ID
                  LIB3431-026-P1-N1-A6
                  BLASTX
Method
                  q4538920
NCBI GI
BLAST score
                  226
                  2.0e-18
E value
Match length
                  59
% identity
NCBI Description
                  (AL049483) nitrogen fixation like protein [Arabidopsis
                  thaliana]
                  399655
Seq. No.
Seq. ID
                  LIB3431-026-P1-N1-A7
Method
                  BLASTX
                  q3913437
NCBI GI
BLAST score
                  196
                  2.0e-15
E value
Match length
                  41
% identity
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                  HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase
                  [Arabidopsis thaliana] >gi 1495271 emb CAA66613 (X97970)
```

RNA helicase [Arabidopsis thaliana]

```
Seq. No.
                  399656
Seq. ID
                  LIB3431-026-P1-N1-A8
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  301
                  3.0e-27
E value
Match length
                  57
% identity
                  100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  399657
                  LIB3431-026-P1-N1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2305114
                  295
BLAST score
E value
                  1.0e-165
                  390 .
Match length
% identity
NCBI Description Oryza sativa ferredoxin mRNA, complete cds
                  399658
Seq. No.
Seq. ID
                  LIB3431-026-P1-N1-B1
Method
                  BLASTN
                  g5360229
NCBI GI
                  393
BLAST score
                  0.0e + 00
E value
Match length
                  393
% identity
                  100
NCBI Description Oryza sativa mRNA for Ran, complete cds
Seq. No.
                  399659
Seq. ID
                  LIB3431-026-P1-N1-B10
Method
                  BLASTX
NCBI GI
                  q1617197
                  230
BLAST score
                  5.0e-19
E value
                  49
Match length
% identity
NCBI Description
                  (Z72488) CP12 [Nicotiana tabacum]
                  399660
Seq. No.
                  LIB3431-026-P1-N1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4588906
BLAST score
                  465
E value
                  2.0e-46
Match length
                  100
% identity
NCBI Description (AF118149) ribosomal protein S7 [Secale cereale]
```

```
399661
Seq. No.
                  LIB3431-026-P1-N1-B2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5478796
                  349
BLAST score
E value
                  0.0e + 00
                  431
Match length
                  100
% identity
                  Oryza sativa CAO mRNA for chlorophyll b synthase, partial
NCBI Description
                  399662
Seq. No.
                  LIB3431-026-P1-N1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1173347
                  250
BLAST score
E value
                  2.0e-21
Match length
                  54
% identity
                  94
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7) P2ASE)
                  >gi 100803 pir S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi 14265 emb CAA46507
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  399663
Seq. ID
                  LIB3431-026-P1-N1-B4
Method
                  BLASTX
NCBI GI
                  q1835731
BLAST score
                  359
E value
                  4.0e-34
Match length
                  80
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                  399664
Seq. ID
                  LIB3431-026-P1-N1-B5
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  359
E value
                  4.0e-34
Match length
                  80
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                  399665
                  LIB3431-026-P1-N1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3929924
BLAST score
                  292
E value
                  3.0e-26
Match length
                  56
% identity
                  98
                   (AB020502) catalase [Oryza sativa]
NCBI Description
```

```
399666
Seq. No.
                  LIB3431-026-P1-N1-B8
Seq. ID
Method
                  BLASTX
                  q517500
NCBI GI
                  401
BLAST score
                  4.0e-39
E value
                  97
Match length
% identity
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
                  399667
Seq. No.
                  LIB3431-026-P1-N1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2072555
                  237
BLAST score
                   9.0e-20
E value
                  44
Match length
                  100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  399668
                  LIB3431-026-P1-N1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5668640
BLAST score
                  332
E value
                   6.0e-31
                  97
Match length
% identity
                   (AL109619) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  399669
                  LIB3431-026-P1-N1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455296
BLAST score
                  241
                   3.0e-20
E value
Match length
                   44
% identity
                   (AL035528) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   399670
                  LIB3431-026-P1-N1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                   301
E value
                   3.0e-27
                  57
Match length
                   100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
```

·

Seq. No.

Seq. ID

```
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

399671
LIB3431-026-P1-N1-C4
BLASTX
```

Method BLASTX
NCBI GI g21839
BLAST score 229
E value 7.0e-19
Match length 47
% identity 96

NCBI Description (X57952) phosphoribulokinase [Triticum aestivum]

Seq. No. 399672

Seq. ID LIB3431-026-P1-N1-C6

Method BLASTN
NCBI GI g2072726
BLAST score 384
E value 0.0e+00
Match length 399
% identity 99

NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2

Seq. No. 399673

Seq. ID LIB3431-026-P1-N1-C7

Method BLASTX
NCBI GI g4512125
BLAST score 243
E value 2.0e-20
Match length 45
% identity 100

NCBI Description (AF133340) putative chlorophyll a/b-binding protein

[Phalaenopsis sp. 'KCbutterfly']

Seq. No. 399674

Seq. ID LIB3431-026-P1-N1-C8

Method BLASTX
NCBI GI g606817
BLAST score 178
E value 6.0e-13
Match length 32
% identity 100

NCBI Description (U08404) carbonic anhydrase [Oryza sativa]

>gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic

anhydrase 3 [Oryza sativa]

Seq. No. 399675

Seq. ID LIB3431-026-P1-N1-D10

Method BLASTX
NCBI GI g4512125
BLAST score 251
E value 2.0e-21
Match length 47
% identity 100

NCBI Description (AF133340) putative chlorophyll a/b-binding protein

BLAST score

E value

218

1.0e-17

[Phalaenopsis sp. 'KCbutterfly'] Seq. No. 399676 LIB3431-026-P1-N1-D3 Seq. ID Method BLASTX q120661 NCBI GI BLAST score 181 3.0e-13 E value 45 Match length 76 % identity GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST NCBI Description PRECURSOR >gi 170237 (M14417) glyceraldehyde-3-phosphate dehydrogenase A-subunit precursor [Nicotiana tabacum] Seq. No. 399677 Seq. ID LIB3431-026-P1-N1-D4 Method BLASTX NCBI GI q3004565 BLAST score 337 E value 2.0e-31 Match length 94 % identity NCBI Description (AC003673) putative protein kinase [Arabidopsis thaliana] 399678 Seq. No. LIB3431-026-P1-N1-D5 Seq. ID Method BLASTX NCBI GI q115787 BLAST score 409 E value 6.0e-40 Match length 77 100 % identity CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi 20182 emb CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] Seq. No. 399679 Seq. ID LIB3431-026-P1-N1-D6 BLASTX Method NCBI GI q543939 BLAST score 160 9.0e-11 E value 39 Match length % identity CHLOROPHYLL A-B BINDING PROTEIN CP24 PRECURSOR NCBI Description >gi 541819_pir__S40210 chlorophyll a/b-binding protein CP24 precursor - spinach >gi_437991_emb_CAA81105.1_ (Z25886) 20 kDa protein of CP24 precursor protein [Spinacia oleracea] 399680 Seq. No. LIB3431-026-P1-N1-D8 Seq. ID Method BLASTX NCBI GI g170131

% identity

100

```
68
Match length
% identity
                  59
NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
                  399681
Seq. No.
                  LIB3431-026-P1-N1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115794
                  501
BLAST score
E value
                  9.0e-51
                  100
Match length
                  93
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
NCBI Description
                  III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding
                  protein type III precursor (cab-13) - tomato
                  >gi 19277 emb CAA42818 (X60275) LHCII type III
                   [Lycopersicon esculentum]
                  399682
Seq. No.
                  LIB3431-026-P1-N1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2673913
BLAST score
                  306
                  7.0e-28
E value
Match length
                  77
% identity
                  75
                  (AC002561) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  399683
                  LIB3431-026-P1-N1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2055273
BLAST score
                  201
E value
                  2.0e-15
Match length
                  52
% identity
NCBI Description (D85339) hydroxypyruvate reductase [Arabidopsis thaliana]
Seq. No.
                  399684
Seq. ID
                  LIB3431-026-P1-N1-E12
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                  402
                  4.0e-39
E value
Match length
                  81
% identity
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
Seq. No.
                  399685
Seq. ID
                  LIB3431-026-P1-N1-E6
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  177
E value
                  9.0e-13
Match length
                  35
```

```
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                  399686
                  LIB3431-026-P1-N1-E7
Seq. ID
Method
                  BLASTX
                  q1617197
NCBI GI
BLAST score
                  164
                  3.0e-11
E value
Match length
                  33
% identity
                  (Z72488) CP12 [Nicotiana tabacum]
NCBI Description
                  399687
Seq. No.
                  LIB3431-026-P1-N1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2754849
BLAST score
                  186
                  8.0e-14
E value
Match length
                  45
% identity
                   (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                   [Fritillaria agrestis]
Seq. No.
                  399688
                  LIB3431-026-P1-N1-F11
Seq. ID
Method
                  BLASTX
                  g3126854
NCBI GI
BLAST score
                  431
                  1.0e-42
E value
Match length
                  82
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  399689
Seq. No.
Seq. ID
                  LIB3431-026-P1-N1-F12
Method
                  BLASTX
                  g482311
NCBI GI
                  508
BLAST score
E value
                  1.0e-51
Match length
                  99
                  100
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >qi 739292 prf 2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                  399690
Seq. No.
Seq. ID
                  LIB3431-026-P1-N1-F2
                  BLASTX
Method
NCBI GI
                  g132105
BLAST score
                  301
                  2.0e-27
E value
Match length
                  57
                  100
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >qi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
```

```
(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
```

```
Seq. No.
                  399691
                  LIB3431-026-P1-N1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  301
E value
                  2.0e-27
Match length
                  57
                  100
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sàtiva] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  399692
Seq. No.
                  LIB3431-026-P1-N1-F7
Seq. ID
Method
                  BLASTX
                  q733454
NCBI GI
BLAST score
                  232
E value
                  3.0e-19
                  48
Match length
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
                  399693
Seq. No.
                  LIB3431-026-P1-N1-G11
Seq. ID
Method
                  BLASTN
                  g2624325
NCBI GI
BLAST score
                  140
                  7.0e-73
E value
Match length
                  168
% identity
                  Oryza sativa mRNA for glycine-rich RNA-binding protein
NCBI Description
                  (OsGRP1)
                  399694
Seq. No.
                  LIB3431-026-P1-N1-G12
Seq. ID
Method
                  BLASTX
                  g517500
NCBI GI
BLAST score
                  272
                  5.0e-24
E value
                  72
Match length
% identity
NCBI Description
                  (M87435) precursor of the oxygen evolving complex 17 kDa
```

OE17 protein [Pisum sativum]

protein [Zea mays] >gi 444338 prf 1906386A photosystem II

```
Seq. No.
                   399695
Seq. ID
                   LIB3431-026-P1-N1-G2
Method
                   BLASTX
NCBI GI
                   q1076724
BLAST score
                   364
                   1.0e-34
E value
Match length
                   70
                   94
% identity
NCBI Description
                   LHCI-680, photosystem I antenna protein - barley
                   >gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I
                   antenna protein [Hordeum vulgare]
                   399696
Seq. No.
                   LIB3431-026-P1-N1-G4
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3885887
BLAST score
                   423
E value
                   0.0e + 00
                   423
Match length
                   100
% identity
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                   complete cds
                   399697
Seq. No.
                  : LIB3431-026-P1-N1-G5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2306980
BLAST score
                   112
E value
                   2.0e-56
Match length
                   125
% identity
                   Oryza sativa photosystem I antenna protein (Lhca) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   399698
                   LIB3431-026-P1-N1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2130089
BLAST score
                   222
                   5.0e-18
E value
Match length
                   42
% identity
                   93
                   2-oxoglutarate/malate translocator (clone OMT103),
NCBI Description
                   mitochondrial membrane - proso millet
>gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate
                   translocator [Panicum miliaceum]
                   399699
Seq. No.
                   LIB3431-026-P1-N1-G7
Seq. ID
Method
                   BLASTX
                   g3036946
NCBI GI
                   300
BLAST score
E value
                   3.0e-27
Match length
                   57
% identity
NCBI Description
                   (AB012637) light harvesting chlorophyll a/b-binding protein
```

% identity

100

[Nicotiana sylvestris] 399700 Seq. No. Seq. ID LIB3431-026-P1-N1-G8 BLASTX Method NCBI GI g3738261 BLAST score 428 3.0e-42E value Match length 95 % identity 92 NCBI Description (AB018412) chloroplast phosphoglycerate kinase [Populus 399701 Seq. No. Seq. ID LIB3431-026-P1-N1-G9 Method BLASTX NCBI GI q131176 BLAST score 187 E value 6.0e-14 Match length 37 97 % identity PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR NCBI Description (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi 72683 pir F1BH4 photosystem I chain IV precursor barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi 226163 prf 1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum] Seq. No. 399702 Seq. ID LIB3431-026-P1-N1-H11 Method BLASTX NCBI GI q3292814 BLAST score 232 E value 3.0e-19 Match length 57 % identity NCBI Description (AL031018) putative protein [Arabidopsis thaliana] Seq. No. 399703 LIB3431-026-P1-N1-H3 Seq. ID Method BLASTX NCBI GI g4490715 BLAST score 147 3.0e-09 E value Match length 99 % identity 34 (AL035680) putative protein [Arabidopsis thaliana] NCBI Description 399704 Seq. No. Seq. ID LIB3431-026-P1-N1-H4 Method BLASTX NCBI GI g3913018 BLAST score 166 E value 2.0e-11 33 Match length

```
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                   (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                   aldolase [Oryza sativa]
                   399705
Seq. No.
Seq. ID
                   LIB3431-026-P1-N1-H5
Method
                   BLASTX
NCBI GI
                   g5007084
BLAST score
                   224
                   3.0e-18
E value
Match length
                   46
% identity
                   100
NCBI Description
                   (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
                   sativa]
                   399706
Seq. No.
                   LIB3431-026-P1-N1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q132105
                   294
BLAST score
                   2.0e-26
E value
                   56
Match length
% identity
                   100
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >qi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   399707
Seq. ID
                   LIB3431-026-P1-N1-H9
Method
                   BLASTX
NCBI GI
                   g1617197
BLAST score
                   212
E value
                   6.0e-17
Match length
                   44
                   89
% identity
NCBI Description
                  (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                   399708
Seq. ID
                   LIB3431-027-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g1173347
BLAST score
                   283
E value
                   3.0e-25
Match length
                   58
% identity
                   88
NCBI Description
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7) P2ASE)
                   >qi 100803 pir S23452 sedoheptulose-bisphosphatase (EC
                   3.1.3.37) precursor - wheat >qi 14265 emb CAA46507
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                   aestivuml
```

```
399709
Seq. No.
Seq. ID
                  LIB3431-027-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q4557229
BLAST score
                  223
E value
                  4.0e-18
Match length
                  112
% identity
                  35
                  angio-associated, migratory cell protein
NCBI Description
                  >gi 3121739 sp Q13685 AAMP HUMAN ANGIO-ASSOCIATED MIGRATORY
                  CELL PROTEIN >gi 2134759 pir I39383 angio-associated
                  migratory cell protein - human >gi 870803 (M95627)
                  angio-associated migratory cell protein [Homo sapiens]
                  399710
Seq. No.
Seq. ID
                  LIB3431-027-P1-K1-A12
                  BLASTX
Method
NCBI GI
                  q2493650
BLAST score .
                  638
                  7.0e-67
E value
                  139
Match length
                  95
% identity
NCBI Description
                  RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD
                  CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)
                  >gi 1167858 emb CAA93139 (Z68903) chaperonin [Secale
                  cereale]
Seq. No.
                  399711
Seq. ID
                  LIB3431-027-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q417103
BLAST score
                  541
                  2.0e-55
E value
Match length
                  124
% identity
                  HISTONE H3.2, MINOR >qi 282871 pir S24346 histone
NCBI Description
                  H3.3-like protein - Arabidopsis thaliana
                  >qi 16324 emb CAA42957 (X60429) histone H3.3 like protein
                  [Arabidopsis thaliana] >gi 404825 emb CAA42958 (X60429)
                  histone H3.3 like protein [Arabidopsis thaliana] >gi 488563
                  (U09458) histone H3.2 [Medicago sativa] >gi 488567 (U09460)
                  histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone
                  H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2
                  [Medicago sativa] >gi 488577 (U09465) histone H3.2
                  [Medicago sativa] >gi 510911 emb CAA56153 (X79714) histone
                  H3 [Lolium temulentum] >gi 1435157 emb CAA58445 (X83422)
                  histone H3 variant H3.3 [Lycopersicon esculentum]
                  >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum]
                  >gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana
                  tabacum] >gi 3885890 (AFO93633) histone H3 [Oryza sativa]
                  >gi 4038469 gb AAC97380 (AF109910) histone H3 [Porteresia
                  coarctata] >gi 4490754 emb CAB38916.1 (AL035708) histone
                  H3.3 [Arabidopsis thaliana] >qi 4490755 emb CAB38917.1
                  (AL035708) Histon H3 [Arabidopsis thaliana]
```

>gi_6006364_dbj_BAA84794.1_ (AP000559) EST D15300(C0425)
corresponds to a region of the predicted gene.; Similar to

histone H3 (AB015760) [Oryza sativa] 399712 Seq. No. Seq. ID LIB3431-027-P1-K1-A4 BLASTX Method g606817 NCBI GI BLAST score 378 1.0e-39 E value 128 Match length 70 % identity (U08404) carbonic anhydrase [Oryza sativa] NCBI Description >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic anhydrase 3 [Oryza sativa] 399713 Seq. No. LIB3431-027-P1-K1-A5 Seq. ID Method BLASTX NCBI GI g2388689 BLAST score 270 1.0e-23 E value Match length 67 76 % identity NCBI Description (AF016633) GH1 protein [Glycine max] Seq. No. 399714 LIB3431-027-P1-K1-A6 Seq. ID Method BLASTX NCBI GI q320618 BLAST score 599 3.0e-62 E value Match length 131 % identity 87 chlorophyll a/b-binding protein I precursor - rice NCBI Description >gi 218172 dbj BAA00536 (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi 227611 prf 1707316A chlorophyll a/b binding protein 1 [Oryza sativa] Seq. No. 399715 Seq. ID LIB3431-027-P1-K1-A7 Method BLASTX NCBI GI g1173347 BLAST score 802 5.0e-86 E value Match length 153 % identity

Seq. No. 399716

NCBI Description

Seq. ID LIB3431-027-P1-K1-A8

aestivum]

Method BLASTX NCBI GI g733454

SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum

NCBI GI

```
476
BLAST score
                  5.0e-70
E value
                  137 -
Match length
                  93
% identity
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                  399717
Seq. No.
                  LIB3431-027-P1-K1-A9
Seq. ID
Method
                  BLASTN
                  g3885891
NCBI GI
BLAST score
                  144
                  3.0e-75
E value
                  197
Match length
% identity
                  99
NCBI Description
                  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                  mRNA, complete cds
                  399718
Seq. No.
                  LIB3431-027-P1-K1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g21843
BLAST score
                  195
E value
                  1.0e-105
Match length
                  412
                  87
% identity
                  Wheat PsbO mRNA for 33kDa oxygen evolving protein of
NCBI Description
                  photosystem II
Seq. No.
                  399719
Seq. ID
                  LIB3431-027-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q2500959
BLAST score
                  424
E value
                  1.0e-41
Match length
                  133
                  62
% identity
NCBI Description
                  ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS)
                  >gi 1653611 dbj BAA18523 (D90915) alanyl-tRNA synthetase
                  [Synechocystis sp.]
Seq. No.
                  399720
                  LIB3431-027-P1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3023816
BLAST score
                  474
                  1.0e-47
E value
Match length
                  90
                  100
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
Seq. No.
                  399721
Seq. ID
                  LIB3431-027-P1-K1-B4
Method
                  BLASTX
```

q2130127

```
BLAST score
                  447
                  2.0e-44
E value
Match length
                  99
% identity
                  90
                  ferritin 1 precursor - maize >gi_1103628_emb_CAA58146
NCBI Description
                  (X83076) ferritin [Zea mays]
Seq. No.
                  399722
                  LIB3431-027-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  257
E value
                  3.0e-29
Match length
                  66
                  100
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >qi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >qi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  399723
Seq. No.
                  LIB3431-027-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  614
                  6.0e-64
E value
                  132
Match length
                  88
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj_BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  399724
Seq. No.
                  LIB3431-027-P1-K1-B7
Seq. ID
Method
                  BLASTX
                  q131388
NCBI GI
BLAST score
                  358
                  6.0e-34
E value
                  121
Match length
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >qi 21844 emb CAA40670 (X57408)
```

33kDa oxygen evolving protein of photosystem II [Triticum

NCBI GI

E value

BLAST score

q82080

1.0e-35

336

399725 Seq. No. LIB3431-027-P1-K1-B8 Seq. ID Method BLASTX NCBI GI g462195 BLAST score 325 4.0e-30 E value 62 Match length 100 % identity PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) NCBI Description >gi 100682 pir S21636 GOS2 protein - rice >gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa] >gi 3789950 (AF094774) translation initiation factor [Oryza sativa] 399726 Seq. No. LIB3431-027-P1-K1-C10 Seq. ID Method BLASTX q1707998 NCBI GI 297 BLAST score 9.0e-27 E value Match length 92 % identity SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR NCBI Description (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi 481944 pir S40218 glycine hydroxymethyltransferase (EC 2.1.2.1) - potato >gi 438247 emb CAA81082 (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum] 399727 Seq. No. LIB3431-027-P1-K1-C11 Seq. ID Method BLASTX NCBI GI g3482977 BLAST score 273 E value 5.0e-24Match length 138 % identity 46 NCBI Description (AL031369) putative protein [Arabidopsis thaliana] Seq. No. 399728 Seq. ID LIB3431-027-P1-K1-C12 Method BLASTX NCBI GI q100796 BLAST score 752 E value 4.0e-80 Match length 152 % identity 94 NCBI Description phosphoribulokinase (EC 2.7.1.19) - wheat Seq. No. 399729 Seq. ID LIB3431-027-P1-K1-C3 Method BLASTX

aestivum]

NCBI GI

BLAST score

q2244926

292

```
118
Match length
                   68
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872 prf__1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                  399730
Seq. No.
                  LIB3431-027-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1669341
BLAST score
                  219
                  1.0e-17
E value
                  133
Match length
                   41
% identity
                   (D45066) AOBP (ascorbate oxidase promoter-binding protein)
NCBI Description
                   [Cucurbita maxima]
Seq. No.
                  399731
Seq. ID
                  LIB3431-027-P1-K1-C5
Method
                  BLASTX
                  g4585882
NCBI GI
BLAST score
                  498
E value
                  2.0e-50
                  150
Match length
% identity
                  64
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  399732
                  LIB3431-027-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5922612
BLAST score
                  282
E value
                  5.0e-25
Match length
                  127
% identity
                   (AP000492) EST AU078118(E3904) corresponds to a region of
NCBI Description
                  the predicted gene.; similar to Arabidopsis thaliana BAC
                  IG002P16; No definition line found. (AF007270) [Oryza
                  sativa]
                  399733
Seq. No.
                  LIB3431-027-P1-K1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q671740
                  219
BLAST score
                  1.0e-17
E value
                  48
Match length
                  88
% identity
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
                  399734
Seq. No.
                  LIB3431-027-P1-K1-D1
Seq. ID
Method
                  BLASTX
```

```
E value
                  3.0e-26
                  98
Match length
% identity
                  58
                  (Z97339) glutaredoxin homolog [Arabidopsis thaliana]
NCBI Description
                  399735
Seq. No.
Seq. ID
                  LIB3431-027-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q1617197
BLAST score
                  304
                  1.0e-27
E value
Match length
                  76
% identity
                  76
NCBI Description
                  (Z72488) CP12 [Nicotiana tabacum]
                  399736
Seq. No.
Seq. ID
                  LIB3431-027-P1-K1-D2
                  BLASTX
Method
NCBI GI
                  q2306981
BLAST score
                  530
                  4.0e-54
E value
                  96
Match length
% identity
                  98
NCBI Description
                  (AF010321) photosystem I antenna protein [Oryza sativa]
                  399737
Seq. No.
                  LIB3431-027-P1-K1-D4
Seq. ID
                  BLASTN
Method
NCBI GI
                  g304219
BLAST score
                  78
                  1.0e-35
E value
                  161
Match length
% identity
                  87
                  Hordeum vulgare chloroplast photosystem I PSK-I subunit
NCBI Description
                  mRNA, complete cds
                  399738
Seq. No.
                  LIB3431-027-P1-K1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1661160
BLAST score
                  458
E value
                  1.0e-45
                  101
Match length
% identity
                  (U74295) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  399739
Seq. No.
                  LIB3431-027-P1-K1-D8
Seq. ID
                  BLASTX
Method
                  q3036951
NCBI GI
BLAST score
                  343
                  1.0e-36
E value
                  80
Match length
% identity
NCBI Description
                  (AB012639) light harvesting chlorophyll a/b-binding protein
```

[Nicotiana sylvestris]

NCBI Description

```
Seq. No.
                  399740
Seq. ID
                  LIB3431-027-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                  163
                  3.0e-22
E value
Match length
                  67
                  78
% identity
                  (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                  399741
Seq. No.
                  LIB3431-027-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4678948
BLAST score
                  192
E value
                  2.0e-14
Match length
                  117
% identity
                  41
                  (AL049711) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  399742
                  LIB3431-027-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g170131
BLAST score
                  260
E value
                  2.0e-22
Match length
                  66
% identity
NCBI Description
                  (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
Seq. No.
                  399743
Seq. ID
                  LIB3431-027-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  702
                  3.0e-74
E value
Match length
                  136
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >qi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  399744
                  LIB3431-027-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2570515
BLAST score
                  569
E value
                  1.0e-58
Match length
                  130
% identity
```

(AF022740) glycolate oxidase [Oryza sativa]

```
399745
Seq. No.
                  LIB3431-027-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5354158
BLAST score
                  384
                  3.0e-43
E value
Match length
                  140
                  64
% identity
                  (AF149841) digalactosyldiacylglycerol synthase [Arabidopsis
NCBI Description
                  thaliana] >gi_5354160_gb_AAD42379.1_AF149842_1 (AF149842)
                  digalactosyldiacylglycerol synthase [Arabidopsis thaliana]
                  >gi 6041825 gb AAF02140.1 AC009918_12 (AC009918)
                  digalactosyldiacylglycerol synthase [Arabidopsis thaliana]
Seq. No.
                  399746
                  LIB3431-027-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q729668
BLAST score
                  241
                  3.0e-20
E value
Match length
                  68
                  63
% identity
                  HISTONE H1 >gi 2147479 pir S65059 histone H1,
NCBI Description
                  drought-inducible - Lycopersicon pennellii >gi 436823
                  (U01890). Solanum pennellii histone H1 [Solanum pennellii]
Seq. No.
                  399747
Seq. ID
                  LIB3431-027-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q1835731
BLAST score
                  412
E value
                  3.0e-40
Match length
                  89
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                  399748
Seq. ID
                  LIB3431-027-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q3885894
BLAST score
                  464
E value
                  2.0e-46
Match length
                  110
% identity
NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
Seq. No.
                  399749
                  LIB3431-027-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076722
BLAST score
                  667
E value
                  4.0e-70
Match length
                  144
% identity
                  90
```

NCBI Description hypothetical protein - barley (fragment)

```
399750
Seq. No.
Seq. ID
                  LIB3431-027-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q1777961
BLAST score
                  504
E value
                  5.0e-51
                  154
Match length
% identity
                  (U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum
NCBI Description
                  vulgare]
                  399751
Seq. No.
Seq. ID
                  LIB3431-027-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
                  9.0e-20
E value
Match length
                  44
                  100
% identity
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  399752
Seq. No.
                  LIB3431-027-P1-K1-F12
Seq. ID
Method ·
                  BLASTX
NCBI GI
                  g3510256
BLAST score
                  157
                  2.0e-10
E value
                  106
Match length
% identity
                  32
NCBI Description (AC005310) unknown protein [Arabidopsis thaliana]
                  399753
Seq. No.
Seq. ID
                  LIB3431-027-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3204108
BLAST score
                  570
E value
                  8.0e-59
                  118
Match length
                  87
% identity
                  (AJ006764) putative deoxycytidylate deaminase [Cicer
NCBI Description
                  arietinum]
                  399754
Seq. No.
                  LIB3431-027-P1-K1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g132105
BLAST score
                  666
                  5.0e-70
E value
                  142
Match length
                  89
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
```

(D00643) small subunit of ribulose-1,5-bisphosphate

```
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]
```

```
399755
Seq. No.
Seq. ID
                  LIB3431-027-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  q3789952
BLAST score
                  307
E value
                  6.0e-28
Match length
                  66
% identity
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
                  399756
Seq. No.
                  LIB3431-027-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076800
BLAST score
                  717
                  5.0e-76
E value
Match length
                  155
                  87
% identity
NCBI Description
                  L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
                  maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate
                  peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate
                  peroxidase [Zea mays]
Seq. No.
                  399757
                  LIB3431-027-P1-K1-F6
Seq. ID
Method
                  BLASTX
                  g1835731
NCBI GI
                  531
BLAST score
                  3.0e-54
E value
Match length
                  101
                  100
% identity
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  399758
Seq. No.
                  LIB3431-027-P1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3126854
BLAST score
                  671
                  1.0e-70
E value
                  126
Match length
                  100
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  399759
Seq. No.
                  LIB3431-027-P1-K1-F9
Seq. ID
                  BLASTX
Method
                  g6066383
NCBI GI
BLAST score
                  236
                  5.0e-20
E value
                  49
Match length
```

98

% identity

BLASTX

```
NCBI Description
                   (AJ011926) Mg-protoporphyrin IX [Hordeum vulgare]
Seq. No.
                   399760
Seq. ID
                  LIB3431-027-P1-K1-G1
Method
                  BLASTX
NCBI GI
                   g2624328
BLAST score
                   542
                   2.0e-55
E value
Match length
                   118
% identity
                   90
NCBI Description
                   (AJ002894) OsGRP2 [Oryza sativa]
                   399761
Seq. No.
                  LIB3431-027-P1-K1-G10
Seq. ID
Method
                  BLASTX
                   g3935168
NCBI GI
BLAST score
                   292
E value
                   3.0e-26
Match length
                   125
% identity
                   53
NCBI Description
                  (AC004557) F17L21.11 [Arabidopsis thaliana]
                   399762
Seq. No.
                  LIB3431-027-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3789952
BLAST score
                   698
E value
                   8.0e-74
Match length
                   139
                   98
% identity
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
                  399763
Seq. No.
                  LIB3431-027-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3789954
BLAST score
                   840
E value
                   2.0e-90
Match length
                  154
                   100
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                  399764
Seq. No.
Seq. ID
                  LIB3431-027-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g2832672
BLAST score
                  263
                   9.0e-23
E value
                  55
Match length
                   95
% identity
                   (AL021712) nifU-like protein [Arabidopsis thaliana]
NCBI Description
                  399765
Seq. No.
                  LIB3431-027-P1-K1-G5
Seq. ID
```

NCBI GI

BLASTX

g3075488

```
g5103831
NCBI GI
BLAST score
                  281
                  5.0e-25
E value
                  94
Match length
                  60
% identity
                  (AC007591) ESTs gb H37032, gb R6425, gb Z34651, gb N37268,
NCBI Description
                  gb AA713172 and gb Z34241 come from this gene. [Arabidopsis
                  thaliana]
                  399766
Seq. No.
                  LIB3431-027-P1-K1-G6
Seq. ID
Method
                  BLASTN
                  g3075487
NCBI GI
BLAST score
                  157
                  5.0e-83
E value
Match length
                  157
                  100
% identity
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                  mRNA, complete cds
                  399767
Seq. No.
                  LIB3431-027-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5815133
BLAST score
                  183
                  2.0e-13
E value
                  99
Match length
% identity
                  37
NCBI Description
                  (AF169386) SPO11 [Mus musculus]
                  399768
Seq. No.
                  LIB3431-027-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3763918
BLAST score
                  236
                  1.0e-19
E value
Match length
                  67
% identity
NCBI Description
                   (AC004450) putative isopropylmalate dehydratase
                   [Arabidopsis thaliana]
                  399769
Seq. No.
                  LIB3431-027-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169544
BLAST score
                  540
E value
                  3.0e-55
Match length
                  154
                  67
% identity
NCBI Description
                  ERD1 PROTEIN PRECURSOR >gi_541859_pir__JN0901 ERD1 protein
                  - Arabidopsis thaliana >gi 497629 dbj BAA04506 (D17582)
                  ERD1 protein [Arabidopsis thaliana]
Seq. No.
                  399770
                  LIB3431-027-P1-K1-H11
Seq. ID
```

NCBI GI

BLASTX q3881189

```
572
BLAST score
                  1.0e-65
E value
                  139
Match length
% identity
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                  399771
Seq. No.
                  LIB3431-027-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3789954
BLAST score
                  148
E value
                  2.0e-19
Match length
                  118
% identity
                  53
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  399772
Seq. No.
                  LIB3431-027-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587571
BLAST score
                  425
                  8.0e-42
E value
                  104
Match length
                  75
% identity
                   (AC006550) Belongs to the PF 01027 Uncharacterized protein
NCBI Description
                  family UPF0005 with 7 transmembrane domains. [Arabidopsis
                  thaliana]
                  399773
Seq. No.
Seq. ID
                  LIB3431-027-P1-K1-H5
                  BLASTX
Method
NCBI GI
                  g115796
BLAST score
                  721
                  2.0e-76
E value
                  138
Match length
                   98
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I
                  CAB) (LHCP) >gi 218174 dbj BAA00537_ (D00642) type II
                  light-harvesting chlorophyll a/b-binding protein [Oryza
                  sativa]
                  399774
Seq. No.
                  LIB3431-027-P1-K1-H6
Seq. ID
Method
                  BLASTX
                  g3789954
NCBI GI
                  186
BLAST score
                  2.0e-14
E value
Match length
                  64
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  399775
Seq. No.
                  LIB3431-027-P1-K1-H7
Seq. ID
```



```
489
BLAST score
                  3.0e-49
E value
Match length
                  144
                  61
% identity
NCBI Description
                   (Z99281) similar to ADP-ribosylation factor; cDNA EST
                  EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337
                  comes from this gene; cDNA EST EMBL: C09829 comes from this
                  gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST y
Seq. No.
                  399776
                  LIB3431-027-P1-K1-H8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q320618
                  489
BLAST score
                  2.0e-49
E value
                  109
Match length
% identity
                  85
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi 218172 dbj BAA00536 (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                  399777
Seq. No.
Seq. ID
                  LIB3431-027-P1-K1-H9
                                             + ji di . +
Method
                  BLASTX
                  q482311
NCBI GI
BLAST score
                  731
E value
                  1.0e-77
                  142
Match length
                  100
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
Seq. No.
                  399778
                  LIB3431-027-P1-N1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g687677
BLAST score
                  230
E value
                  4.0e-19
Match length
                  51
% identity
NCBI Description
                  (U19925) unknown [Arabidopsis thaliana]
Seq. No.
                  399779
Seq. ID
                  LIB3431-027-P1-N1-A11
Method
                  BLASTX
NCBI GI
                  g3413423
BLAST score
                  169
E value
                  7.0e-12
Match length
                  64
% identity
                  (AJ006309) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

399780

LIB3431-027-P1-N1-A12

Seq. No. Seq. ID

```
BLASTX
Method
                  g2493650
NCBI GI
                  299
BLAST score
                   5.0e-36
E value
                  90
Match length
                   77
% identity
                  RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD
NCBI Description
                  CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)
                  >gi 1167858 emb CAA93139 (Z68903) chaperonin [Secale
                  cereale]
Seq. No.
                   399781
                  LIB3431-027-P1-N1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4574208
BLAST score
                  265
E value
                   4.0e-23
Match length
                  53
                   100
% identity
NCBI Description
                   (AF093108) histone H3 [Tortula ruralis]
                  399782
Seq. No.
Seq. ID
                  LIB3431-027-P1-N1-A4
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  177
                   9.0e-13
E value
Match length
                   41
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
Seq. No.
                  399783
                  LIB3431-027-P1-N1-A6
Seq. ID
Method
                  BLASTN
                  g20177
NCBI GI
BLAST score
                   399
                   0.0e+00
E value
Match length
                   433
                   99
% identity
                  Rice cab1R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
Seq. No.
                  399784
                  LIB3431-027-P1-N1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1173347
BLAST score
                  284
E value
                  2.0e-25
Match length
                  61
% identity
                   95
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7) P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
```

aestivum]

Seq. ID

```
Seq. No.
                  399785
                  LIB3431-027-P1-N1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                  271
E value
                  8.0e-24
Match length
                  56
% identity
NCBI Description
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                  [Zea mays]
                  399786
Seq. No.
                  LIB3431-027-P1-N1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3885892
BLAST score
                  338
                  1.0e-31
E value
Match length
                  65
                  100
% identity
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
                  399787
Seq. No.
                  LIB3431-027-P1-N1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q482311
BLAST score
                  186
E value
                  6.0e-14
Match length
                  36
                  100
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                  (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                  399788
Seq. No.
Seq. ID
                  LIB3431-027-P1-N1-B10
Method
                  BLASTN
NCBI GI
                  g169798
BLAST score
                  42
E value
                  3.0e-14
Match length
                  94
                  86
% identity
NCBI Description Oryza sativa 16.9 kDa heat shock protein gene, complete cds
                  399789
Seq. No.
                  LIB3431-027-P1-N1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g482311
BLAST score
                  154
E value
                  4.0e-10
Match length
                  44
                  73
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                  (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                  399790
Seq. No.
```

LIB3431-027-P1-N1-B3

```
BLASTN
Method
NCBI GI
                  g6006355
BLAST score
                  351
                  0.0e+00
E value
                  375
Match length
                  98
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
NCBI Description
Seq. No.
                  399791
                  LIB3431-027-P1-N1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q455510
BLAST score
                  173
E value
                  3.0e-92
Match length
                  201
                  97
% identity
NCBI Description Rice mRNA for ferritin, partial sequence
                  399792
Seq. No.
Seq. ID
                  LIB3431-027-P1-N1-B5
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  734
E value
                  6.0e-78
Match length
                  160
% identity
                  88
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  399793
Seq. ID
                  LIB3431-027-P1-N1-B6
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  339
E value
                  1.0e-42
Match length
                  89
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

Seq. No. 399794

Seq. ID LIB3431-027-P1-N1-B7

Method BLASTX

```
NCBI GI
                  q482311
BLAST score
                  345
                  1.0e-32
E value
Match length
                  75
                  91
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                  399795
Seq. No.
Seq. ID
                  LIB3431-027-P1-N1-B8
                  BLASTN
Method
NCBI GI
                  q3789949
BLAST score
                  288
E value
                  1.0e-161
                  292
Match length
% identity
                  100
                  Oryza sativa translation initiation factor (GOS2) mRNA,
NCBI Description
                  complete cds
                  399796
Seq. No.
                  LIB3431-027-P1-N1-C10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1346155
BLAST score
                  168
E value
                  1.0e-11
Match length
                  33
% identity
                  SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL 1 PRECURSOR
NCBI Description
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi_481942 pir__S40212 glycine
                  hydroxymethyltransferase (EC 2.1.2.1) - Flaveria pringlei
                  >gi_437995_emb_CAA81078_ (Z25859) glycine
                  hydroxymethyltransferase [Flaveria pringlei]
                  399797
Seq. No.
Seq. ID
                  LIB3431-027-P1-N1-C3
Method
                  BLASTX
NCBI GI
                  q115813
BLAST score
                  227
E value
                  1.0e-18
Match length
                  53
% identity
                  83
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                  399798
                  LIB3431-027-P1-N1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115813
BLAST score
                  243
E value
                  2.0e-20
Match length
                  55
                  85
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
```

4.5

```
399799
Seq. No.
                  LIB3431-027-P1-N1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g6063542
BLAST score
                  225
                  2.0e-18
E value
                  41
Match length
                  98
% identity
                   (AP000615) EST C74302(E30840) corresponds to a region of
NCBI Description
                  the predicted gene.; similar to glyceraldehyde-3-phosphate
                  dehydrogenase. (M64118) [Oryza sativa]
                  399800
Seq. No.
Seq. ID
                  LIB3431-027-P1-N1-C9
Method
                  BLASTN ·
NCBI GI
                  g218209
BLAST score
                  41
                  1.0e-13
E value
                  131
Match length
                  81
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
                  399801
Seq. No.
Seq. ID
                  LIB3431-027-P1-N1-D1
Method
                  BLASTX
                  g2244926
NCBI GI
                  292
BLAST score
                   3.0e-26
E value
                  88
Match length
% identity
                   (Z97339) glutaredoxin homolog [Arabidopsis thaliana]
NCBI Description
                   399802
Seq. No.
                  LIB3431-027-P1-N1-D10
Seq. ID
Method
                  BLASTX
                  q4115337
NCBI GI
BLAST score
                  201
                   1.0e-15
E value
                   41
Match length
% identity
                   (L81141) ubiquitin [Pisum sativum]
NCBI Description
                   399803
Seq. No.
                  LIB3431-027-P1-N1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  212
                   6.0e-17
E value
Match length
                   44
% identity
                   (Z72488) CP12 [Nicotiana tabacum]
NCBI Description
```

chlorophyll a/b-binding protein [Lycopersicon esculentum]

399804

57.00

Seq. No.

```
LIB3431-027-P1-N1-D2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1076724
BLAST score
                  284
                  2.0e-25
E value
Match length
                  56
                  95
% identity
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                  >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                  399805
                  LIB3431-027-P1-N1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  484
E value
                  1.0e-48
Match length
                  126
                  79
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055_pir__A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
                  399806
Seq. No.
Seq. ID
                  LIB3431-027-P1-N1-D7
Method
                  BLASTX
                  g3036951
NCBI GI
BLAST score
                  343
                  2.0e-32
E value
Match length
                  65
                  100
% identity
                   (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
                  399807
Seq. No.
Seq. ID
                  LIB3431-027-P1-N1-D8
Method
                  BLASTX
NCBI GI
                  q421916
BLAST score
                  243
                  1.0e-20
E value
                  45
Match length
                  100
% identity
                  chlorophyll a/b-binding protein - English ivy (fragment)
NCBI Description
                  >gi_12582_emb_CAA48410_ (X68333) light harvesting
                  chlorophyll a /b binding protein [Hedera helix]
Seq. No.
                  399808
                  LIB3431-027-P1-N1-E1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2570510
                  150
BLAST score
                  8.0e-79
E value
Match length
                  226
% identity
                  92
NCBI Description Oryza sativa chlorophyll a-b binding protein mRNA, complete
```

cds 399809 Seq. No. Seq. ID LIB3431-027-P1-N1-E11 Method BLASTX NCBI GI q170131 BLAST score 213 5.0e-17 E value Match length 61 % identity 66 NCBI Description (M55322) ribosomal protein 30S subunit [Spinacia oleracea] 399810 Seq. No. LIB3431-027-P1-N1-E12 Seq. ID Method BLASTX NCBI GI g132105 BLAST score 169 2.0e-20 E value 55 Match length 98 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa] Seq. No. 399811 LIB3431-027-P1-N1-E4 Seq. ID Method BLASTN NCBI GI q2570514 BLAST score 266 E value 1.0e-148 Match length 369 % identity 98 NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds Seq. No. 399812 Seq. ID LIB3431-027-P1-N1-E5 Method BLASTX NCBI GI q451193 BLAST score 284 2.0e-25 E value Match length 87 % identity NCBI Description (L28008) wali7 [Triticum aestivum] >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]

Seq. No. 399813

Seq. ID LIB3431-027-P1-N1-E6

Method BLASTX
NCBI GI g5354158
BLAST score 155
E value 3.0e-10

```
42
Match length
                  60
% identity
                   (AF149841) digalactosyldiacylglycerol synthase [Arabidopsis
NCBI Description
                  thaliana] >gi 5354160 gb_AAD42379.1_AF149842_1 (AF149842)
                  digalactosyldiacylglycerol synthase [Arabidopsis thaliana]
                  >gi 6041825 gb AAF02140.1 AC009918 12 (AC009918)
                  digalactosyldiacylglycerol synthase [Arabidopsis thaliana]
                  399814
Seq. No.
                  LIB3431-027-P1-N1-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1835731
BLAST score
                  359
                  4.0e-34
E value
Match length
                  80
                  88
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza satīva]
NCBI Description
Seq. No.
                  399815
                  LIB3431-027-P1-N1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885894
BLAST score
                  398
E value
                  1.0e-38
                  90
Match length
% identity
                   (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
Seq. No.
                  399816
Seq. ID
                  LIB3431-027-P1-N1-F1
                  BLASTX
Method
                  g3328221
NCBI GI
BLAST score
                  348
                  7.0e-33
E value
Match length
                   69
% identity
                   (AF076920) thioredoxin peroxidase [Secale cereale]
NCBI Description
                  399817
Seq. No.
Seq. ID
                  LIB3431-027-P1-N1-F10
                  BLASTX
Method
NCBI GI
                  q2826842
                  268
BLAST score
                  2.0e-23
E value
                  75
Match length
% identity
                   (AJ002236) loxc homologue [Lycopersicon pimpinellifolium]
NCBI Description
                  399818
Seq. No.
                  LIB3431-027-P1-N1-F11
Seq. ID
Method
                  BLASTN
                  g2072554
NCBI GI
                   361
BLAST score
E value
                  0.0e + 00
Match length
                   389
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
```

BLAST score

% identity

NCBI Description

E value Match length 326 3.0e-30

73

```
cds
                   399819
Seq. No.
Seq. ID
                  LIB3431-027-P1-N1-F2
Method
                  BLASTX
NCBI GI
                   q3204108
BLAST score
                   344
E value
                   2.0e-32
Match length
                   94
% identity
                   70
NCBI Description
                   (AJ006764) putative deoxycytidylate deaminase [Cicer
                   arietinum]
                  399820
Seq. No.
                  LIB3431-027-P1-N1-F3
Seq. ID
Method
                  BLASTN
                  g218207
NCBI GI
BLAST score
                  195
E value
                   1.0e-105
Match length
                  315
                   90
% identity
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
Seq. No.
                  399821
Seq. ID
                  LIB3431-027-P1-N1-F4
Method
                  BLASTN
NCBI GI
                  q3789951
BLAST score
                  134
E value
                   4.0e-69
Match length
                  318
% identity
                  86
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
Seq. No.
                  399822
Seq. ID
                  LIB3431-027-P1-N1-F5
Method
                  BLASTN
NCBI GI
                  q433216
BLAST score
                  223
                  1.0e-122
E value
Match length
                  232
                  99
% identity
                  Rice mRNA for ascorbate peroxidase (gene name SS622),
NCBI Description
                  partial cds
Seq. No.
                  399823
                  LIB3431-027-P1-N1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1835731
```

(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. ID

```
399824
Seq. No.
                   LIB3431-027-P1-N1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3126854
BLAST score
                   333
E value
                   5.0e - 31
Match length
                   63
                   100
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   399825
Seq. No.
Seq. ID
                   LIB3431-027-P1-N1-F9
Method
                   BLASTX
NCBI GI
                   g6066383
BLAST score
                   236
                   5.0e-20
E value
                   49
Match length
                   98
% identity
                   (AJ011926) Mg-protoporphyrin IX [Hordeum vulgare]
NCBI Description
Seq. No.
                   399826
                   LIB3431-027-P1-N1-G1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2624327
BLAST score
                   319
E value
                   1.0e-179
Match length
                   322
                   100
% identity
                  Oryza sativa mRNA for glycine rich RNA-binding protein 2
NCBI Description
                   (OsGRP2)
                   399827
Seq. No.
                   LIB3431-027-P1-N1-G11
Seq. ID
                   BLASTN
Method
                   g3789951
NCBI GI
                   193
BLAST score
E value
                   1.0e-104
Match length
                   391
% identity
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
                   399828
Seq. No.
                   LIB3431-027-P1-N1-G12
Seq. ID
Method
                  BLASTX
                  g3789954
NCBI GI
BLAST score
                   339
                   9.0e-32
E value
                  63
Match length
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   399829
Seq. No.
```

LIB3431-027-P1-N1-G4

BLAST score

347

```
BLASTX
Method
NCBI GI
                   g2832672
BLAST score
                   183
E value
                   2.0e-13
Match length
                   37
                   97
% identity
                   (AL021712) nifU-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   399830
                   LIB3431-027-P1-N1-G6
Seq. ID
Method
                   BLASTN
                   g3075487
NCBI GI
BLAST score
                   149
E value
                   3.0e-78
Match length
                   157
% identity
                   99
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                  mRNA, complete cds
                   399831
Seq. No.
Seq. ID
                   LIB3431-027-P1-N1-G8
Method
                   BLASTX
NCBI GI
                   g3763918
BLAST score
                   225
E value
                   3.0e-18
                   70
Match length
% identity
                   64
                   (AC004450) putative isopropylmalate dehydratase
NCBI Description
                   [Arabidopsis thaliana]
                   399832
Seq. No.
Seq. ID
                   LIB3431-027-P1-N1-H1
Method
                   BLASTX.
NCBI GI
                   g733454
BLAST score
                   383
E value
                   6.0e-37
Match length
                  80
% identity
                   93
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                   399833
Seq. No.
                  LIB3431-027-P1-N1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3075487
BLAST score
                   310
                   1.0e-174
E value
Match length
                   314
                  100
% identity
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                  mRNA, complete cds
                   399834
Seq. No.
                  LIB3431-027-P1-N1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g517500
```

BLASTX

```
9.0e-33
E value
                  87
Match length
                  79
% identity
                  (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
                  399835
Seq. No.
                                                                  LIB3431-027-P1-N1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  300
                  2.0e-27
E value
                  57
Match length
                  100
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  399836
                  LIB3431-027-P1-N1-H6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3789953
BLAST score
                  227
                  1.0e-125
E value
                  291
Match length
                  95
% identity
                  Oryza sativa chlorophyll a/b-binding protein precursor
NCBI Description
                  (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  399837
Seq. No.
                  LIB3431-027-P1-N1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3881189
BLAST score
                  292
                  4.0e-26
E value
                  107
Match length
                  48
% identity
NCBI Description
                  (Z99281) similar to ADP-ribosylation factor; cDNA EST
                  EMBL: C08179 comes from this gene; cDNA EST EMBL: C08337
                  comes from this gene; cDNA EST EMBL:C09829 comes from this
                  gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST y
                  399838
Seq. No.
                  LIB3431-027-P1-N1-H9
Seq. ID
Method
                  BLASTX
                  g482311
NCBI GI
                  426
BLAST score
                  6.0e-42
E value
Match length
                  84
                  100
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                  (strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
Seq. No.
                  399839
                  LIB3431-028-P1-K1-A1
Seq. ID
```

% identity

51

```
NCBI GI
                  g2570497
                  373
BLAST score
E value
                  7.0e-36
Match length
                  76
                  97
% identity
                   (AF022731) H protein subunit of glycine decarboxylase
NCBI Description
                   [Oryza sativa]
                  399840
Seq. No.
                  LIB3431-028-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4680203
BLAST score
                  377
                  4.0e-36
E value
Match length
                  153
% identity
                  49
                   (AF114171) TNP2-like protein [Sorghum bicolor]
NCBI Description
                  399841
Seq. No.
                  LIB3431-028-P1-K1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  35
E value
                  5.0e-10
Match length
                  35
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  399842
                  LIB3431-028-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4325041
BLAST score
                  630
E value
                  7.0e-66
Match length
                  144
% identity
                   (AF117339) FtsH-like protein Pftf precursor [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                  399843
Seq. ID
                  LIB3431-028-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q1835731
BLAST score
                  594
E value
                  1.0e-61
Match length
                  126
% identity
                  91
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                  399844
                  LIB3431-028-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4127348
BLAST score
                  289
                  6.0e-26
E value
Match length
                  117
```

```
NCBI Description (AJ010449) glutathione transferase [Alopecurus myosuroides]
                  399845
Seq. No.
                  LIB3431-028-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1698548
BLAST score
                  456
                  2.0e-45
E value
                  137
Match length
                  60
% identity
NCBI Description (U58971) calmodulin-binding protein [Nicotiana tabacum]
                  399846
Seq. No.
                  LIB3431-028-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3345477
                  147
BLAST score
                  3.0e-09
E value
                  28
Match length
                  100
% identity
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
                  399847
Seq. No.
                  LIB3431-028-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5921189
BLAST score
                  364
E value
                  1.0e-34
Match length
                  153
                  49
% identity
                  CYTOCHROME P450 71C4 >qi 550542 emb CAA57425 (X81831)
NCBI Description
                  cytochrome P450 [Zea mays] >gi_1850903 emb CAA72196
                  (Y11368) cytochrome p450 [Zea mays]
                  399848
Seq. No.
                  LIB3431-028-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  408
                  7.0e-40
E value
                  98
Match length
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  399849
                  LIB3431-028-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI ·
                  g6002102
BLAST score
                  322
                  1.0e-29
E value
Match length
                  91
% identity
                  68
NCBI Description (AJ249833) Acyl-CoA binding protein (ACBP) [Digitalis
```

```
lanata]
                  399850
Seq. No.
Seq. ID
                  LIB3431-028-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g20262
BLAST score
                  69
E value
                  3.0e-30
Match length
                  89
% identity
                  94
NCBI Description O.sativa light-induced mRNA
                  399851
Seq. No.
                  LIB3431-028-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2499775
                  188
BLAST score
E value
                  5.0e-14
Match length
                  84
% identity
                  49
                  51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL
NCBI Description
                  CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE) >gi_915280
                  (U16959) FKBP51 [Mus musculus] >gi_1020307 (U36220) FK506
                  binding protein 51 [Mus musculus]
Seq. No.
                  399852
Seq. ID
                  LIB3431-028-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g5802955
BLAST score
                  194
E value
                  8.0e-15
Match length
                  79
                  47
% identity
NCBI Description (AF178990) stress related protein [Vitis riparia]
                  399853
Seq. No.
Seq. ID
                  LIB3431-028-P1-K1-C10
Method
                  BLASTX
                  g2734085
NCBI GI
BLAST score
                  154
E value
                  5.0e-10
Match length
                  107
% identity
                  28
                  (AF003136) contains similarity to ATP synthase subunit B
NCBI Description
                  [Caenorhabditis elegans]
Seq. No.
                  399854
Seq. ID
                  LIB3431-028-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g6015437
                  35
BLAST score
E value
                  6.0e-10
Match length .
                  35
% identity
                  100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
```

399855

Seq. No.

Seq. ID

```
LIB3431-028-P1-K1-C3
Seq. ID
                  BLASTN
Method
                  g5822826
NCBI GI
                  265
BLAST score
                  1.0e-147
E value
Match length
                  265
                  100
% identity
NCBI Description Oryza sativa D1 gene for alpha-subunit of GTP-binding
                  protein, wild type, partial sequence
Seq. No.
                  399856
                  LIB3431-028-P1-K1-C4
Seq. ID
                  BLASTN
Method
NCBI GI
                  g218171
                  59
BLAST score
                  1.0e-24
E value
                  139
Match length
% identity
                  86
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                  a/b binding protein of photosystem II (LHCPII), complete
                  399857
Seq. No.
                  LIB3431-028-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  573
E value
                  3.0e-59
Match length
                  109
% identity
                  100
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                  399858
Seq. No.
                  LIB3431-028-P1-K1-C7
Seq. ID
Method
                  BLASTX
                  g167097
NCBI GI
BLAST score
                  313
                  3.0e-41
E value
Match length
                  102
% identity
                   (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                   [Hordeum vulgare]
                  399859
Seq. No.
                  LIB3431-028-P1-K1-C8
Seq. ID
Method
                  BLASTX
                  g548770
NCBI GI
                  755
BLAST score
                  2.0e-80
E value
Match length
                  145
                  100
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
NCBI Description
                  protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                  ribosomal protein L3 [Oryza sativa]
                  399860
Seq. No.
                  LIB3431-028-P1-K1-D1
```

```
BLASTN
Method
                  g6015437
NCBI GI
                  36
BLAST score
                  1.0e-10
E value
Match length
                  36
                  100
% identity
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
                  399861
Seq. No.
Seq. ID
                  LIB3431-028-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g5441889
BLAST score
                  661
                  2.0e-69
E value
                  148
Match length
                  89
% identity
                  (AP000367) Similar to SEC7 protein, Saccharomyces
NCBI Description
                  cerevisiae, PIR2:S49764; Contains Immunoglobulins and major
                  histocompatibility complex proteins signature. (AL022604)
                  [Oryza sativa]
Seq. No.
                  399862
                  LIB3431-028-P1-K1-D12
Seq. ID
Method
                  BLASTX
                  g82080
NCBI GI
BLAST score
                  422
                  1.0e-41
E value
Match length
                  120
                  68
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >qi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  399863
Seq. No.
                  LIB3431-028-P1-K1-D2
Seq. ID
Method
                  BLASTX
                  g2072555
NCBI GI
BLAST score
                  237
E value
                  9.0e-20
Match length
                  44
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  399864
Seq. No.
                  LIB3431-028-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548605
BLAST score
                  435
E value
                  4.0e-43
Match length
                  112
                  80
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
```

- barley >gi_304220 (L12707) photosystem I PSI-K subunit

```
[Hordeum vulgare]
                  399865
Seq. No.
                  LIB3431-028-P1-K1-D5
Seq. ID
                  BLASTN
Method
                  g3885891
NCBI GI
BLAST score
                  119
                  2.0e-60
E value
                  156
Match length
                  100
% identity
                  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
NCBI Description
                  mRNA, complete cds
                  399866
Seq. No.
                  LIB3431-028-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2501189
                  164
BLAST score
                  7.0e-12
E value
                  33
Match length
                  91
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
Seq. No.
                  399867
                  LIB3431-028-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3341692
BLAST score
                  324
                   6.0e-30
E value
Match length
                  141
% identity
                   (AC003672) unknown protein [Arabidopsis thaliana]
NCBI Description
                  399868
Seq. No.
Seq. ID
                  LIB3431-028-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2570511
                   660
BLAST score
                   9.0e-72
E value
                  138
Match length
% identity
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                  399869
Seq. No.
                  LIB3431-028-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1076800
BLAST score
                  561
                  1.0e-57
E value
Match length
                  121
                  85
% identity
                  L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme -
NCBI Description
                  maize >gi 600116 emb CAA84406 (Z34934) cytosolic ascorbate
```

peroxidase [Zea mays] >gi 1096503 prf 2111423A ascorbate

Method

BLAST score

E value

peroxidase [Zea mays] 399870 Seq. No. LIB3431-028-P1-K1-E1 Seq. ID BLASTX Method NCBI GI g132105 699 BLAST score 6.0e-74 E value 149 Match length 89 % identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxy \overline{l} ase (EC $4.\overline{1}.1.39$) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa] 399871 Seq. No. LIB3431-028-P1-K1-E2 Seq. ID BLASTX Method g2633727 NCBI GI 148 BLAST score 2.0e-09 E value Match length 137 % identity 28 (Z99111) ykrT [Bacillus subtilis] NCBI Description 399872 Seq. No. LIB3431-028-P1-K1-E3 Seq. ID BLASTX Method g25704.97 NCBI GI BLAST score 565 3.0e-58 E value 123 Match length 93 % identity (AF022731) H protein subunit of glycine decarboxylase NCBI Description [Oryza sativa] 399873 Seq. No. LIB3431-028-P1-K1-E4 Seq. ID

g1661160 NCBI GI BLAST score 382 8.0e-37 E value 89 Match length 80 % identity (U74295) chlorophyll a/b binding protein [Oryza sativa] NCBI Description 399874 Seq. No. LIB3431-028-P1-K1-E5 Seq. ID BLASTX Method g836954 NCBI GI

BLASTX

452

6.0e-45

```
Match length
                  154
% identity
                   60
NCBI Description
                  (U20948) receptor protein kinase [Ipomoea trifida]
                  399875
Seq. No.
Seq. ID
                  LIB3431-028-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  q3789953
BLAST score
                  55
                   5.0e-22
E value
Match length
                  77
% identity
                  Oryza sativa chlorophyll a/b-binding protein precursor
NCBI Description
                   (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                   399876
Seq. No.
                  LIB3431-028-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3560529
BLAST score
                  336
E value
                   2.0e-31
                  87
Match length
                   75
% identity
NCBI Description
                   (AF039598) light harvesting chlorophyll A/B binding protein
                   [Prunus persica]
                  399877
Seq. No.
                  LIB3431-028-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2407281
BLAST score
                   349
                   7.0e-33
E value
Match length
                   65
                   100
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
                   399878
Seq. No.
Seq. ID
                  LIB3431-028-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g3329386
BLAST score
                  334
E value
                   4.0e-31
                  138
Match length
% identity
                   (AF038958) synaptic glycoprotein SC2 spliced variant [Homo
NCBI Description
                   sapiens]
                  399879
Seq. No.
Seq. ID
                  LIB3431-028-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                   644
                  3.0e-67
E value
                  136
Match length
```

95

% identity

Match length

81

```
(AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                   399880
Seq. No.
                   LIB3431-028-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q671740
BLAST score
                   547
                   4.0e-56
E value
Match length
                   101
                   98
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   399881
Seq. No.
Seq. ID
                   LIB3431-028-P1-K1-F2
Method
                   BLASTX
                   q132672
NCBI GI
                   459
BLAST score
                   8.0e-46
E value
Match length
                   97
% identity
                   95
                   CHLOROPLAST 50S RIBOSOMAL PROTEIN L14 >gi_71224_pir__R5RZ14
NCBI Description
                   ribosomal protein L14 - rice chloroplast >gi_12023_emb_CAA33932_ (X15901) ribosomal protein L14
                   [Oryza sativa] >gi_226644_prf__1603356BU ribosomal protein
                   L14 [Oryza sativa]
                   399882
Seq. No.
                   LIB3431-028-P1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5442410
BLAST score
                   243
E value
                   2.0e-20
Match length
                   108
                   48
% identity
                   (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]
NCBI Description
Seq. No.
                   399883
                   LIB3431-028-P1-K1-F5
Seq. ID
Method
                   BLASTX
                   q548603
NCBI GI
BLAST score
                   158
E value
                   1.0e-10
                   34
Match length
                   91
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                   >gi 478404_pir__JQ2247 photosystem I chain D precursor -
                   barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]
                   399884
Seq. No.
                   LIB3431-028-P1-K1-F6
Seq. ID
Method
                   BLASTX
                   g2673920
NCBI GI
BLAST score
                   248
                   5.0e-21
E value
```

```
% identity
                   (AC002561) similar to Drosophila couch potato protein
NCBI Description
                   [Arabidopsis thaliana]
                  399885
Seq. No.
                  LIB3431-028-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3033382
BLAST score
                  257
E value
                  4.0e-22
Match length
                  101
% identity
                  49
                  (AC004238) unknown protein [Arabidopsis thaliana]
NCBI Description
                  399886
Seq. No.
                  LIB3431-028-P1-K1-G1
Seq. ID
Method
                  BLASTX
                  g6006894
NCBI GI
BLAST score
                  404
                  2.0e-39
E value
Match length
                  113
                  .75
% identity
                  (AC008153) unknown protein [Arabidopsis thaliana]
NCBI Description
                  399887
Seq. No.
                  LIB3431-028-P1-K1-G10
Seq. ID
Method
                  BLASTX
                  g168523
NCBI GI
                  274
BLAST score
                  3.0e-24
E value
                  113
Match length
% identity
                   (M31483) glyceraldehyde-3-phosphate dehydrogenase precursor
NCBI Description
                  [Zea mays]
                  399888
Seq. No.
Seq. ID
                  LIB3431-028-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g2072555
                  237
BLAST score
                  7.0e-20
E value
                  44
Match length
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  399889
Seq. No.
                  LIB3431-028-P1-K1-G2
Seq. ID
                  BLASTX
Method
                  q2293480
NCBI GI
BLAST score
                  413
                  1.0e-40
E value
                  86
Match length
% identity
                  93
```

NCBI Description (AF011331) glycine-rich protein [Oryza sativa]

BLAST score

174

```
399890
Seq. No.
                  LIB3431-028-P1-K1-G3
Seq. ID
Method
                  BLASTX
                  q5902394
NCBI GI
BLAST score
                  155
                   3.0e-10
E value
Match length
                  37
                  86
% identity
                   (AC008148) Putative phosphoglucomutase [Arabidopsis
NCBI Description
                  thaliana]
                  399891
Seq. No.
                  LIB3431-028-P1-K1-G4
Seq. ID
Method
                  BLASTX
                  g3126854
NCBI GI
BLAST score
                   645
                   1.0e-67
E value
Match length
                  121
% identity
                   100
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  399892
Seq. ID
                  LIB3431-028-P1-K1-G5
Method
                  BLASTX
NCBI GI
                   g3668091
BLAST score
                   519
E value
                   8.0e-53
Match length
                   149
% identity
                   (AC004667) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  399893
                  LIB3431-028-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2780746
BLAST score
                  717
                   5.0e-76
E value
Match length
                  138
% identity
                   (AB005290) plastid RNA polymerase sigma factor [Oryza
NCBI Description
                  sativa]
Seq. No.
                   399894
                  LIB3431-028-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q710308
BLAST score
                   699
E value
                   6.0e-74
Match length
                   153
% identity
                   (U11693) victorin binding protein [Avena sativa]
NCBI Description
Seq. No.
                   399895
                  LIB3431-028-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4510406
```

```
1.0e-12
E value
Match length
                  104
                  48
% identity
                  (AC006587) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  399896
Seq. No.
                  LIB3431-028-P1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g586038
BLAST score
                  537
                  6.0e-55
E value
Match length
                  148
                  72
% identity
                  SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN, CHLOROPLAST
NCBI Description
                  PRECURSOR (SRP54) (54 CHLOROPLAST PROTEIN) (54CP) (FFC)
                  >gi 480296 pir S36637 signal recognition particle 54CP
                  protein precursor - Arabidopsis thaliana
                  >gi 396701 emb CAA79981.1 (Z21970) 54CP [Arabidopsis
                  thaliana]
Seq. No.
                  399897
                  LIB3431-028-P1-K1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g132105
                  609
BLAST score
                  2.0e-63
E value
Match length
                  131
% identity
                  88
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  399898
                  LIB3431-028-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170606
BLAST score
                  314
                  8.0e-29
E value
                  81
Match length
% identity
                  ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                  >gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3),
```

chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A,

Adenylate Kinase From Maize In Complex With The Inhibitor

P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)

>gi 3114422 pdb 1ZAK B Chain B, Adenylate Kinase From Maize

In Complex With The Inhibitor

P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)

Seq. No. 399899

LIB3431-028-P1-K1-H12 Seq. ID



```
BLASTN
Method
NCBI GI
                  q20262
                  186
BLAST score
E value
                  1.0e-100
Match length
                  333
                  90
% identity
NCBI Description O.sativa light-induced mRNA
                  399900
Seq. No.
                  LIB3431-028-P1-K1-H2
Seq. ID
Method
                  BLASTX
                  g2499614
NCBI GI
BLAST score
                  720
                  2.0e-76
E value
                  146
Match length
                  90
% identity
                  MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG NTF3 (P43)
NCBI Description
                  >gi_481830_pir__S39559 mitogen-activated protein kinase 3
                  homolog ntf3 - common tobacco >gi_406751_emb_CAA49592_
                   (X69971) NTF3 [Nicotiana tabacum]
                  399901
Seq. No.
                  LIB3431-028-P1-K1-H3
Seq. ID
                  BLASTX
Method
                  g4079798
NCBI GI
BLAST score
                  565
                  3.0e-58
E value
Match length
                  109
                  100
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                  399902
Seq. No.
                  LIB3431-028-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1351270
                  542
BLAST score
                  1.0e-55
E value
Match length
                  113
                   93
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi_478410_pir__JQ2255 triose-phosphate isomerase (EC
                   5.3.1.1) - rice >gi 169821 (M87064) triosephosphate
                   isomerase [Oryza sativa]
                   399903
Seq. No.
                  LIB3431-028-P1-K1-H5
Seq. ID
                  BLASTX
Method
NCBI GI
                   g871931
                   452
BLAST score
                   6.0e-45
E value
Match length
                   117
                   79
% identity
                   (D30763) ferredoxin [Oryza sativa]
NCBI Description
```

399904

LIB3431-028-P1-K1-H6

Seq. No.

Seq. ID

BLAST score

E value

410 0.0e+00

```
Method
                  BLASTX
NCBI GI
                  g417260
BLAST score
                   323
E value
                   5.0e-30
Match length
                  106
                   64
% identity
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                  lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
                  399905
Seq. No.
                  LIB3431-028-P1-K1-H7
Seq. ID
Method
                  BLASTX
                  g1498315
NCBI GI
BLAST score
                  364
                  1.0e-34
E value
Match length
                  135
% identity
                  54
                  (U56419) IAP100 [Pisum sativum]
NCBI Description
                  399906
Seq. No.
Seq. ID
                  LIB3431-028-P1-K1-H8
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
                  1.0e-10
E value
Match length
                  47
% identity
                   66
NCBI Description Xenopus laevis cDNA clone 27A6-1
                  399907
Seq. No.
Seq. ID
                  LIB3431-028-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g4079798
BLAST score
                  416
                  7.0e-41
E value
Match length
                  111
% identity
NCBI Description
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                  sativa]
                  399908
Seq. No.
                  LIB3431-028-P1-N1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2887286
                  273
BLAST score
                  3.0e-24
E value
Match length
                  61
% identity
                  82
NCBI Description
                  (Z99530) H protein [Flaveria anomala]
                  399909
Seq. No.
Seq. ID
                  LIB3431-028-P1-N1-A10
Method
                  BLASTN
NCBI GI
                  g6041757
```

```
418
Match length
% identity
                  100
NCBI Description
                  Genomic Sequence For Oryza sativa Clone 10P20, Lemont
                  Strain, Complete Sequence, complete sequence
                  399910
Seq. No.
Seq. ID
                  LIB3431-028-P1-N1-A11
Method
                  BLASTX
NCBI GI
                  g2462750
BLAST score
                  173
E value
                  2.0e-12
Match length
                  51
% identity
                  67
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                  399911
Seq. No.
                  LIB3431-028-P1-N1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3643602
BLAST score
                  246
                  7.0e-21
E value
                  78
Match length
                  58
% identity
                   (AC005395) putative tonoplast intrinsic protein
NCBI Description
                   [Arabidopsis thaliana]
                  399912
Seq. No.
Seq. ID
                  LIB3431-028-P1-N1-A4
Method
                  BLASTX
NCBI GI
                  g3808101
BLAST score
                  344
                  2.0e-32
E value
                  79
Match length
                  90
% identity
                   (AJ012165) chloroplast protease [Capsicum annuum]
NCBI Description
Seq. No.
                  399913
                  LIB3431-028-P1-N1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  286
E value
                  1.0e-25
                  65
Match length
                  85
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                  399914
Seq. No.
                  LIB3431-028-P1-N1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  277
E value
                  1.0e-24
Match length
                  52
                  100
% identity
```

NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]

```
Seq. No.
                   399915
                   LIB3431-028-P1-N1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g289920
BLAST score
                   298
                   5.0e-27
E value
                   58
Match length
                   98
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   399916
Seq. No.
                   LIB3431-028-P1-N1-B2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g6002102
BLAST score
                   213
                   3.0e-17
E value
                   47
Match length
                   83
% identity
                   (AJ249833) Acyl-CoA binding protein (ACBP) [Digitalis
NCBI Description
                   lanata]
Seq. No.
                   399917
                   LIB3431-028-P1-N1-B3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g20262
BLAST score
                   343
E value
                   0.0e + 00
Match length
                   363
                   99
% identity
NCBI Description O.sativa light-induced mRNA
                   399918
Seq. No.
                   LIB3431-028-P1-N1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131176
                   275
BLAST score
                   2.0e-24
E value
Match length
                   57
% identity
                   93
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                   >gi 72683 pir F1BH4 photosystem I chain IV precursor -
                   barley >gi 19087 emb CAA68782 (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi 226163 prf 1413233A
                   10.8kD photosystem I protein [Hordeum vulgare var.
                   distichum]
Seq. No.
                   399919
                   LIB3431-028-P1-N1-C10
Seq. ID
                   BLASTX
Method
                   g1136416
NCBI GI
BLAST score
                   144
                   7.0e-09
E value
Match length
                   51
% identity
NCBI Description (D80000) similar to mitosis-specific chromosome segregation
```

Seq. ID Method

protein SMC1 of S.cerevisiae. [Homo sapiens]

399920

Seq. No.

```
LIB3431-028-P1-N1-C12
Seq. ID
Method
                   BLASTX
                   g134034
NCBI GI
                   238
BLAST score
                   5.0e-20
E value
                   70
Match length
                   64
% identity
                   30S RIBOSOMAL PROTEIN S30, CHLOROPLAST PRECURSOR (CS-S5)
NCBI Description
                   (CS5) (S22) (RIBOSOMAL PROTEIN 1) (PSRP-1)
                   >gi_279640_pir__R3SPS5 ribosomal protein CS-S22 precursor,
                   chloroplast - spinach >gi_12316_emb_CAA41960_ (X59270)
                   chloroplast ribosomal protein S\overline{2}2 [\overline{S}pinacia \overline{o}leracea]
                   >gi 18031 emb CAA33403 (X15344) spinach S22 r-protein
                   [Spinacia oleracea]
                   399921
Seq. No.
                   LIB3431-028-P1-N1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g693920
                   327
BLAST score
                   2.0e-30
E value
                   64
Match length
                   98
% identity
                   (U21113) chlorophyll a/b binding protein [Solanum
NCBI Description
                   tuberosum]
                   399922
Seq. No.
                   LIB3431-028-P1-N1-C5
Seq. ID
                   BLASTX
Method
NÇBI GI
                   g1835731
                   330
BLAST score
                   1.0e-30
E value
                   74
Match length
                   86
% identity
NCBI Description
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                   399923
Seq. No.
                   LIB3431-028-P1-N1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132166
BLAST score
                   160
                   6.0e-11
E value
Match length
                   31
                   87
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                   CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                   >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase
                   actīvase precursor - Arabidopsis thaliana
                   >gi 16471 emb CAA32429 (X14212) rubisco activase (AA 1 -
                   473) [Arabidopsis thaliana]
                   399924
Seq. No.
```

LIB3431-028-P1-N1-C8

BLASTX

Seq. ID

```
g548770
NCBI GI
BLAST score
                   321
                   9.0e-30
E value
Match length
                   63
                   100
% identity
                   60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
NCBI Description
                   protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
                   ribosomal protein L3 [Oryza sativa]
Seq. No.
                   399925
Seq. ID
                   LIB3431-028-P1-N1-D10
Method
                   BLASTN
                   g433216
NCBI GI
BLAST score
                   55
E value
                   4.0e-22
Match length
                   138
                   85
% identity
NCBI Description
                  Rice mRNA for ascorbate peroxidase (gene name SS622),
                  partial cds
Seq. No.
                   399926
Seq. ID
                   LIB3431-028-P1-N1-D11
Method
                   BLASTN
NCBI GI
                   g5441876
BLAST score
                   357
E value
                   0.0e+00
Match length
                   439
                   97
% identity
                  Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
NCBI Description
                   (contig b)
Seq. No.
                   399927
Seq. ID
                  LIB3431-028-P1-N1-D12
Method
                   BLASTX
NCBI GI
                   g115813
BLAST score
                   238
E value
                   5.0e-20
Match length
                   54
                   85
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                   CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
                   399928
Seq. No.
                  LIB3431-028-P1-N1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2072555
BLAST score
                   224
E value
                   3.0e-18
Match length
                   44
                   95
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                   399929
```

LIB3431-028-P1-N1-D5

```
BLASTX
Method
                   q3885892
NCBI GI
BLAST score
                   261
                   1.0e-22
E value
Match length
                   53
% identity
                   98
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
                   399930
Seq. No.
                   LIB3431-028-P1-N1-D6
Seq. ID
                   BLASTX
Method
                   q2501190
NCBI GI
                   198
BLAST score
                   3.0e-15
E value
Match length
                   57
                   74
% identity
                   THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
NCBI Description
                   >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
                   - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                   [Zea mays]
                   399931
Seq. No.
Seq. ID
                   LIB3431-028-P1-N1-D8
Method .
                   BLASTX
                   g115793
NCBI GI
BLAST score
                   396
                   2.0e-38
E value
Match length
                   78
% identity
                   95
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR
NCBI Description
                   (CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_
                   (X63197) type III LHCII CAB precursor protein [Hordeum
                   vulgare]
                   399932
Seq. No.
                   LIB3431-028-P1-N1-D9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g433216
BLAST score
                   165
                   9.0e-88
E value
Match length
                   171
                   99
% identity
                   Rice mRNA for ascorbate peroxidase (gene name SS622),
NCBI Description
                   partial cds
Seq. No.
                   399933
                   LIB3431-028-P1-N1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   301
                   2.0e-27
E value
Match length
                   57
% identity
                   100
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
```

ribulose-bisphosphate carboxy \overline{l} ase ($\overline{E}C$ 4.1.1.39) small chain

```
sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  399934
Seq. No.
Seq. ID
                  LIB3431-028-P1-N1-E3
Method
                  BLASTX
NCBI GI
                  g2499417
BLAST score
                  323
                  5.0e-30
E value
Match length
                  74
                  82
% identity
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
NCBI Description
                  >gi 1085826_pir S49248 H-protein - Flaveria anomala
                  >gi 547558 emb CAA85761 (Z37524) H-protein [Flaveria
                  anomala]
Seq. No.
                  399935
                  LIB3431-028-P1-N1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  315
                  5.0e-29
E value
Match length
                  64
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  399936
Seq. No.
                  LIB3431-028-P1-N1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129703
BLAST score
                  189
                  3.0e-14
E value
Match length
                  87
% identity
                  49
NCBI Description
                  receptor kinase - Arabidopsis thaliana
                  >gi_2129704_pir__S71184 receptor kinase - Arabidopsis
                  thaliana >gi 166692 (M80238) receptor kinase [Arabidopsis
                  thaliana] >gi 445123 prf 1908429A receptor kinase
                   [Arabidopsis thaliana]
                  399937
Seq. No.
                  LIB3431-028-P1-N1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789954
                  357
BLAST score
E value
                  7.0e-34
Match length
                  66
                  100
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
```

precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

(D00643) small subunit of ribulose-1,5-bisphosphate

399938

Seq. No.

Seq. ID

```
LIB3431-028-P1-N1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3126853
BLAST score
                  171
E value
                  3.0e-91
Match length
                  209
                  100
% identity
NCBI Description
                  Oryza sativa chlorophyll a/b binding protein (RCABP89)
                  mRNA, nuclear gene encoding chloroplast protein, complete
                  399939
Seq. No.
Seq. ID
                  LIB3431-028-P1-N1-E8
Method
                  BLASTN
NCBI GI
                  q218209
BLAST score
                  149
E value
                  4.0e-78
Match length
                  313
                  97
% identity
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
Seq. No.
                  399940
Seq. ID
                  LIB3431-028-P1-N1-F10
Method
                  BLASTX
NCBI GI
                  a115794
BLAST score
                  611
E value
                  2.0e-63
Match length
                  127
% identity
                  91
                  CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
NCBI Description
                  III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding
                  protein type III precursor (cab-13) - tomato
                  >gi_19277_emb_CAA42818_ (X60275) LHCII type III
                  [Lycopersicon esculentum]
                  399941
Seq. No.
Seq. ID
                  LIB3431-028-P1-N1-F11
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  406
                  1.0e-39
E value
Match length
                  76
                  99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  399942
Seq. No.
```

LIB3431-028-P1-N1-F3

Seq. ID

```
BLASTX
Method
NCBI GI
                  g5442410
BLAST score
                  182
                  2.0e-13
E value
                  78
Match length
                  50
% identity
                   (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]
NCBI Description
Seq. No.
                  399943
                  LIB3431-028-P1-N1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q548603
BLAST score
                  158
E value
                  1.0e-10
Match length
                  34
% identity
                  91
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                  barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
                  399944
Seq. No.
Seq. ID
                  LIB3431-028-P1-N1-F8
Method
                  BLASTX
NCBI GI
                  q3033382
BLAST score
                  359
E value
                   3.0e-34
Match length
                  76
% identity
NCBI Description
                   (AC004238) unknown protein [Arabidopsis thaliana]
                  399945
Seq. No.
                  LIB3431-028-P1-N1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076724
BLAST score
                  374
E value
                  7.0e-36
Match length
                  72
                  94
% identity
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                  >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
                  399946
Seq. No.
                  LIB3431-028-P1-N1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q120661
BLAST score
                  180
E value
                   4.0e-13
Match length
                  38
                  87
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
NCBI Description
                  PRECURSOR >qi 170237 (M14417) glyceraldehyde-3-phosphate
                  dehydrogenase A-subunit precursor [Nicotiana tabacum]
Seq. No.
```

LIB3431-028-P1-N1-G12

```
Method
                   BLASTX
                   g2072555
NCBI GI
BLAST score
                   231
E value
                   5.0e-19
Match length
                   44
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   399948
Seq. ID
                   LIB3431-028-P1-N1-G2
Method
                   BLASTN
NCBI GI
                   q2331130
BLAST score
                   247
E value
                   1.0e-136
Match length
                   275
% identity
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
                   399949
Seq. No.
                   LIB3431-028-P1-N1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g534982
BLAST score
                   340
                   6.0e-32
E value
                   100
Match length
                   68
% identity
                   (X75898) phosphoglucomutase [Spinacia oleracea]
NCBI Description
                   399950
Seq. No.
                   LIB3431-028-P1-N1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3126854
BLAST score
                   370
E value
                   2.0e-35
Match length
                   70
% identity
                   100
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   399951
Seq. No.
                  LIB3431-028-P1-N1-G5
Seq. ID
Method
                   BLASTN
                   g4680488
NCBI GI
BLAST score
                   45
                   5.0e-16
E value
                  114
Match length
                  84
% identity
                  Oryza sativa BAC clone 1.H19, complete sequence
NCBI Description
Seq. No.
                   399952
                  LIB3431-028-P1-N1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2780746
BLAST score
                  279
```

8.0e-25

E value

NCBI Description

```
56
Match length
                   96
% identity
                   (AB005290) plastid RNA polymerase sigma factor [Oryza
NCBI Description
                   sativa]
                   399953
Seq. No.
                   LIB3431-028-P1-N1-G8
Seq. ID
Method
                   BLASTX · /
NCBI GI
                   g710308
BLAST score
                   318
E value
                   2.0e-29
Match length
                   58
% identity
                   97
                   (U11693) victorin binding protein [Avena sativa]
NCBI Description
                   399954
Seq. No.
                   LIB3431-028-P1-N1-H10
Seq. ID
                   BLASTX
Method
                   g671740
NCBI GI
                   508
BLAST score
                   2.0e-51
E value
Match length
                   91
                   100
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
Seq. No.
                   399955
                   LIB3431-028-P1-N1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g671740
BLAST score
                   256
                   5.0e-22
E value
Match length
                   55
                   89
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
Seq. No.
                   399956
Seq. ID
                   LIB3431-028-P1-N1-H12
                   BLASTN
Method
NCBI GI
                   g3063523
                   72
BLAST score
                   2.0e-32
E value
Match length
                   88
                   95
% identity
                   Oryza sativa ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
Seq. No.
                   399957
                   LIB3431-028-P1-N1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4914323
                   206
BLAST score
                   4.0e-16
E value
                   44
Match length
                   77
% identity
                   (AC005489) F14N23.9 [Arabidopsis thaliana]
```

```
Seq. No.
                  399958
Seq. ID
                  LIB3431-028-P1-N1-H3
Method
                  BLASTX
NCBI GI
                  q4079798
BLAST score
                  183
E value
                  1.0e-13
Match length
                  34
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
                  399959
Seq. No.
                  LIB3431-028-P1-N1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351270
BLAST score
                  149
                  1.0e-09
E value
Match length
                  30
                  100
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
NCBI Description
                  >gi_478410_pir__JQ2255 triose-phosphate isomerase (EC
                  5.3.1.1) - rice >gi_169821 (M87064) triosephosphate
                  isomerase [Oryza sativa]
                  399960
Seq. No.
Seq. ID
                  LIB3431-028-P1-N1-H5
                  BLASTX
Method
                  q871931
NCBI GI
BLAST score
                  199
E value
                  2.0e-15
Match length
                  65
                  66
% identity
                  (D30763) ferredoxin [Oryza sativa]
NCBI Description
                  399961
Seq. No.
Seq. ID
                  LIB3431-028-P1-N1-H6
Method
                  BLASTX
NCBI GI
                  g417260
BLAST score
                  247
E value
                  5.0e-21
                  65
Match length
                  71
% identity
                  LIGHT REGULATED PROTEIN PRECURSOR >qi 422003 pir S33632
NCBI Description
                  lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                  light-regulated gene [Oryza sativa]
                  399962
Seq. No.
                  LIB3431-028-P1-N1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4079798
                  268
BLAST score
                  2.0e-23
E value
                  52
Match length
% identity
                  98
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
```

```
Seq. No.
                   399963
Seq. ID
                  LIB3431-029-P1-K1-A1
Method
                  BLASTN
NCBI GI
                   g2570516
BLAST score
                   55
                   2.0e-22
E value
                   125
Match length
% identity
                   87
                  Oryza sativa thioredoxin F isoform mRNA, complete cds
NCBI Description
                   399964
Seq. No.
                  LIB3431-029-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2982362
BLAST score
                   444
                   4.0e-44
E value
                   91
Match length
                   89
% identity
                   (AF053311) glutathione peroxidase [Zantedeschia aethiopica]
NCBI Description
                   399965
Seq. No.
                  LIB3431-029-P1-K1-A11
Seq. ID
                  BLASTN
Method
                   g473980
NCBI GI
BLAST score
                   74
E value
                   1.0e-33
Match length
                   115
                   90
% identity
                  Rice mRNA, partial homologous to glycine-rich protein gene
NCBI Description
                   399966
Seq. No.
Seq. ID
                  LIB3431-029-P1-K1-A5
Method
                   BLASTX
                   g2501189
NCBI GI
                   383
BLAST score
                   6.0e-37
E value
Match length
                   111
% identity
                   69
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                   >gi 2130146 pir S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
Seq. No.
                   399967
                  LIB3431-029-P1-K1-A8
Seq. ID
Method
                   BLASTX
                   g3075488
NCBI GI
BLAST score
                   270
E value
                   2.0e-47
                   117
Match length
% identity
NCBI Description
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                   399968
Seq. No.
                   LIB3431-029-P1-K1-B1
Seq. ID
```

BLASTX

Method

```
q3292814
NCBI GI
                  540
BLAST score
                  3.0e-55
E value
Match length
                  144
% identity
                  72
                  (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
                  399969
Seq. No.
                  LIB3431-029-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2662343
BLAST score
                  639
                  7.0e-67
E value
Match length
                  124
                  100
% identity
                 (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                  399970
Seq. No.
                  LIB3431-029-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5734634
BLAST score
                  286
                  2.0e-25
E value
                  83
Match length
                  60
% identity
NCBI Description (AP000391) Similar to putative lipase (AC006232) [Oryza
                  sativa]
                  399971
Seq. No.
                  LIB3431-029-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1084455
                  527
BLAST score
                  9.0e-54
E value
                  115
Match length
                  88
% identity
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                  >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]
                   399972
Seq. No.
                  LIB3431-029-P1-K1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                   q132105
                   566
BLAST score
                   2.0e-58
E value
                  131
Match length
                   82
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{EC} 4\overline{.1}.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
```

carboxylase S [Oryza sativa]

```
Seq. No.
                   399973
Seq. ID
                   LIB3431-029-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   g3747044
BLAST score
                   157
E value
                   2.0e-10
Match length
                   51
% identity
NCBI Description
                   (AF093537) blue copper protein [Zea mays]
Seq. No.
                   399974
Seq. ID
                   LIB3431-029-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   q115815
BLAST score
                   457
                   8.0e-46
E value
Match length
                   86
                   99
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN M9 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll a/b-binding protein precursor - maize
                   >gi_22355_emb_CAA39376_ (X55892) light-harvesting
                   chlorophyll a/b binding protein [Zea mays]
                   399975
Seq. No.
Seq. ID
                   LIB3431-029-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   q3288821
BLAST score
                   473
E value
                   2.0e-47
Match length
                   115
% identity
NCBI Description
                   (AF063901) alanine:glyoxylate aminotransferase;
                   transaminase [Arabidopsis thaliana]
                   >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
                   alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
Seq. No.
                   399976
                   LIB3431-029-P1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1001253
BLAST score
                   222
E value
                   5.0e-18
Match length
                   130
% identity
NCBI Description
                   (D64003) hypothetical protein [Synechocystis sp.]
                   399977
Seq. No.
                   LIB3431-029-P1-K1-C8
Seq. ID
Method
                   BLASTX
                   g2407281
NCBI GI
BLAST score
                   682
E value
                   6.0e-72
Match length
                   129
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
```

```
Seq. No.
                  399978
Seq. ID
                  LIB3431-029-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g2708741
BLAST score
                  391
E value
                   6.0e-38
Match length
                  122
% identity
NCBI Description
                   (AC003952) hypothetical protein [Arabidopsis thaliana]
                  399979
Seq. No.
                  LIB3431-029-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5923674
BLAST score
                   468
E value
                   7.0e-47
                  135
Match length
                   65
% identity
NCBI Description
                   (AC009326) unknown protein [Arabidopsis thaliana]
                  399980
Seq. No.
Seq. ID
                  LIB3431-029-P1-K1-D12
Method
                  BLASTN
                   q6063530
NCBI GI
BLAST score
                   310
                   1.0e-174
E value
Match length
                   321
                   99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
                  399981
Seq. No.
                  LIB3431-029-P1-K1-D2
Seq. ID
Method
                  BLASTX
                   q464986
NCBI GI
BLAST score
                   491
E value
                   2.0e-49
                   95
Match length
                   92
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                  >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana
                  >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                  enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
                  >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
                  enzyme E2 [Arabidopsis Thaliana]
                  >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                  ligase UBC9 [Arabidopsis thaliana]
                  399982
Seq. No.
Seq. ID
                  LIB3431-029-P1-K1-D3
Method ·
                  BLASTX
                  q482311
NCBI GI
                  707
BLAST score
                  8.0e-75
E value
```

NCBI GI

BLAST score

```
Match length
                  142
                  97
% identity
NCBI Description
                  photosystem II oxygen-evolving complex protein 1 - rice
                  (strain Nihonbare) >gi_739292 prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                  399983
Seq. No.
                  LIB3431-029-P1-K1-D8 .
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  565
E value
                  3.0e-58
Match length
                  124
                  85
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  399984
Seq. ID
                  LIB3431-029-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  609
                  2.0e-63
E value
Match length
                  131
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  399985
                  LIB3431-029-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617206
BLAST score
                  190
                  6.0e-23
E value
                  74
Match length
% identity
NCBI Description
                  (Z72489) CP12 [Pisum sativum]
Seq. No.
                  399986
                  LIB3431-029-P1-K1-E12
Seq. ID
Method
                  BLASTX
```

q2407281

497

```
2.0e-50
E value
Match length
                  98
% identity
                  98
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
Seq. No.
                  399987
Seq. ID
                  LIB3431-029-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g5262204
BLAST score
                  288
E value
                  9.0e-26
Match length
                  75
                  77
% identity
NCBI Description
                  (AL080252) putative protein [Arabidopsis thaliana]
                  399988
Seq. No.
                  LIB3431-029-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2624328
BLAST score
                  489
                  2.0e-49
E value
Match length
                  115
% identity
                  (AJ002894) OsGRP2 [Oryza sativa]
NCBI Description
                  399989
Seq. No.
                  LIB3431-029-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2501190
BLAST score
                  606
E value
                  5.0e-63
Match length
                  142
                  85
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
NCBI Description
                  >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
                  - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                  [Zea mays]
                  399990
Seq. No.
                  LIB3431-029-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2306981
BLAST score
                  277
E value
                  1.0e-24
Match length
                  54
                  89
% identity
NCBI Description
                  (AF010321) photosystem I antenna protein [Oryza sativa]
                  399991
Seq. No.
                  LIB3431-029-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4567279
BLAST score
                  412
E value
                  3.0e-40
Match length
                  138
```

60

% identity

```
(AC006841) putative serine/threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
                   399992
Seq. No.
                   LIB3431-029-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3063447
BLAST score
                   244
E value
                   2.0e-33
Match length
                   155
% identity
                   24
                   (AC003981) F22013.9 [Arabidopsis thaliana]
NCBI Description
                   399993
Seq. No.
Seq. ID
                   LIB3431-029-P1-K1-F2
Method
                   BLASTX
                   q1617197
NCBI GI
BLAST score
                   304
                   1.0e-27
E value
Match length
                   76
                   76
% identity
                   (Z72488) CP12 [Nicotiana tabacum]
NCBI Description
                   399994
Seq. No.
                   LIB3431-029-P1-K1-F3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2407266
BLAST score
                   102
                   3.0e-50
E value
Match length
                   158
                   91
% identity
                   Oryza sativa low molecular early light-inducible protein
NCBI Description
                   mRNA, complete cds
                   399995
Seq. No.
Seq. ID
                   LIB3431-029-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   q729478
                   230
BLAST score
                   5.0e-19
E value
                   120
Match length
% identity
                   42
                   FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                   >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1
                   (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
                   a region of the predicted gene.; similar to
                   ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
                   399996
Seq. No.
                   LIB3431-029-P1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3789954
BLAST score
                   654
                   1.0e-68
E value
Match length
                   121
```

100

% identity

Match length

80

```
(AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   399997
Seq. No.
                   LIB3431-029-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2570511
BLAST score
                   514
                                                                                   3<sup>65</sup>
E value
                   2.0e-52
Match length
                   98
% identity
                   99
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                   399998
Seq. No.
                   LIB3431-029-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q131176
BLAST score
                   322
E value
                   9.0e-30
Match length
                   62
                   98
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                   >gi_72683_pir__F1BH4 photosystem I chain IV precursor -
                   barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A
                   10.8kD photosystem I protein [Hordeum vulgare var.
                   distichuml
                   399999
Seq. No.
Seq. ID
                   LIB3431-029-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   q3850621
BLAST score
                   450
                   9.0e-45
E value
Match length
                   127
% identity
                   (Y15382) putative RNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   400000
Seq. No.
Seq. ID
                   LIB3431-029-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   q3075488
BLAST score
                   713
                   1.0e-75
E value
Match length
                   143
% identity
NCBI Description
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                   400001
Seq. No.
Seq. ID
                   LIB3431-029-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   q4406764
BLAST score
                   293
                   3.0e-26
E value
```

```
% identity
                  (AC006836) putative uridylyl transferase [Arabidopsis
NCBI Description
                  thaliana]
                  400002
Seq. No.
                  LIB3431-029-P1-K1-G12
Seq. ID
Method
                  BLASTN
                  g20262
NCBI GI
BLAST score
                  166
E value
                  3.0e-88
                  274
Match length
                  91
% identity
NCBI Description O.sativa light-induced mRNA
                  400003
Seq. No.
                  LIB3431-029-P1-K1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q115787
                  545
BLAST score
                  7.0e-56
E value
Match length
                  104
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  400004
Seq. No.
                  LIB3431-029-P1-K1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2982243
BLAST score
                  405
                  2.0e-39
E value
Match length
                  137
% identity
NCBI Description (AF051204) hypothetical protein [Picea mariana]
                  400005
Seq. No.
                  LIB3431-029-P1-K1-G7
Seq. ID
Method
                  BLASTX
                  g548604
NCBI GI
BLAST score
                  158
E value
                  1.0e-10
                  59
Match length
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F)
                  >gi 1076728 pir S51813 photosystem-I PSI-F chain precursor
                  - barley >gi 469560 (U08135) photosystem-I PSI-F subunit
                  precursor [Hordeum vulgare]
                  400006
Seq. No.
                  LIB3431-029-P1-K1-G8
Seq. ID
Method
                  BLASTX
                  g1835731
NCBI GI
```

200g.

391

BLAST score

```
8.0e-38
E value
Match length
                   86
% identity
                   86
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                   400007
Seq. No.
                   LIB3431-029-P1-K1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3618310
BLAST score
                   461
E value
                   5.0e-46
Match length
                   123
                   72
% identity
NCBI Description
                   (AB001883) zinc finger protein [Oryza sativa]
                   400008
Seq. No.
                   LIB3431-029-P1-K1-H1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3980400
BLAST score
                   253
                   1.0e-21
E value
                   134
Match length
% identity
                   42
NCBI Description
                   (AC004561) putative tropinone reductase [Arabidopsis
                   thaliana]
                   400009
Seq. No.
                   LIB3431-029-P1-K1-H10
Seq. ID
Method
                   BLASTN
                   q3885887
NCBI GI
BLAST score
                   265
                   1.0e-147
E value
                   265
Match length
                   100
% identity
                   Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                   complete cds
                   400010
Seq. No.
                   LIB3431-029-P1-K1-H11
Seq. ID
Method
                   BLASTX
                   q3126854
NCBI GI
BLAST score
                   581
                   3.0e-60
E value
                   109
Match length
% identity
                   100
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   400011
Seq. ID
                   LIB3431-029-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   q2191138
                   249
BLAST score
E value
                   3.0e-21
                   76
Match length
% identity
                   68
                   (AF007269) A IG002N01.18 gene product [Arabidopsis
NCBI Description
```

thaliana]

```
Seq. No.
                  400012
                  LIB3431-029-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  546
                  6.0e-56
E value
Match length
                  122
                  84
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  400013
Seq. No.
Seq. ID
                  LIB3431-029-P1-K1-H5
Method
                  BLASTN
                  g168500
NCBI GI
BLAST score
                  62
E value
                  3.0e-26
Match length
                  118
% identity
                  88
NCBI Description Maize (Zea mays) histone H4 gene (H4Cl4), complete cds
                  400014
Seq. No.
                  LIB3431-029-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5926740
BLAST score
                  455
                  2.0e-45
E value
Match length
                  89
                  98
% identity -
NCBI Description
                  (AB025310) asparaginyl endopeptidase [Oryza sativa]
                  400015
Seq. No.
Seq. ID
                  LIB3431-029-P1-N1-A10
Method
                  BLASTX
                  g2982362
NCBI GI
                  306
BLAST score
E value
                  6.0e-28
                  63
Match length
                  89
% identity
                  (AF053311) glutathione peroxidase [Zantedeschia aethiopica]
NCBI Description
                  400016
Seq. No.
                  LIB3431-029-P1-N1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4469021
BLAST score
                  271
                  6.0e-24
E value
                  75
Match length
```

71

% identity

Seq. ID

```
NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]
                  400017
Seq. No.
                  LIB3431-029-P1-N1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4585992
                  195
BLAST score
                  6.0e-15
E value
                  49
Match length
                  78
% identity
                  (AC005287) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  400018
Seq. No.
                  LIB3431-029-P1-N1-A7
Seq. ID
Method
                  BLASTX
                  g82167
NCBI GI
BLAST score
                  152
                   6.0e-10
E value
Match length
                  27
                  100
% identity
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
NCBI Description
                   (phosphorylating) (EC 1.2.1.13) A, chloroplast - common
                  tobacco (fragment)
                  400019
Seq. No.
                  LIB3431-029-P1-N1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3075488
BLAST score
                  143
                   6.0e-09
E value
                  29
Match length
% identity
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                   400020
Seq. No.
                  LIB3431-029-P1-N1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3075487
BLAST score
                  37
E value
                   1.0e-11
Match length
                   133
% identity
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                  mRNA, complete cds
Seq. No.
                   400021
Seq. ID
                  LIB3431-029-P1-N1-B1
                  BLASTX
Method
NCBI GI
                  g3292814
BLAST score
                   174
E value
                   2.0e-12
Match length
                   43
                  79
% identity
                   (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   400022
```

LIB3431-029-P1-N1-B11

Seq. ID

```
Method
                  BLASTN
NCBI GI
                  q2662344
BLAST score
                  319
E value
                  1.0e-179
Match length
                  323
                  100
% identity
                  Oryza sativa mRNA for EF-1 alpha, complete cds
NCBI Description
Seq. No.
                  400023
                  LIB3431-029-P1-N1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3183079
BLAST score
                  180
E value
                  2.0e-15
Match length
                  62
% identity
                  66
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
NCBI Description
                  >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate
                  dehydrogenase [Oryza sativa]
Seq. No.
                  400024
Seq. ID
                  LIB3431-029-P1-N1-B3
Method
                  BLASTN
NCBI GI
                  g600766
BLAST score
                  329
                  0.0e + 00
E value
Match length
                  368
% identity
                  98
                  Oryza sativa cyclophilin 2 (Cyp2) gene, complete cds
NCBI Description
                  400025
Seq. No.
Seq. ID
                  LIB3431-029-P1-N1-B4
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  135
E value
                  6.0e-70
Match length
                  199
% identity
                  92
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
                  400026
Seq. No.
Seq. ID
                  LIB3431-029-P1-N1-B6
Method
                  BLASTX
                  g1076308
NCBI GI
                  156
BLAST score
                  2.0e-10
E value
Match length
                  74
% identity
                  45
NCBI Description
                  RNA-binding protein cp33 precursor - Arabidopsis thaliana
                  >gi 681910 dbj BAA06522 (D31714) cp33 [Arabidopsis
                  thaliana] >gi 4886289 emb CAB43448.1 (AL050300)
                  RNA-binding protein cp33 precursor [Arabidopsis thaliana]
                  400027
Seq. No.
```

LIB3431-029-P1-N1-B9

Seq. ID

```
Method
                  BLASTN
NCBI GI
                  g20181
BLAST score
                  66
E value
                  1.0e-28
Match length
                  126
% identity
                  88
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
Seq. No.
                  400028
                  LIB3431-029-P1-N1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218171
BLAST score
                  166
                  3.0e-88
E value
                  242
Match length
                  93
% identity
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                  a/b binding protein of photosystem II (LHCPII), complete
Seq. No.
                  400029
Seq. ID
                  LIB3431-029-P1-N1-C4
Method
                  BLASTN
NCBI GI
                  q218154
BLAST score
                  76
E value
                  1.0e-34
Match length
                  138
% identity
                  99
NCBI Description
                  Oryza sativa gene for cytoplasmic aldolase, complete cds,
                  clone:Aldp
Seq. No.
                  400030
Seq. ID
                  LIB3431-029-P1-N1-C5
Method
                  BLASTN
NCBI GI
                  q218154
BLAST score
                  84
E value
                  2.0e-39
Match length
                  124
% identity
                  92
NCBI Description
                  Oryza sativa gene for cytoplasmic aldolase, complete cds,
                  clone:Aldp
Seq. No.
                  400031
Seq. ID
                  LIB3431-029-P1-N1-C8
Method
                  BLASTN
NCBI GI
                  q218209
BLAST score
                  155
E value
                  1.0e-81
Match length
                  338
% identity
                  96
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
Seq. No.
                  400032
```

LIB3431-029-P1-N1-D1

```
BLASTN
Method
                   a3789953
NCBI GI
                   214
BLAST score
E value
                   1.0e-117
                   293
Match length
% identity
                  Oryza sativa chlorophyll a/b-binding protein precursor
NCBI Description
                   (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
                   400033
Seq. No.
                   LIB3431-029-P1-N1-D12
Seq. ID
Method
                   BLASTN
                   g6063530
NCBI GI
BLAST score
                   115
E value
                   7.0e-58
                   299
Match length
                   83
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
                   400034
Seq. No.
                   LIB3431-029-P1-N1-D2
Seq. ID
Method
                   BLASTX
                   g464986
NCBI GI
BLAST score
                   351
                   3.0e-33
E value
Match length
                   70
% identity
                   91
                   UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN
NCBI Description
                   LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B)
                   >gi_421857_pir__S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana
                   >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating
                   enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639)
                   ubiquitin conjugating enzyme [Arabidopsis thaliana]
                   >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating
                   enzyme E2 [Arabidopsis thaliana]
                   >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein
                   ligase UBC9 [Arabidopsis thaliana]
                   400035
Seq. No.
                   LIB3431-029-P1-N1-D3
Seq. ID
                   BLASTX
Method
                   g482311
NCBI GI
                   238
BLAST score
                   5.0e-20
E value
                   48
Match length
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                   complex protein 1 [Oryza sativa]
                   400036
Seq. No.
                   LIB3431-029-P1-N1-D5
Seq. ID
Method
                   BLASTN
                   g4079797
NCBI GI
```

125

BLAST score

```
E value
                   6.0e-64
Match length
                   243
% identity
                   100
                   Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
NCBI Description
                   complete cds
Seq. No.
                   400037
Seq. ID
                   LIB3431-029-P1-N1-D6
Method
                   BLASTX
NCBI GI
                   g2570511
BLAST score
                   163
E value
                   1.0e-20
Match length
                   62
% identity
                   79
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                   400038
Seq. No.
                   LIB3431-029-P1-N1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   161
                   5.0e-11
E value
Match length
                   34
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   400039
Seq. No.
Seq. ID
                   LIB3431-029-P1-N1-D9
Method
                   BLASTX
                   q4038034
NCBI GI
                   142
BLAST score
                   8.0e-09
E value
                   42
Match length
% identity
                   (AC005936) unknown protein [Arabidopsis thaliana]
NCBI Description
                   400040
Seq. No.
                   LIB3431-029-P1-N1-E10
Seq. ID
Method
                   BLASTX
                   g671740
NCBI GI
BLAST score
                   164
                   2.0e-11
E value
Match length
                   33
% identity
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
                   400041
Seq. No.
                   LIB3431-029-P1-N1-E4
Seq. ID
```

. .

BLAST score

163

```
Method
                   BLASTX
NCBI GI
                  q5733874
BLAST score
                   225
E value
                   2.0e-18
                   75
Match length
                   53
% identity
                   (AC007932) F11A17.8 [Arabidopsis thaliana]
NCBI Description
                   400042
Seq. No.
                   LIB3431-029-P1-N1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2407279
BLAST score
                   182
                   1.0e-13
E value
Match length
                   37
% identity
                   100
                  (AF017362) aldolase [Oryza sativa]
NCBI Description
                   400043
Seq. No.
                   LIB3431-029-P1-N1-E6
Seq. ID
Method
                   BLASTN
                   g218171
NCBI GI
BLAST score
                   84
                   2.0e-39
E value
Match length
                   239
% identity
NCBI Description
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
                   a/b binding protein of photosystem II (LHCPII), complete
                   400044
Seq. No.
                   LIB3431-029-P1-N1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3980415
BLAST score
                   196
                   4.0e-15
E value
Match length
                   75
% identity
                   53
                   (AC004561) putative tropinone reductase [Arabidopsis
NCBI Description
                   thaliana]
                   400045
Seq. No.
Seq. ID
                   LIB3431-029-P1-N1-E8
Method
                   BLASTN
NCBI GI
                   g2624327
BLAST score
                   210
                   1.0e-114
E value
Match length
                   222
                   99
% identity
                  Oryza sativa mRNA for glycine rich RNA-binding protein 2
NCBI Description
                   (OsGRP2)
                   400046
Seq. No.
Seq. ID
                   LIB3431-029-P1-N1-F10
                   BLASTX
Method
                   q1076724
NCBI GI
```

```
3.0e-11
E value
                  34
Match length
                  82
% identity
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                  >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
                  400047
Seq. No.
                  LIB3431-029-P1-N1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g729477
                  294
BLAST score
                  1.0e-26
E value
                  58
Match length
                  90
% identity
                  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR)
NCBI Description
                  >gi_320548_pir__A44974 ferredoxin--NADP+ reductase (EC
                  1.18.1.2) precursor - common ice plant >gi_167256 (M25528)
                  ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
                  [Mesembryanthemum crystallinum] >qi 226768 prf 1604475A
                  ferredoxin NADP reductase [Mesembryanthemum crystallinum]
                  400048
Seq. No.
                  LIB3431-029-P1-N1-F5
Seq. ID
                  BLASTN
Method
                  q3789953
NCBI GI
                  301
BLAST score
E value
                  1.0e-169
Match length
                  321
                  98
% identity
                  Oryza sativa chlorophyll a/b-binding protein precursor
NCBI Description
                  (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  400049
Seq. No.
                  LIB3431-029-P1-N1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2570511
BLAST score
                  163
                  8.0e-22
E value
Match length
                  63
% identity
                  (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                  400050
Seq. No.
                  LIB3431-029-P1-N1-F8
Seq. ID
                  BLASTN
Method
                  g19086
NCBI GI
BLAST score
                  51
                  1.0e-19
E value
Match length
                  75
                  92
% identity
NCBI Description
                  Hordeum vulgare pot. psaE mRNA
                  400051
Seq. No.
                  LIB3431-029-P1-N1-F9
Seq. ID
```

BLASTX

Method

```
NCBI GI
                   q3850621
BLAST score
                   177
E value
                   7.0e-13
Match length
                   39
% identity
                   87
NCBI Description
                   (Y15382) putative RNA binding protein [Arabidopsis
                   thaliana]
Seq. No.
                   400052
Seq. ID
                  LIB3431-029-P1-N1-G1
Method
                   BLASTX
NCBI GI
                   g115813
BLAST score
                   233
                   2.0e-19
E value
Match length
                   53
% identity
                   85
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                   CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
                   400053
Seq. No.
                  LIB3431-029-P1-N1-G10
Seq. ID
Method
                  BLASTN
                   g3075487
NCBI GI
BLAST score
                   75
E value
                   5.0e-34
Match length
                   94
                   97
% identity
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                  mRNA, complete cds
Seq. No.
                   400054
Seq. ID
                  LIB3431-029-P1-N1-G12
Method
                  BLASTN
                   g20262
NCBI GI
BLAST score
                   173
E value
                   2.0e-92
Match length
                   345
                   88
% identity
                  O.sativa light-induced mRNA
NCBI Description
                   400055
Seq. No.
Seq. ID
                  LIB3431-029-P1-N1-G2
```

Method BLASTX g3036946 NCBI GI BLAST score 314 E value 6.0e-29 Match length 61 98 % identity

NCBI Description (AB012637) light harvesting chlorophyll a/b-binding protein

[Nicotiana sylvestris]

400056 Seq. No.

Seq. ID LIB3431-029-P1-N1-G3

Method BLASTN NCBI GI q2072554 BLAST score 142

```
E value
                  4.0e-74
Match length
                  194
% identity
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                  cds
                  400057
Seq. No.
                  LIB3431-029-P1-N1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2982243
BLAST score
                  294
E value
                  2.0e-26
                  83
Match length
                  66
% identity
                  (AF051204) hypothetical protein [Picea mariana]
NCBI Description
                  400058
Seq. No.
                  LIB3431-029-P1-N1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885892
BLAST score
                  242
                  2.0e-20
E value
                  53
Match length
                  92
% identity
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.
                  400059
                  LIB3431-029-P1-N1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
                  280
BLAST score
                  6.0e-25
E value
                  64
Match length
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                  400060
Seq. No.
Seq. ID
                  LIB3431-029-P1-N1-G9
Method
                  BLASTN
NCBI GI
                  g3618309
                  270
BLAST score
                  1.0e-150
E value
Match length
                  306
% identity
                  Oryza sativa mRNA for zinc finger protein, complete cds,
NCBI Description
                  clone:E10707
                  400061
Seq. No.
                  LIB3431-029-P1-N1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3126853
BLAST score
                  155
                  6.0e-82
E value
Match length
                  197
                  99
% identity
NCBI Description Oryza sativa chlorophyll a/b binding protein (RCABP89)
```

mRNA, nuclear gene encoding chloroplast protein, complete

cds Seq. No. 400062 Seq. ID LIB3431-029-P1-N1-H2 Method BLASTX NCBI GI q687677 BLAST score 234 1.0e-19 E value Match length 58 76 % identity (U19925) unknown [Arabidopsis thaliana] NCBI Description 400063 Seq. No. LIB3431-029-P1-N1-H3 Seq. ID Method BLASTX NCBI GI q347451 173 BLAST score 2.0e-12 E value Match length 33 100 % identity (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza NCBI Description sativa] 400064 Seq. No. Seq. ID LIB3431-029-P1-N1-H5 Method BLASTX NCBI GI g223793 BLAST score 190 E value 2.0e-14 Match length 37 100 % identity NCBI Description histone H4 [Physarum polycephalum] 400065 Seq. No. Seq. ID LIB3431-029-P1-N1-H6 Method BLASTN NCBI GI g20177 BLAST score 137 E value 3.0e-71 Match length 172 95 % identity Rice cab1R gene for light harvesting chlorophyll NCBI Description a/b-binding protein 400066 Seq. No. LIB3431-029-P1-N1-H7 Seq. ID Method BLASTN NCBI GI g5926739 BLAST score 369 E value 0.0e + 00393 Match length

% identity

Oryza sativa mRNA for asparaginyl endopeptidase, complete NCBI Description

cds

400067 Seq. No.

LIB3431-029-P1-N1-H9 Seq. ID

E value

3.0e-16

```
Method
                  BLASTX
NCBI GI
                  g5103833
BLAST score
                  156
E value
                  1.0e-10
Match length
                  43
                  70
% identity
                   (AC007591) ESTs gb R65145, gb N96612 and gb R90096 come
NCBI Description
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  400068
Seq. ID
                  LIB3431-030-P1-K2-A11
Method
                  BLASTX
NCBI GI
                  q4586039
BLAST score
                  419
E value
                  4.0e-41
Match length
                  130
% identity
                  62
NCBI Description
                   (AC007109) unknown protein [Arabidopsis thaliana]
Seq. No.
                  400069
Seq. ID
                  LIB3431-030-P1-K2-A3
Method
                  BLASTN
NCBI GI
                  q4206059
BLAST score
                  33
E value
                  3.0e-09
Match length
                  3.3
                  100
% identity
NCBI Description
                  Homo sapiens map 20q13.3; 51cR from D20S173 repeat region,
                  complete sequence
Seq. No.
                  400070
Seq. ID
                  LIB3431-030-P1-K2-A5
Method
                  BLASTN
NCBI GI
                  g5922603
BLAST score
                  84
E value
                  3.0e-39
Match length
                  107
% identity
                  Oryza sativa genomic DNA, chromosome 1, clone:P0705D01
NCBI Description
                  400071
Seq. No.
Seq. ID
                  LIB3431-030-P1-K2-A6
Method
                  BLASTX
NCBI GI
                  q729479
BLAST score
                  473
                  1.0e-47
E value
Match length
                  105
% identity
NCBI Description
                  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi 551131
                  (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]
                  400072
Seq. No.
Seq. ID
                  LIB3431-030-P1-K2-A7
Method
                  BLASTX
                  g871931
NCBI GI
BLAST score
                  204
```

```
Match length
                   66
                   68
% identity
                   (D30763) ferredoxin [Oryza sativa]
NCBI Description
                   400073
Seq. No.
                  LIB3431-030-P1-K2-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q671740
BLAST score
                   638
E value
                   9.0e-67
Match length
                  119
% identity
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
                   400074
Seq. No.
                  LIB3431-030-P1-K2-B1
Seq. ID
Method
                  BLASTN
                   g2407280
NCBI GI
BLAST score
                   43
E value
                   2.0e-15
Match length
                  90
                   88
% identity
                  Oryza sativa ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   400075
Seq. No.
Seq. ID
                  LIB3431-030-P1-K2-B2
Method
                  BLASTX
                   g2832681
NCBI GI
BLAST score
                   414
E value
                   2.0e-40
Match length
                   89
                   82
% identity
                   (AL021712) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   400076
                  LIB3431-030-P1-K2-B3
Seq. ID
Method
                  BLASTN
                   g6103440
NCBI GI
                   87
BLAST score
E value
                   1.0e-41
Match length
                   95
                   98
% identity
                  Oryza sativa metallothionein-like protein (ML2) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   400077
Seq. ID
                  LIB3431-030-P1-K2-B4
Method
                  BLASTN
NCBI GI
                   g5734616
BLAST score
                   227
E value
                   1.0e-125
Match length
                   235
% identity
                   99
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
```

```
Seq. No.
                   400078
Seq. ID
                   LIB3431-030-P1-K2-B8
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   547
                   4.0e-56
E value
Match length
                   120
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf_ 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   400079
Seq. No.
Seq. ID
                   LIB3431-030-P1-K2-C10
Method
                   BLASTX
NCBI GI
                   q4678303
BLAST score
                   184
E value
                   1.0e-13
Match length
                   52
                   63
% identity
NCBI Description (AL049655) putative protein [Arabidopsis thaliana]
                   400080
Seq. No.
                   LIB3431-030-P1-K2-C11
Seq. ID
Method
                   BLASTN
                   g19086
NCBI GI
                   78
BLAST score
E value
                   1.0e-35
Match length
                   126
% identity
NCBI Description Hordeum vulgare pot. psaE mRNA
                   400081
Seq. No.
                   LIB3431-030-P1-K2-C2
Seq. ID
Method
                   BLASTN
                   g19094
NCBI GI
BLAST score
                   54
E value
                   1.0e-21
Match length
                   66
% identity
NCBI Description H.vulgare mRNA PsaN for photosystem I subunit N
                   400082
Seq. No.
                   LIB3431-030-P1-K2-C4
Seq. ID
Method
                   BLASTX
                   g4678303
NCBI GI
BLAST score
                   205
E value
                   4.0e-16
Match length
                   57
% identity
                   (AL049655) putative protein [Arabidopsis thaliana]
NCBI Description
```

```
400083
Seq. No.
Seq. ID
                  LIB3431-030-P1-K2-C6
Method
                  BLASTX
NCBI GI
                   g2501189
BLAST score
                   618
E value
                   2.0e-64
Match length
                   129
% identity
                   92
NCBI Description
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                   >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thil-1
                   - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
Seq. No.
                   400084
Seq. ID
                   LIB3431-030-P1-K2-C7
Method
                   BLASTX
NCBI GI
                   q4960154
BLAST score
                   316
E value
                   3.0e-29
                   97
Match length
% identity
                   65
NCBI Description
                   (AF153283) putative progesterone-binding protein homolog
                   [Arabidopsis thaliana]
                   400085
Seq. No.
                  LIB3431-030-P1-K2-C8
Seq. ID
Method
                  BLASTX
                   g3776581
NCBI GI
BLAST score
                   335
E value
                   3.0e-31
Match length
                  100
                   61
% identity
                   (ACO05388) Similar to Beta integral membrane protein
NCBI Description
                  homolog gb_U43629 from A. thaliana. [Arabidopsis thaliana]
Seq. No.
                   400086
                  LIB3431-030-P1-K2-C9
Seq. ID
Method
                  BLASTN
                  g6016845
NCBI GI
BLAST score
                   271.
E value
                  1.0e-151
Match length
                  285
                   99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                  400087
Seq. No.
Seq. ID
                  LIB3431-030-P1-K2-D10
Method
                  BLASTX
                  g3126854
NCBI GI
BLAST score
                   650
                   3.0e-68
E value
Match length
                  124
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
```

400088

Seq. No.

Match length

103

```
Seq. ID
                  LIB3431-030-P1-K2-D11
Method
                  BLASTX
NCBI GI
                  q1488297
BLAST score
                  516
E value
                  2.0e-52
Match length
                  129
% identity
NCBI Description
                  (U63530) osRAD23 [Oryza sativa]
                  400089
Seq. No.
Seq. ID
                  LIB3431-030-P1-K2-D2
                  BLASTX
Method
NCBI GI
                  a3121731
BLAST score
                  642
E value
                  3.0e-67
Match length
                  143
% identity
                  83
                  ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE)
NCBI Description
                  (ACONITASE) >gi 2145473 emb_CAA65735 (X97012) aconitate
                  hydratase [Solanum tuberosum]
                  400090
Seq. No.
Seq. ID
                  LIB3431-030-P1-K2-D3
Method
                  BLASTX
                  g132105
NCBI GI
BLAST score
                  149
E value
                  4.0e-10
Match length
                  31
                  97
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400091
Seq. ID
                  LIB3431-030-P1-K2-D4
Method
                  BLASTX
                  g671740
NCBI GI
BLAST score
                  554
E value
                  6.0e-57
Match length
                  109
                  95
% identity
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                  400092
                  LIB3431-030-P1-K2-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1654144
BLAST score
                  292
E value
                  4.0e-37
```

% identity

99

```
% identity
                  (U38471) small GTP-binding protein rab [Brassica rapa]
NCBI Description
                  400093
Seq. No.
                  LIB3431-030-P1-K2-D7
Seq. ID
                  BLASTN
Method
                  g2062705
NCBI GI
BLAST score
                  35
E value
                  7.0e-11
Match length
                  35
                  100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  400094
Seq. No.
                  LIB3431-030-P1-K2-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3023816
BLAST score
                  584
E value
                  2.0e-60
Match length
                  132
                  86
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_968996 (U31676) glyceraldehyde-3-phosphate
                  dehydrogenase [Oryza sativa]
Seq. No.
                  400095
                  LIB3431-030-P1-K2-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1709620
BLAST score
                  505
E value
                  3.0e-51
Match length
                  116
                  82
% identity
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) >gi 508975
NCBI Description
                   (U11496) protein disulfide isomerase [Triticum aestivum]
                  >gi 1094851 prf 2106410A protein disulfide isomerase
                   [Triticum aestivum]
Seq. No.
                   400096
Seq. ID
                  LIB3431-030-P1-K2-E2
Method
                  BLASTN
NCBI GI
                  g167086
BLAST score
                  69
E value
                   1.0e-30
Match length
                  167
                  85
% identity
NCBI Description
                  Hordeum vulgare photosystem I protein (PSI-L) mRNA,
                  complete cds
                   400097
Seq. No.
Seq. ID
                  LIB3431-030-P1-K2-E4
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                   628
E value
                  7.0e-72
Match length
                  135
```

```
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400098
Seq. ID
                  LIB3431-030-P1-K2-E6
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  737
                  3.0e-78
E value
                  163
Match length
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400099
Seq. ID
                  LIB3431-030-P1-K2-E7
Method
                  BLASTX
NCBI GI
                  g2583108
BLAST score
                  351
E value
                  4.0e-33
Match length
                  144
% identity
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
                  400100
Seq. No.
Seq. ID
                  LIB3431-030-P1-K2-E8
                  BLASTX
Method
NCBI GI
                  g5802606
BLAST score
                  704
E value
                  2.0e-74
Match length
                  147
% identity
NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]
                  400101
Seq. No.
Seq. ID
                  LIB3431-030-P1-K2-E9
Method
                  BLASTX
NCBI GI
                  g3183079
BLAST score
                  157
E value
                  9.0e-11
Match length
                  86
                  47
% identity
```

NCBI Description MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR

```
Seq. No.
                     400102
Seq. ID
                    LIB3431-030-P1-K2-F1
Method
                     BLASTX
NCBI GI
                     g133999
BLAST score
                     489
E value
                     2.0e-49
Match length
                     99
% identity
                     100
NCBI Description
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi_70904_pir__R3RZ7
                    ribosomal protein S7 - rice chloroplast
>gi_12037_emb_CAA33942_ (X15901) ribosomal protein S7
[Oryza sativa] >gi_12065_emb_CAA33919_ (X15901) ribosomal protein S7 [Oryza sativa] >gi_226657_prf__1603356CH
                     ribosomal protein S7 [Oryza sativa]
                     400103
Seq. No.
Seq. ID
                    LIB3431-030-P1-K2-F10
Method
                    BLASTX
NCBI GI
                     q132105
BLAST score
                     706
E value
                     1.0e-74
Match length
                     131
% identity
NCBI Description
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                     (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                     ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                     (D00643) small subunit of ribulose-1,5-bisphosphate
                     carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                     ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                     sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                     carboxylase S [Oryza sativa]
Seq. No.
                     400104
                    LIB3431-030-P1-K2-F12
Seq. ID
Method
                    BLASTX
NCBI GI
                     q1519251
BLAST score
                     443
E value
                     6.0e-44
Match length
                    111
                     83
% identity
NCBI Description
                     (U65957) GF14-c protein [Oryza sativa]
Seq. No.
                     400105
Seq. ID
                    LIB3431-030-P1-K2-F2
Method
                    BLASTN
                    g3789951
NCBI GI
                     71
BLAST score
E value
                     3.0e-32
Match length
                     91
% identity
                    Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
```

>gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate

dehydrogenase [Oryza sativa]

complete cds

(Cab27) mRNA, nuclear gene encoding chloroplast protein,

```
Seq. No.
                  400106
                  LIB3431-030-P1-K2-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2570523
BLAST score
                  567
E value
                  2.0e-58
Match length
                  128
% identity
                  80
NCBI Description
                   (AF022873) inorganic phosphate transporter [Lycopersicon
                  esculentum]
Seq. No.
                  400107
Seq. ID
                  LIB3431-030-P1-K2-F5
Method
                  BLASTX
NCBI GI
                  g134944
BLAST score
                  718
                  6.0e-82
E value
Match length
                  179
% identity
                  ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR
NCBI Description
                  (STEAROYL-ACP DESATURASE) >gi_100502_pir__A39173
                  acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6)
                  precursor - safflower >gi_167197 (M61109)
                  stearoyl-acyl-carrier protein desaturase [Carthamus
                  tinctorius]
                  400108
Seq. No.
                  LIB3431-030-P1-K2-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3777598
BLAST score
                  314
                  6.0e-29
E value
Match length
                  104
% identity
                  67
NCBI Description
                  (AF095707) 30S ribosomal protein S17 [Oryza sativa]
Seq. No.
                  400109
                  LIB3431-030-P1-K2-F7
Seq. ID
Method
                  BLASTX
                  q3789952
NCBI GI
BLAST score
                  279
E value
                  1.0e-45
Match length
                  102
% identity
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
Seq. No.
                  400110
                  LIB3431-030-P1-K2-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024697
BLAST score
                  274
                  2.0e-24
E value
                  91
Match length
% identity
                  65
                  T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON)
NCBI Description
```

% identity

60

```
thaliana]
Seq. No.
                   400111
                  LIB3431-030-P1-K2-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q20177
BLAST score
                   40
E value
                   2.0e-13
Match length
                   94
                   88
% identity
                  Rice cablR gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
                   400112
Seq. No.
Seq. ID
                  LIB3431-030-P1-K2-G1
Method
                  BLASTX
NCBI GI
                   g1084455
                  517
BLAST score
                  1.0e-52
E value
                  116
Match length
% identity
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
NCBI Description
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                   400113
                  LIB3431-030-P1-K2-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4185499
                   167
BLAST score
                   1.0e-11
E value
Match length
                   65
                   49
% identity
NCBI Description
                   (AF096095) fertilization-independent seed 2 protein
                   [Arabidopsis thaliana] >gi_4185501 (AF096096)
                   fertilization-independent seed 2 protein [Arabidopsis
                   thaliana]
Seq. No.
                   400114
Seq. ID
                  LIB3431-030-P1-K2-G5
Method
                  BLASTX
NCBI GI
                   g1353352
BLAST score
                   527
                   1.0e-53
E value
Match length
                  150
% identity
                   (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
Seq. No.
                   400115
                  LIB3431-030-P1-K2-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2316016
BLAST score
                  198
                   1.0e-18
E value
Match length
                  86
```

(CCT-EPSILON) >gi 2213618 (AC000103) F21J9.12 [Arabidopsis

Seq. ID

```
NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
                  400116
Seq. No.
Seq. ID
                  LIB3431-030-P1-K2-G9
Method
                  BLASTX
                  g132105
NCBI GI
BLAST score
                  179
E value
                  2.0e-13
Match length
                  49
% identity
                  69
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400117
Seq. ID
                  LIB3431-030-P1-K2-H1
Method
                  BLASTN
NCBI GI
                  g1398998
BLAST score
                  190
                  1.0e-102
E value
Match length
                  275
% identity
                  100
                  Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II,
NCBI Description
                  complete cds
Seq. No.
                  400118
Seq. ID
                  LIB3431-030-P1-K2-H12
Method
                  BLASTX
NCBI GI
                  g2407279
BLAST score
                  319
                  9.0e-30
E value
Match length
                  65
% identity
                  100
NCBI Description
                  (AF017362) aldolase [Oryza sativa]
Seq. No.
                  400119
                  LIB3431-030-P1-K2-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115787
                  535
BLAST score
                  8.0e-55
E value
                  121
Match length
% identity
                  86
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                  400120
```

LIB3431-030-P1-K2-H3

```
BLASTN
Method
NCBI GI
                  g20262
BLAST score
                  306
                  1.0e-172
E value
                  341
Match length
% identity
                  98
NCBI Description O.sativa light-induced mRNA
Seq. No.
                  400121
Seq. ID
                  LIB3431-030-P1-K2-H5
Method
                  BLASTX
NCBI GI
                  g2130127
BLAST score
                  322
E value
                  1.0e-29
Match length
                  70
                  86
% identity
                  ferritin 1 precursor - maize >gi 1103628 emb CAA58146
NCBI Description
                   (X83076) ferritin [Zea mays]
Seq. No.
                  400122
                  LIB3431-030-P1-K2-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4079798
BLAST score
                  214
                  1.0e-17
E value
Match length
                  43
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
Seq. No.
                  400123
                  LIB3431-030-P1-K2-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2407281
                  399
BLAST score
E value
                  8.0e-39
Match length
                  112
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
Seq. No.
                  400124
                  LIB3431-030-P1-K2-H9
Seq. ID
Method
                  BLASTX
                  g1262847
NCBI GI
BLAST score
                  166
E value
                  1.0e-11
Match length
                  42
                  71
% identity
                   (U51632) type 2 light-harvesting chlorophyll a/b-binding
NCBI Description
                  polypeptide [Pinus palustris]
Seq. No.
                  400125
                  LIB3431-030-P1-N1-A1
Seq. ID
Method
                  BLASTN
                  g169820
NCBI GI
```

277

BLAST score

Seq. ID

```
E value
                    1.0e-154
Match length
                    345
% identity
NCBI Description
                    Oryza sativa triosephosphate isomerase (Rictpi) mRNA,
                    complete cds
                    400126
Seq. No.
                    LIB3431-030-P1-N1-A2
Seq. ID
Method
                    BLASTX
NCBI GI
                    q115787
BLAST score
                    403
E value
                    3.0e-39
                    76
Match length
                    100
% identity
                    CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                    CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
Seq. No.
                    400127
                    LIB3431-030-P1-N1-A4
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3126854
BLAST score
                    339
                    1.0e-31
E value
Match length
                    64
% identity
                    100
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                    400128
Seq. No.
Seq. ID
                    LIB3431-030-P1-N1-A5
Method
                    BLASTN
NCBI GI
                    g5922603
BLAST score
                    57
E value
                    4.0e-23
Match length
                    80
% identity
                    94
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0705D01
                    400129
Seq. No.
                    LIB3431-030-P1-N1-A6
Seq. ID
Method
                    BLASTX
                    g729478
NCBI GI
                    323
BLAST score
                    6.0e-30
E value
                    73
Match length
                    79
% identity
                    FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                    >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_
                    (AP000616) ESTs AU078647(E15\overline{5}7),C724\overline{0}0(E\overline{1}557) correspond to
                    a region of the predicted gene.; similar to
                    ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
                    400130
Seq. No.
```

LIB3431-030-P1-N1-A7

```
BLASTN
Method
NCBI GI
                  g2305114
BLAST score
                  321
                  1.0e-180
E value
Match length
                  400
                  95
% identity
NCBI Description Oryza sativa ferredoxin mRNA, complete cds
                  400131
Seq. No.
                  LIB3431-030-P1-N1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
                  387
BLAST score
                  2.0e-37
E value
                  73
Match length
                  99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400132
Seq. ID
                  LIB3431-030-P1-N1-A9
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  460
                  8.0e-46
E value
Match length
                  86
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  400133
Seq. No.
                  LIB3431-030-P1-N1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2344897
BLAST score
                  273
                  6.0e-24
E value
Match length
                  92
% identity
                  (AC002388) unknown protein [Arabidopsis thaliana]
NCBI Description
                  400134
Seq. No.
                  LIB3431-030-P1-N1-B3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2072555
BLAST score
                  237
                  9.0e-20
E value
Match length
                  44
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
```

>gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like

Match length

114

protein [Oryza sativa] Seq. No. 400135 Seq. ID LIB3431-030-P1-N1-B4 Method BLASTN NCBI GI q5734616 BLAST score 409 0.0e + 00E value 499 Match length 100 % identity NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01 400136 Seq. No. LIB3431-030-P1-N1-B5 Seq. ID BLASTX Method NCBI GI g3345477 BLAST score 331 9.0e-31 E value Match length 62 100 % identity (AB016283) carbonic anhydrase [Oryza sativa] NCBI Description Seq. No. 400137 LIB3431-030-P1-N1-B7 Seq. ID Method BLASTX NCBI GI g3510256 BLAST score 229 E value 9.0e-19 Match length 79 % identity 56 (AC005310) unknown protein [Arabidopsis thaliana] NCBI Description 400138 Seq. No. LIB3431-030-P1-N1-B8 Seq. ID Method BLASTX NCBI GI g132105 BLAST score 207 8.0e-23 E value Match length 56 % identity 93 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >qi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa] Seq. No. 400139 LIB3431-030-P1-N1-B9 Seq. ID Method BLASTX NCBI GI q4115536 BLAST score 293 E value 2.0e-26

NCBI Description

```
% identity
                  47
                   (AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna
NCBI Description
                  mungo]
Seq. No.
                  400140
                  LIB3431-030-P1-N1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3789954
                  259
BLAST score
                  2.0e-22
E value
Match length
                  48
                  98
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  400141
Seq. No.
                  LIB3431-030-P1-N1-C12
Seq. ID
Method
                  BLASTX
                  g2191138
NCBI GI
                  318
BLAST score
                  3.0e-29
E value
                  75
Match length
                  79
% identity
                   (AF007269) A IG002N01.18 gene product [Arabidopsis
NCBI Description
                  thaliana]
                  400142
Seq. No.
Seq. ID
                  LIB3431-030-P1-N1-C2
Method
                  BLASTN
                  g19094
NCBI GI
BLAST score
                  58
                   5.0e-24
E value
Match length
                   66
% identity
                   97
                  H.vulgare mRNA PsaN for photosystem I subunit N
NCBI Description
Seq. No.
                   400143
                  LIB3431-030-P1-N1-C4
Seq. ID
Method
                  BLASTX
                  g3914466
NCBI GI
BLAST score
                   455
                   3.0e-45
E value
Match length
                   84
                   98
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >qi 2981214 (AF052429) photosystem I complex PsaN
                   subunit precursor [Zea mays]
                   400144
Seq. No.
Seq. ID
                  LIB3431-030-P1-N1-C6
Method
                  BLASTX
NCBI GI
                   g2501190.
BLAST score
                   155
                   3.0e-10
E value
Match length
                   51
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
```

```
Seq. No.
                   400145
                   LIB3431-030-P1-N1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3776581
BLAST score
                   350
E value
                   5.0e-33
Match length
                   118
% identity
                   (AC005388) Similar to Beta integral membrane protein
NCBI Description
                   homolog gb U43629 from A. thaliana. [Arabidopsis thaliana]
                   400146
Seq. No.
                   LIB3431-030-P1-N1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1184112
BLAST score
                   410
                   4.0e-40
E value
Match length
                   111
% identity
                   75
NCBI Description
                   (U46138) Zn-induced protein [Oryza sativa]
                   400147
Seq. No.
                   LIB3431-030-P1-N1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q131176
BLAST score
                   352
E value
                   2.0e-33
                   70
Match length
% identity
                   96
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                   >gi_72683_pir__F1BH4 photosystem I chain IV precursor -
                   barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A
                   10.8kD photosystem I protein [Hordeum vulgare var.
                   distichum]
Seq. No.
                   400148
                   LIB3431-030-P1-N1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3126854
BLAST score
                   635
E value
                   2.0e-66
Match length
                   123
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   400149
Seq. No.
Seq. ID
                   LIB3431-030-P1-N1-D11
Method
                   BLASTX
NCBI GI
                   q1488297
BLAST score
                   257
```

[Zea mays]

>gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
- maize >gi_596080 (U17351) thiamine biosynthetic enzyme

4.0e-22

E value

```
Match length
                    60
% identity
NCBI Description (U63530) osRAD23 [Oryza sativa]
                    400150
Seq. No.
Seq. ID
                    LIB3431-030-P1-N1-D12
Method
                    BLASTX
NCBI GI
                    q461595
BLAST score
                    183
                    2.0e-13
E value
Match length
                    95
% identity
                    44
                    ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II)

>gi_479533_pir__S34473 H+-transporting ATP synthase (EC 3.6.1.34) chain 9 - spinach >gi_394755_emb_CAA50520_
NCBI Description
                    (X71397) CF(o)II ATP synthase subunit 9 [Spinacia oleracea]
Seq. No.
                    400151
                    LIB3431-030-P1-N1-D2
Seq. ID
Method
                    BLASTX
NCBI GI
                    q6093830
BLAST score
                    164
E value
                    2.0e-11
Match length
                    50
% identity
                    38
NCBI Description
                    PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
                    [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
                    PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor;
                    putative photosytem II peptide [Spinacia oleracea]
Seq. No.
                    400152
                    LIB3431-030-P1-N1-D3
Seq. ID
Method
                    BLASTX
NCBI GI
                    g132105
BLAST score
                    398
E value
                    1.0e-38
Match length
                    73
% identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi_226375 prf__1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
Seq. No.
                    400153
Seq. ID
                    LIB3431-030-P1-N1-D4
Method
                    BLASTX
NCBI GI
                    a132105
BLAST score
                    301
                    2.0e-27
E value
Match length
                    57
                    100
% identity
```

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

```
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]
400154
LIB3431-030-P1-N1-D6
BLASTX
g1362066
546
6.0e-56
126
86
```

% identity 86
NCBI Description small GTP-binding protein - garden pea

>gi 871510 emb CAA90080 (Z49900) small GTP-binding protein

[Pisum sativum]

 Seq. No.
 400155

 Seq. ID
 LIB3431-030-P1-N1-D7

 Method
 BLASTX

 NCBI GI
 g167097

 BLAST score
 151

BLAST score 151 E value 1.0e-20 Match length 61 % identity 87

Seq. No.

Seq. ID Method

NCBI GI BLAST score

E value Match length

NCBI Description (M55449) ribulose 1,5-bisphosphate carboxylase activase

[Hordeum vulgare]

Seq. No. 400156

Seq. ID LIB3431-030-P1-N1-D8

Method BLASTX
NCBI GI g4586021
BLAST score 271
E value 8.0e-24
Match length 61
% identity 77

NCBI Description (AC007170) putative cytoplasmic aconitate hydratase

[Arabidopsis thaliana]

Seq. No. 400157

Seq. ID LIB3431-030-P1-N1-E1

Method BLASTX
NCBI GI g2493650
BLAST score 438
E value 3.0e-43
Match length 89
% identity 97

NCBI Description RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD

CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)

>gi 1167858 emb CAA93139 (Z68903) chaperonin [Secale

cereale]

Seq. No. 400158

```
LIB3431-030-P1-N1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1709620
BLAST score
                  178
E value
                  9.0e-13
Match length
                  55
                  71
% identity
NCBI Description
                  PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) >gi 508975
                  (U11496) protein disulfide isomerase [Triticum aestivum]
                  >gi_1094851_prf__2106410A protein disulfide isomerase
                  [Triticum aestivum]
                  400159
Seq. No.
                  LIB3431-030-P1-N1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131225
                  337
BLAST score
E value
                  2.0e-31
Match length
                  94
% identity
                  70
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  400160
Seq. No.
Seq. ID
                  LIB3431-030-P1-N1-E4
Method
                  BLASTX
                  q347451
NCBI GI
BLAST score
                  152
E value
                  7.0e-10
Match length
                  38
% identity
                  79
NCBI Description
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa]
Seq. No.
                  400161
                  LIB3431-030-P1-N1-E6
Seq. ID
Method
                  BLASTX
                  g671740
NCBI GI
BLAST score
                  512
E value
                  6.0e-52
Match length
                  94
% identity
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                  400162
Seq. ID
                  LIB3431-030-P1-N1-E8
Method
                  BLASTX
NCBI GI
                  g5802606
BLAST score
                  498
E value
                  3.0e-50
Match length
                  104
                  86
% identity
NCBI Description (AF174486) methylenetetrahydrofolate reductase [Zea mays]
```

:. .

Seq. ID

Method

BLASTX

```
400163
Seq. No.
                  LIB3431-030-P1-N1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3183079
BLAST score
                  341
                  6.0e-32
E value
                  83
Match length
                  78
% identity
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
NCBI Description
                  >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate
                  dehydrogenase [Oryza sativa]
                  400164
Seq. No.
                  LIB3431-030-P1-N1-F1
Seq. ID
                  BLASTX
Method
                  g1173275
NCBI GI
                  590
BLAST score
                  4.0e-61
E value
                  136
Match length
                  90
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
NCBI Description
                  >gi_2119068_pir__S58630 ribosomal protein S7 - maize
                  chloroplast >gi 902274 emb CAA60339 (X86563) ribosomal
                  protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563)
                  ribosomal protein S7 [Zea mays]
                  400165
Seq. No.
Seq. ID
                  LIB3431-030-P1-N1-F10
Method
                  BLASTX
                  g132105
NCBI GI
                  386
BLAST score
                  1.0e-47
E value
Match length
                  93
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  400166
Seq. No.
                  LIB3431-030-P1-N1-F12
Seq. ID
                  BLASTX
Method
                  g1519251
NCBI GI
                  244
BLAST score
                  1.0e-20
E value
Match length
                  47
                  100
% identity
                  (U65957) GF14-c protein [Oryza sativa]
NCBI Description
                  400167
Seq. No.
                  LIB3431-030-P1-N1-F2
```

51225

```
NCBI GI
                   q1587206
BLAST score
                   186
                   1.0e-13
E value
Match length
                  39
                   97
% identity
NCBI Description T complex protein [Cucumis sativus]
                   400168
Seq. No.
Seq. ID
                  LIB3431-030-P1-N1-F4
Method
                  BLASTX
NCBI GI
                   q5053118
BLAST score
                   495
                   5.0e-58
E value
Match length
                   165
                   72
% identity
NCBI Description
                   (AF156695) inorganic phosphate transporter [Solanum
                   tuberosum]
                   400169
Seq. No.
                  LIB3431-030-P1-N1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2281099
BLAST score
                   181
                   3.0e-13
E value
Match length
                   45
% identity
                   76
NCBI Description
                  (AC002333) stearoyl-ACP desaturase [Arabidopsis thaliana]
                   400170
Seq. No.
                  LIB3431-030-P1-N1-F6
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3777598
                   327
BLAST score
                   2.0e-30
E value
                  78
Match length
                   85
% identity
NCBI Description
                  (AF095707) 30S ribosomal protein S17 [Oryza sativa]
                   400171
Seq. No.
                  LIB3431-030-P1-N1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3789952
BLAST score
                   230
                   6.0e-19
E value
                   44
Match length
                   98
% identity
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
                   400172
Seq. No.
                  LIB3431-030-P1-N1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g115787
BLAST score
                   505
                   4.0e-51
E value
                   96
Match length
```

100

% identity

BLAST score

488

```
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   400173
Seq. No.
                  LIB3431-030-P1-N1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1084455
BLAST score
                   379
                   2.0e-36
E value
                  72
Match length
                  100
% identity
NCBI Description
                  peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                  >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
                   400174
Seq. No.
                  LIB3431-030-P1-N1-G11
Seq. ID
Method
                  BLASTX
                   g4185499
NCBI GI
BLAST score
                   226
E value
                   2.0e-18
Match length
                   68
% identity
                   51
                   (AF096095) fertilization-independent seed 2 protein
NCBI Description
                   [Arabidopsis thaliana] >gi_4185501 (AF096096)
                   fertilization-independent seed 2 protein [Arabidopsis
                   thaliana]
                   400175
Seq. No.
Seq. ID
                  LIB3431-030-P1-N1-G4
Method
                  BLASTX
NCBI GI
                   g3643602
                  .263
BLAST score
                  7.0e-23
E value
Match length
                   88
% identity
                   57
                   (AC005395) putative tonoplast intrinsic protein.
NCBI Description
                   [Arabidopsis thaliana]
                   400176
Seq. No.
Seq. ID
                  LIB3431-030-P1-N1-G5
Method
                  BLASTX
NCBI GI
                  g1353352
BLAST score
                  184
E value
                   1.0e-13
Match length
                   51
                  71
% identity
NCBI Description
                   (U31975) alanine aminotransferase [Chlamydomonas
                  reinhardtii]
                   400177
Seq. No.
Seq. ID
                  LIB3431-030-P1-N1-G9
Method
                  BLASTX
                  g671740
NCBI GI
```

```
4.0e-49
E value
Match length
                  90
                  99
% identity
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
                  400178
Seq. No.
                  LIB3431-030-P1-N1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1398998
BLAST score
                  162
                  8.0e-86
E value
                  275
Match length
% identity
NCBI Description
                  Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II,
                  complete cds
                  400179
Seq. No.
                  LIB3431-030-P1-N1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2331130
BLAST score
                  259
E value
                  1.0e-144
Match length
                  271
                  99
% identity
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
Seq. No.
                  400180
                  LIB3431-030-P1-N1-H2
Seq. ID
Method
                  BLASTX
                  g3036951
NCBI GI
BLAST score
                  451
E value
                  9.0e-45
Match length
                  86
% identity
NCBI Description
                   (AB012639) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
                  400181
Seq. No.
                  LIB3431-030-P1-N1-H3
Seq. ID
Method
                  BLASTX
                  g417260
NCBI GI
BLAST score
                  303
E value
                  2.0e-27
Match length
                  77
                  74
% identity
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                  lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
                  400182
Seq. No.
                  LIB3431-030-P1-N1-H6
Seq. ID
Method
                  BLASTX
                  g4079798
NCBI GI
BLAST score
                  301
```

2.0e-27

E value

```
61
Match length
                  93
% identity
NCBI Description
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                  sativa]
                  400183
Seq. No.
                  LIB3431-030-P1-N1-H8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3377792
BLAST score
                  269
E value
                  1.0e-149
Match length
                  399
                  92
% identity
                  Oryza sativa ribulose-1,5-bisphosphate
NCBI Description
                  carboxylase/oxygenase activase (rca) mRNA, complete cds
                  400184
Seq. No.
Seq. ID
                  LIB3431-030-P1-N1-H9
Method
                  BLASTX
NCBI GI
                  g6093827
BLAST score
                  156
                  2.0e-10
E value
                  61
Match length
                  29
% identity
                  PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
NCBI Description
                   [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
                  PROTEIN PSBY-2] >gi_2956690_emb_CAA11248_
                                                              (AJ223306) PSBY
                   [Arabidopsis thaliana] >gi 3414928 (AF079800) PsbY
                  precursor [Arabidopsis thaliana]
                  400185
Seq. No.
Seq. ID
                  LIB3431-031-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g2913893
BLAST score
                  262
                  8.0e-23
E value
                  56
Match length
% identity
                  82
                   (AB011368) LIP5 [Oryza sativa]
NCBI Description
                  400186
Seq. No.
                  LIB3431-031-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2072555
                  237
BLAST score
                  8.0e-20
E value
                  44
Match length
                  100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  400187
Seq. No.
                  LIB3431-031-P1-K1-A2
Seq. ID
Method
                  BLASTX
                  g134595
NCBI GI
```

236

BLAST score

NCBI GI

BLAST score

g134595 615

```
1.0e-19
E value
Match length
                     71
% identity
                     66
                     SUPEROXIDE DISMUTASE-1 [CU-ZN] >gi_280412_pir__S22508 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodA - rice >gi_218224_dbj_BAA00799_ (D00999) copper/zinc-superoxide dismutase [Oryza sativa] >gi_685242 (L19435) cytosolic
NCBI Description
                     copper/zinc-superoxide dismutase [Oryza sativa]
                     >gi 1096504 prf__2111424A Cu/Zn superoxide dismutase [Oryza
                     satīva]
                     400188
Seq. No.
                     LIB3431-031-P1-K1-A3
Seq. ID
Method
                     BLASTN
NCBI GI
                     g19094
BLAST score
                     53
E value
                     9.0e-21
Match length
                     65
                     95
% identity
NCBI Description
                     H.vulgare mRNA PsaN for photosystem I subunit N
                     400189
Seq. No.
                     LIB3431-031-P1-K1-A4
Seq. ID
Method
                     BLASTN
NCBI GI
                     q20262
BLAST score
                     193
E value
                     1.0e-104
                     300
Match length
                     100
% identity
NCBI Description O.sativa light-induced mRNA
                     400190
Seq. No.
Seq. ID
                     LIB3431-031-P1-K1-A5
Method
                     BLASTX
                     g2407281
NCBI GI
BLAST score
                     641
E value
                     3.0e-67
Match length
                     120
                     99
% identity
                     (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                     subunit [Oryza sativa]
Seq. No.
                     400191
                     LIB3431-031-P1-K1-A6
Seq. ID
Method
                     BLASTX
NCBI GI
                     g4914452
                     420
BLAST score
                     3.0e-41
E value
                     127
Match length
% identity
                     (AL050398) putative protein [Arabidopsis thaliana]
NCBI Description
                     400192
Seq. No.
                     LIB3431-031-P1-K1-A7
Seq. ID
Method
                     BLASTX
```

NCBI Description

```
E value
                   4.0e-64
Match length
                   116
                   100
% identity
NCBI Description
                   SUPEROXIDE DISMUTASE-1 [CU-ZN] >gi_280412_pir__S22508
                   superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodA - rice
                   >gi_218224_dbj_BAA00799_ (D00999) copper/zinc-superoxide
dismutase [Oryza sativa] >gi_685242 (L19435) cytosolic
                   copper/zinc-superoxide dismutase [Oryza sativa]
                   >gi 1096504_prf 2111424A Cu/Zn superoxide dismutase [Oryza
                   satīva]
Seq. No.
                   400193
                   LIB3431-031-P1-K1-A8
Seq. ID
Method
                   BLASTX
                   g5903036
NCBI GI
BLAST score
                   316
                   4.0e-29
E value
                   132
Match length
                   52
% identity
                   (AC008016) F6D8.5 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   400194
                   LIB3431-031-P1-K1-B1
Seq. ID
                   BLASTX
Method
                   g5702231
NCBI GI
BLAST score
                   195
                   7.0e-15
E value
Match length
                   110
                   45
% identity
                   (AF145386) hypersensitive reaction associated Ca2+-binding
NCBI Description
                   protein [Phaseolus vulgaris]
Seq. No.
                   400195
                   LIB3431-031-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g320618
                   285
BLAST score
                   5.0e-26
E value
Match length
                   62
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   400196
Seq. No.
                   LIB3431-031-P1-K1-B2
Seq. ID
Method
                   BLASTX
                   g2754849
NCBI GI
                   254
BLAST score
                   7.0e-22
E value
                   56
Match length
% identity
```

[Fritillaria agrestis]

(AF039000) putative serine-glyoxylate aminotransferase

```
Seq. ID
                  LIB3431-031-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  q4138289
BLAST score
                  177
                  8.0e-95
E value
Match length
                  281
% identity
                  91
                  Oryza sativa mRNA for thioredoxin M
NCBI Description
                  400198
Seq. No.
Seq. ID
                  LIB3431-031-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q228403
BLAST score
                  655
E value
                  8.0e-69
Match length
                  145
                  89
% identity
                  glycolate oxidase [Lens culinaris]
NCBI Description
                  400199
Seq. No.
                  LIB3431-031-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  577
E value
                  1.0e-59
Match length
                  124
                  87
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR.
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  400200
Seq. No.
                  LIB3431-031-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  536
                  7.0e-55
E value
                  118
Match length
                  86
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  400201
Seq. No.
Seq. ID
                  LIB3431-031-P1-K1-C3
Method
                  BLASTX
                  g2072555
NCBI GI
BLAST score
                  237
```

400197

Seq. No.

% identity

```
E value
                   8.0e-20
Match length
                   44
% identity
                   100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   400202
Seq. ID
                   LIB3431-031-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   512
E value
                   5.0e-52
Match length
                   110
% identity
                   85
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   400203
Seq. ID
                   LIB3431-031-P1-K1-C7
Method
                   BLASTN
NCBI GI
                   q2780342
BLAST score
                   102
E value
                   1.0e-50
Match length
                   102
                   100
% identity
NCBI Description
                   Oryza sativa gene for PBZ1, complete cds
                   >gi_3251321_dbj_E12488_E12488 Nucleotide sequence of Oryza
                   sativa PBZ1 gene
                   400204
Seq. No.
Seq. ID
                   LIB3431-031-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   q3660469
BLAST score
                   608
E value
                   3.0e-63
Match length
                   132
% identity
NCBI Description
                   (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
                   thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569)
                   succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
Seq. No.
                   400205
Seq. ID
                   LIB3431-031-P1-K1-D1
Method
                   BLASTN
NCBI GI
                   q3126853
BLAST score
                   47
E value
                   1.0e-17
Match length
                   63
```

```
NCBI Description Oryza sativa chlorophyll a/b binding protein (RCABP89)
                  mRNA, nuclear gene encoding chloroplast protein, complete
                  cds
                  400206
Seq. No.
                  LIB3431-031-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1658315
BLAST score
                  580
E value
                   5.0e-60
Match length
                  134
                  76
% identity
NCBI Description
                   (Y08988) osr40q3 [Oryza sativa]
Seq. No.
                   400207
Seq. ID
                  LIB3431-031-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                   607
E value
                   3.0e-63
                  128
Match length
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  400208
Seq. No.
                  LIB3431-031-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1296955
                  596
BLAST score
E value
                   6.0e-62
Match length
                  134
% identity
                   (X95402) duplicated domain structure protein [Oryza sativa]
NCBI Description
Seq. No.
                  400209
                  LIB3431-031-P1-K1-E12
Seq. ID
Method
                  BLASTX
                  q986969
NCBI GI
BLAST score
                  318
                  3.0e-29
E value
Match length
                  127
% identity
                  51
                  (L28005) TGACG-motif-binding protein [Glycine max]
NCBI Description
Seq. No.
                  400210
Seq. ID
                  LIB3431-031-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  q3126854
                  686
BLAST score
E value
                  2.0e-72
Match length
                  128
                  100
% identity
```

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

```
Seq. No.
                  400211
Seq. ID
                  LIB3431-031-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g417260
BLAST score
                  372
E value
                  1.0e-35
Match length
                  121
% identity
NCBI Description
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
                  lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
                  400212
Seq. No.
                  LIB3431-031-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914466
                  258
BLAST score
E value
                  6.0e-24
Match length
                  60
                  92
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                   (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
                  subunit precursor [Zea mays]
Seq. No.
                  400213
                  LIB3431-031-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3913018
BLAST score
                  579
                  6.0e-60
E value
                  117
Match length
                  100
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
Seq. No.
                  400214
Seq. ID
                  LIB3431-031-P1-K1-F10
Method
                  BLASTX
                  g2688824
NCBI GI
                  146
BLAST score
                  3.0e-09
E value
Match length
                  76
% identity
                  (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                  armeniaca]
                  400215
Seq. No.
                  LIB3431-031-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2944178
BLAST score
                  346
                  1.0e-32
E value
Match length
                  116
% identity
                  (AF007778) trehalose-6-phosphate phosphatase [Arabidopsis
NCBI Description
```

thaliana]

```
Seq. No.
                   400216
Seq. ID
                   LIB3431-031-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   559
E value
                   1.0e-57
Match length
                   122
% identity
                   86
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf_ 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   400217
                   LIB3431-031-P1-K1-F2
Seq. ID
Method
                   BLASTN
                   g20369
NCBI GI
BLAST score
                   335
E value
                   0.0e + 00
Match length
                   351
% identity
                   99
                   Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
NCBI Description
                   synthetase (EC 6.3.1.2) (clone lambda-GS31)
                   >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of
                   chloroplast localising glutamine synthetase
Seq. No.
                   400218
                   LIB3431-031-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1661160
BLAST score
                   178
E value
                   3.0e-13
Match length
                   59
                   71
% identity
                   (U74295) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   400219
                   LIB3431-031-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4507223
BLAST score
                   460
E value
                   5.0e-46
Match length
                   135
% identity
                   71
                   signal recognition particle receptor ('docking protein')
NCBI Description
                   >gi_134892_sp_P08240_SRPR_HUMAN SIGNAL RECOGNITION PARTICLE
                   RECEPTOR ALPHA SUBUNIT (SR-ALPHA) (DOCKING PROTEIN ALPHA)
                   (DP-ALPHA) >gi_88607_pir__A29440 signal recognition
                   particle receptor - human >gi_30866_emb_CAA29608_ (X06272)
```

docking protein [Homo sapiens]

Seq. ID

```
Seq. No.
                  400220
                  LIB3431-031-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82080.
BLAST score
                  333
E value
                  4.0e-31
Match length
                  104
% identity
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  400221
Seq. No.
                  LIB3431-031-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
                  600
BLAST score
                  2.0e-62
E value
                  129
Match length
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  400222
Seq. No.
Seq. ID
                  LIB3431-031-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g2130127
BLAST score
                  397
E value
                  1.0e-38
Match length.
                  92
% identity
                  ferritin 1 precursor - maize >gi 1103628 emb CAA58146
NCBI Description
                  (X83076) ferritin [Zea mays]
                  400223
Seq. No.
                  LIB3431-031-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115787
                  614
BLAST score
                  5.0e-64
E value
                  137
Match length
                  89
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  400224
Seq. No.
```

LIB3431-031-P1-K1-H11

NCBI GI

```
Method
                   BLASTX
NCBI GI
                   q217909
BLAST score
                   353
E value
                   2.0e-33
Match length
                   105
                   69
% identity
NCBI Description
                   (D14044) glycolate oxidase [Cucurbita sp.]
Seq. No.
                   400225
Seq. ID
                   LIB3431-031-P1-N1-A3
Method
                   BLASTX
NCBI GI
                   q3914466
BLAST score
                   472
                   2.0e-47
E value
Match length
                   90
% identity
                   96
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
                   subunit precursor [Zea mays]
Seq. No.
                   400226
                   LIB3431-031-P1-N1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g417260
BLAST score
                   338
E value
                   2.0e-31
Match length
                   115
% identity
                   62
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                   lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                   light-regulated gene [Oryza sativa]
                   400227
Seq. No.
                   LIB3431-031-P1-N1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g671740
BLAST score
                   227
E value
                   2.0e-18
Match length
                   45
% identity
                   96
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   400228
Seq. No.
Seq. ID
                  LIB3431-031-P1-N1-A6
Method
                   BLASTX
NCBI GI
                   g4914452
BLAST score
                   274
E value
                   6.0e-24
Match length
                   75
% identity
                   68
                   (AL050398) putative protein [Arabidopsis thaliana]
NCBI Description
                   400229
Seq. No.
Seq. ID
                  LIB3431-031-P1-N1-A7
Method
                  BLASTX
```

g538430 ·

NCBI GI

```
BLAST score
                   279
E value
                   1.0e-24
Match length
                   55
% identity
                   (L36320) superoxide dismutase [Oryza sativa]
NCBI Description
                   400230
Seq. No.
                   LIB3431-031-P1-N1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   632
E value
                   6.0e-66
Match length
                   121
                   100
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   400231
                   LIB3431-031-P1-N1-B11
Seq. ID
                   BLASTN
Method
                   q218171
NCBI GI
BLAST score
                   80
                   3.0e-37
E value
Match length
                   168
% identity
                   Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                   a/b binding protein of photosystem II (LHCPII), complete
                   400232
Seq. No.
                   LIB3431-031-P1-N1-B5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2062705
BLAST score
                   33
E value
                   3.0e-09
                   41
Match length
                   95
% identity
                   Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
                   400233
Seq. No.
                   LIB3431-031-P1-N1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5734790
                   335
BLAST score
                   2.0e-31
E value
                   76
Match length
% identity
                   (AC007980) ATP-dependent metalloprotease [Arabidopsis
NCBI Description
                   thaliana]
                   400234
Seq. No.
                   LIB3431-031-P1-N1-B9
Seq. ID
Method
                   BLASTX
```

q4138290

```
398
BLAST score
E value
                   1.0e-38
Match length
                   77
                   100
% identity
                   (AJ005841) thioredoxin M [Oryza sativa]
NCBI Description
                   400235
Seq. No.
                   LIB3431-031-P1-N1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2570515
BLAST score
                   196
E value
                   5.0e-15
Match length
                   41
% identity
                   93
                   (AF022740) glycolate oxidase [Oryza sativa]
NCBI Description
Seq. No.
                   400236
                   LIB3431-031-P1-N1-C10
Seq. ID
Method
                   BLASTX
                   g131397
NCBI GI
BLAST score
                   158
E value
                   2.0e-10
                   147
Match length
                   28
% identity
                   OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) (16 KD
NCBI Description
                   SUBUNIT OF OXYGEN-EVOLVING SYSTEM OF PHOTOSYSTEM II)
                   >gi 81480 pir S00008 photosystem II oxygen-evolving
                   complex protein 3 precursor - spinach
                   >gi 755802 emb CAA29056 (X05512) 16 kDa protein of the
                   photosynthetic oxygen- evolving protein (OEC) [Spinacia
                   oleracea] >gi 225597 prf 1307179B luminal protein 16kD
                   [Spinacia oleracea]
                   400237
Seq. No.
                   LIB3431-031-P1-N1-C12
Seq. ID
                   BLASTN
Method
                   g218207
NCBI GI
BLAST score
                   327
E value
                   0.0e + 00
                   399
Match length
                   95
% identity
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS1139
                   400238
Seq. No.
                   LIB3431-031-P1-N1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   432
                   1.0e-42
E value
Match length
                   82
                   100
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
```

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

Seq. ID Method

```
[Oryza sativa]
                   400239
Seq. No.
Seq. ID
                   LIB3431-031-P1-N1-C3
Method
                   BLASTN
NCBI GI
                   g2072554
BLAST score
                   389
E value
                   0.0e + 00
Match length
                   389
% identity
                   100
                   Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   400240
Seq. No.
                   LIB3431-031-P1-N1-C4
Seq. ID
Method
                   BLASTX
                   g132105
NCBI GI
BLAST score
                   653
                   2.0e-68
E value
                   124
Match length
                   98
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4\overline{.1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   400241
Seq. ID
                   LIB3431-031-P1-N1-C6
Method
                   BLASTX
NCBI GI
                   g347451
BLAST score
                   386
                   3.0e-37
E value
Match length
                   71
% identity
                   99
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                   sativa]
                   400242
Seq. No.
                   LIB3431-031-P1-N1-C7
Seq. ID
Method
                   BLASTN
                   g2780342
NCBI GI
BLAST score
                   419
                   0.0e+00
E value
Match length
                   427
                   100
% identity
                   Oryza sativa gene for PBZ1, complete cds
NCBI Description
                   >gi 3251321 dbj E12488 E12488 Nucleotide sequence of Oryza
                   sativa PBZ1 gene
                   400243
Seq. No.
```

LIB3431-031-P1-N1-D1

BLASTN

Seq. ID

Method

```
g3126853
NCBI GI
BLAST score
                  124
                  2.0e-63
E value
                  162
Match length
                  100
% identity
                  Oryza sativa chlorophyll a/b binding protein (RCABP89)
NCBI Description
                  mRNA, nuclear gene encoding chloroplast protein, complete
                  400244
Seq. No.
                  LIB3431-031-P1-N1-D10
Seq. ID
                  BLASTX
Method
                  g1296955
NCBI GI
BLAST score
                  308
                  3.0e-28
E value
                  56
Match length
                  46
% identity
                  (X95402) duplicated domain structure protein [Oryza sativa]
NCBI Description
                  400245
Seq. No.
                  LIB3431-031-P1-N1-D6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g218154
BLAST score
                  117
                  6.0e-59
E value
                  169
Match length
                  100
% identity
NCBI Description
                  Oryza sativa gene for cytoplasmic aldolase, complete cds,
                  clone:Aldp
                  400246
Seq. No.
                  LIB3431-031-P1-N1-D7
Seq. ID
Method
                  BLASTX
                  g289920
NCBI GI
                  300
BLAST score
                  3.0e-27
E value
                  57
Match length
% identity
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                  400247
Seq. No.
                  LIB3431-031-P1-N1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  216
                  2.0e-17
E value
                  56
Match length
                  73
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  400248
Seq. No.
```

LIB3431-031-P1-N1-D9

BLASTN

Seq. ID

```
NCBI GI
                  g3885887
BLAST score
                  425
                  0.0e + 00
E value
                  429
Match length
                  100
% identity
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                  complete cds
                  400249
Seq. No.
                  LIB3431-031-P1-N1-E12
Seq. ID
                  BLASTX
Method
                  g1076422
NCBI GI
                  229
BLAST score
                  1.0e-18
E value
Match length
                  85
% identity
                   60
                  transcription factor OBF4 - Arabidopsis thaliana
NCBI Description
                  >gi 414613 emb CAA49524 (X69899) ocs-element binding
                  factor 4 [Arabidopsis thaliana]
                   400250
Seq. No.
                  LIB3431-031-P1-N1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g133019
BLAST score
                   256
                   4.0e-22
E value
Match length
                  79
% identity
                   60S RIBOSOMAL PROTEIN L7 >gi 71122 pir R5D07 ribosomal
NCBI Description
                  protein L7 - slime mold (Dictyostelium discoideum)
                  >qi 7357 emb CAA33035 (X14909) ribosomal protein L7 (AA 1
                   246) [Dictyostelium discoideum]
Seq. No.
                   400251
                  LIB3431-031-P1-N1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3126854
BLAST score
                   507
E value
                   1.0e-68
Match length
                   135
                   99
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   400252
Seq. ID
                  LIB3431-031-P1-N1-E6
Method
                  BLASTN
NCBI GI
                   g218209
BLAST score
                   53
E value
                   9.0e-21
Match length
                   69
% identity
                   94
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
Seq. No.
                   400253
```

LIB3431-031-P1-N1-E8

Match length

87

```
Method
                  BLASTX
NCBI GI
                  q417260
BLAST score
                  300
E value
                  4.0e-27
Match length
                  76
% identity
                  75
NCBI Description
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
                  lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                  light-regulated gene [Oryza sativa]
Seq. No.
                  400254
                  LIB3431-031-P1-N1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914466
BLAST score
                  342
                  4.0e-32
E value
Match length
                  63
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                  (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
                  subunit precursor [Zea mays]
Seq. No.
                  400255
Seq. ID
                  LIB3431-031-P1-N1-F1
Method
                  BLASTX
NCBI GI
                  g2407279
BLAST score
                  182
E value
                  2.0e-13
Match length
                  37
                  100
% identity
NCBI Description
                  (AF017362) aldolase [Oryza sativa]
Seq. No.
                  400256
                  LIB3431-031-P1-N1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  354
E value
                  6.0e-44
Match length
                  94
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400257
Seq. ID
                  LIB3431-031-P1-N1-F5
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  459
E value
                  8.0e-46
```

Method

BLASTX

```
100
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   400258
Seq. No.
Seq. ID
                   LIB3431-031-P1-N1-F6
Method
                   BLASTX
NCBI GI
                   q3036949
BLAST score
                   300
E value
                   4.0e-27
Match length
                   57
                   100
% identity
NCBI Description
                   (AB012638) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
                   400259
Seq. No.
Seq. ID
                   LIB3431-031-P1-N1-F8
Method
                   BLASTX
NCBI GI
                   g2911886
BLAST score
                   198
                   3.0e-15
E value
Match length
                   52
% identity
NCBI Description
                   (AF047663) Contains similarity to Pfam domain: PF00448
                   (SRP54), Score=14.7, E-value=2.7e-12, N=1 [Caenorhabditis
                   elegans]
                   400260
Seq. No.
Seq. ID
                   LIB3431-031-P1-N1-F9
Method
                   BLASTX
                   g82080
NCBI GI
BLAST score
                   336
                   2.0e-31
E value
Match length
                   79
% identity
                   82
NCBI Description
                   chlorophyll a/b-binding protein type III precursor - tomato
                   >gi_226872_prf__1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                   400261
Seq. No.
                   LIB3431-031-P1-N1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g606817
                   266
BLAST score
E value
                   3.0e-23
                   50
Match length
                   100
% identity
                   (U08404) carbonic anhydrase [Oryza sativa]
NCBI Description
                   >gi_5917783_gb AAD56038.1_AF182806 1 (AF182806) carbonic
                   anhydrase 3 [Oryza sativa]
Seq. No.
                   400262
                   LIB3431-031-P1-N1-G3
Seq. ID
```

```
NCBI GI
                  q671740
                  508
BLAST score
                  2.0e-51
E value
Match length
                  91
                  100
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  400263
Seq. No.
                  LIB3431-031-P1-N1-G4
Seq. ID
Method
                  BLASTN
                  g455510
NCBI GI
                  58
BLAST score
                  8.0e-24
E value
                  102
Match length
                  89
% identity
NCBI Description Rice mRNA for ferritin, partial sequence
                   400264
Seq. No.
                  LIB3431-031-P1-N1-G5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g289920
BLAST score
                  300
                   4.0e-27
E value
                  57
Match length
% identity
                  100
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                   400265
Seq. No.
                  LIB3431-031-P1-N1-G6
Seq. ID
Method
                  BLASTX
                  g132105
NCBI GI
BLAST score
                   301
                   2.0e-27
E value
                  57
Match length
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   400266
Seq. No.
                  LIB3431-031-P1-N1-G7
Seq. ID
Method
                  BLASTX
                  q548603
NCBI GI
                   449
BLAST score
E value
                  1.0e-44
Match length
                  89
                   97
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
```

(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)

```
barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
                   400267
Seq. No.
                   LIB3431-031-P1-N1-H1
Seq. ID
Method
                   BLASTX
                   g4886443
NCBI GI
BLAST score
                   219
                   1.0e-17
E value
Match length
                   62
                   76
% identity
                   (AL050268) hypothetical protein [Homo sapiens]
NCBI Description
Seq. No.
                   400268
                   LIB3431-031-P1-N1-H11
Seq. ID
Method
                   BLASTX
                   q1486472
NCBI GI
BLAST score
                   168
                   9.0e-12
E value
                   33
Match length
                   85
% identity
                   (X99853) oxoglutarate malate translocator [Solanum
NCBI Description
                   tuberosum]
                   400269
Seq. No.
Seq. ID
                   LIB3431-031-P1-N1-H12
Method
                   BLASTX
NCBI GI
                   g2570515
BLAST score
                   148
                   2.0e-09
E value
                   38
Match length
                   71
% identity
                   (AF022740) glycolate oxidase [Oryza sativa]
NCBI Description
                   400270
Seq. No.
                  LIB3431-031-P1-N1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g733454
BLAST score
                   446
                   3.0e-44
E value
Match length
                   91
                   95
% identity
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                   400271
Seq. No.
                  LIB3431-031-P1-N1-H7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g5295987
BLAST score
                   124
                   4.0e-63
E value
                   359
Match length
% identity
                   84
                   Oryza sativa mRNA for MADS box-like protein, complete cds,
NCBI Description
                   clone:S10304
```

>gi_478404_pir__JQ2247 photosystem I chain D precursor -

400272

Seq. No.

% identity

95

```
Seq. ID
                   LIB3431-031-P1-N1-H8
Method
                   BLASTX
NCBI GI
                   q4587556
BLAST score
                   161
E value
                   7.0e-11
Match length
                   40
% identity
NCBI Description
                   (AC006577) Similar to gi_1653162 (p)ppGpp
                   3-pyrophosphohydrolase from Synechocystis sp genome
                   gb_D90911. EST gb_W43807 comes from this gene.
                   [Arabidopsis thaliana]
                   400273
Seq. No.
Seq. ID
                   LIB3431-033-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   q3789948
                   673
BLAST score
                   7.0e-71
E value.
                   133
Match length
                   95
% identity
                   (AF094773) translation initiation factor 5A [Oryza sativa]
NCBI Description
                   400274
Seq. No.
                   LIB3431-033-P1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   397
E value
                   1.0e-38
Match length
                   102
                   79
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   400275
Seq. ID
                   LIB3431-033-P1-K1-A12
Method
                   BLASTX
                   g548603
NCBI GI
BLAST score
                   223
E value
                   3.0e-18
Match length
                   93
                   58
% identity
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                   >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                   barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                   400276
Seq. ID
                   LIB3431-033-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g1076724
BLAST score
                   580
E value
                   5.0e-60
Match length
                   109
```

```
NCBI Description
                  LHCI-680, photosystem I antenna protein - barley
                  >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                   400277
                  LIB3431-033-P1-K1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2286153
BLAST score
                  529
E value
                   4.0e-60
                  138
Match length
                  80
% identity
                   (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
NCBI Description
                   400278
Seq. No.
                  LIB3431-033-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1419090
BLAST score
                   431
                  1.0e-42
E value
                  116
Match length
% identity
                   (X94968) 37kDa chloroplast inner envelope membrane
NCBI Description
                  polypeptide precursor [Nicotiana tabacum]
Seq. No.
                   400279
Seq. ID
                  LIB3431-033-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g710308
                   377
BLAST score
                   3.0e-36
E value
                  72
Match length
                   94
% identity
                   (U11693) victorin binding protein [Avena sativa]
NCBI Description
Seq. No.
                  400280
                  LIB3431-033-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5733866
BLAST score
                   442
                  8.0e-44
E value
Match length
                  140
                   62
% identity
NCBI Description
                   (AC007932) Contains similarity to gb M73488
                   1-aminocyclopropane-1-carboxylate deaminase from
                  Pseudomonas sp. ESTs gb Z18033 and gb Z34214 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  400281
                  LIB3431-033-P1-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218207
                  246
BLAST score
                  1.0e-136
E value
Match length
                  246
                  100
% identity
NCBI Description Oryza sativa mRNA for the small subunit of
```

```
p0SSS1139
Seq. No.
                  400282
                  LIB3431-033-P1-K1-B4
Seq. ID
Method
                  BLASTX
                  q2244749
NCBI GI
                  574
BLAST score
E value
                   2.0e-59
                  132
Match length
% identity
                   81
                  (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  400283
                  LIB3431-033-P1-K1-B5
Seq. ID
Method
                  BLASTX
                  g1421730
NCBI GI
BLAST score
                  531
                   6.0e-63
E value
Match length
                  143
                  87
% identity
                  (U43082) RF2 [Zea mays]
NCBI Description
                  400284
Seq. No.
                  LIB3431-033-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3212854
BLAST score
                  453
                   4.0e-45
E value
                  137
Match length
                   66
% identity
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                   400285
Seq. No.
                  LIB3431-033-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3281853
BLAST score
                  231
                   4.0e-19
E value
                  90
Match length
                   51
% identity
                  (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   400286
                  LIB3431-033-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5915836
BLAST score
                  157
E value
                  1.0e-10
Match length
                  55
% identity
                  62
                  CYTOCHROME P450 71D7 >gi_1762144 (U48435) putative
NCBI Description
                  cytochrome P450 [Solanum chacoense]
Seq. No.
                   400287
                  LIB3431-033-P1-K1-C2
Seq. ID
```

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

BLASTX

Method

```
g6006363
NCBI GI
BLAST score
                  228
E value
                  1.0e-18
Match length
                  42
% identity
                  100
                  (AP000559) ESTs AU078183(C62904), C73912(E21020) correspond
NCBI Description
                  to a region of the predicted gene.; Similar to water stress
                  inducible protein (U74296) [Oryza sativa]
                  400288
Seq. No.
                  LIB3431-033-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2501356
BLAST score
                  475
                  1.0e-47
E value
                  115
Match length
                  79
% identity
                  TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK)
NCBI Description
                  >gi 1658322 emb CAA90427 (Z50099) transketolase precursor
                  [Solanum tuberosum]
                  400289
Seq. No.
                  LIB3431-033-P1-K1-C4
Seq. ID
                  BLASTX
Method
                  g1076724
NCBI GI
BLAST score
                  655
                  8.0e-69
E value
Match length
                  141
% identity
                  85
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                  >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                  400290
                  LIB3431-033-P1-K1-C6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3821780
BLAST score
                  35
E value
                  5.0e-10
Match length
                  35
                  100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                  400291
Seq. No.
                  LIB3431-033-P1-K1-C7
Seq. ID
                  BLASTX
Method
                  g131388
NCBI GI
BLAST score
                  329
                  1.0e-30
E value
Match length
                  115
                  65
% identity
NCBI Description
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir $16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408)
                  33kDa oxygen evolving protein of photosystem II [Triticum
```

Method

BLASTX

aestivum]

```
400292
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g131388
                  308
BLAST score
E value
                  4.0e-28
Match length
                  115
% identity
                  63
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
                  33kDa oxygen evolving protein of photosystem II [Triticum
                  aestivum]
Seq. No.
                  400293
Seq. ID
                  LIB3431-033-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q2507455
BLAST score
                  617
                  2.0e-64
E value
Match length
                  141
                  82
% identity
                  FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE
NCBI Description
                  SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350
                  formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach
                  >gi 170145 (M83940) 10-formyltetrahydrofolate synthetase
                  [Spinacia oleracea]
                  400294
Seq. No.
                  LIB3431-033-P1-K1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3789953
BLAST score
                  317
E value
                  1.0e-178
                  317
Match length
                  100
% identity
                  Oryza sativa chlorophyll a/b-binding protein precursor
NCBI Description
                  (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  400295
Seq. No.
                  LIB3431-033-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3201656
BLAST score
                  178
E value
                  6.0e-13
                  85
Match length
% identity
                  (AF005933) galactokinase [Lactobacillus casei]
NCBI Description
                  400296
Seq. No.
                  LIB3431-033-P1-K1-D11
Seq. ID
```

BLAST score

662

```
g3885888
NCBI GI
BLAST score
                  180
                  4.0e-13
E value
                  83
Match length
                  52
% identity
                  (AF093632) high mobility group protein [Oryza sativa]
NCBI Description
                  400297
Seq. No.
                  LIB3431-033-P1-K1-D12
Seq. ID
                  BLASTX
Method
                  g2407281
NCBI GI
                  674
BLAST score
                  5.0e-71
E value
Match length
                  127
                  98
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  400298
Seq. No.
                  LIB3431-033-P1-K1-D2
Seq. ID
                  BLASTN
Method
                  g20262
NCBI GI
                  225
BLAST score
                  1.0e-123
E value
                  225
Match length
                  100
% identity
                  O.sativa light-induced mRNA
NCBI Description
Seq. No.
                  400299
                  LIB3431-033-P1-K1-D4
Seq. ID
                  BLASTX
Method
                  q5729802
NCBI GI
                  254
BLAST score
                  8.0e-22
E value
                  53
Match length
                  83
% identity
                  similar to S. pombe dim1+ >gi 2565275 (AF023611) Dim1p
NCBI Description
                  homolog [Homo sapiens]
                  400300
Seq. No.
                  LIB3431-033-P1-K1-D5
Seq. ID
                  BLASTX
Method
                  g1169798
NCBI GI
                  688
BLAST score
                  1.0e-72
E value
                  145
Match length
                  92
% identity
                  GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC B (GPI-B)
NCBI Description
                   (PHOSPHOGLUCOSE ISOMERASE B) (PGI-B) (PHOSPHOHEXOSE
                  ISOMERASE B) (PHI-B) >gi_639686_dbj_BAA08149_ (D45218)
                  phosphoglucose isomerase (Pgi-b) [Oryza sativa]
                  400301
Seq. No.
                  LIB3431-033-P1-K1-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3345477
```

```
E value
                  1.0e-69
Match length
                  125
% identity
                  100
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
                  400302
Seq. No.
                  LIB3431-033-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5923670
                  296
BLAST score
E value
                  8.0e-27
                  99
Match length
                  57
% identity
                  (AC009326) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  400303
                  LIB3431-033-P1-K1-D8
Seq. ID
Method
                  BLASTX
                  q3885513
NCBI GI
                  276
BLAST score
                  2.0e-24
E value
                 . 74
Match length
% identity
                  62
                   (AF084201) similar to chloroplast 50S ribosomal protein L31
NCBI Description
                   [Medicago sativa]
Seq. No.
                  400304
Seq. ID
                  LIB3431-033-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g3980417
BLAST score
                  385
                  4.0e-37
E value
Match length
                  118
% identity
NCBI Description (AC004561) pumilio-like protein [Arabidopsis thaliana]
                  400305
Seq. No.
                  LIB3431-033-P1-K1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3885891
BLAST score
                  121
                  2.0e-61
E value
Match length
                  170
% identity
NCBI Description
                  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                  mRNA, complete cds
Seq. No.
                  400306
Seq. ID
                  LIB3431-033-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  579
                  7.0e-60
E value
Match length
                  106
% identity
                  100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
```

```
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
```

```
400307
Seq. No.
                  LIB3431-033-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  436
                  4.0e-43
E value
Match length
                  124
% identity
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >qi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  400308
Seq. No.
                  LIB3431-033-P1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3345477
                  630
BLAST score
                  6.0e-66
E value
                  135
Match length
% identity
                  (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                  400309
Seq. No.
                  LIB3431-033-P1-K1-E4
Seq. ID
Method
                  BLASTX
                  q417260
NCBI GI
BLAST score
                  410
E value
                  5.0e-40
                  128
Match length
% identity
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                  lir1 protein - rice >qi 20263 emb CAA48706 (X68807)
                  light-regulated gene [Oryza sativa]
                  400310
Seq. No.
                  LIB3431-033-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  a115787
                  376
BLAST score
                  4.0e-36
E value
                  73
Match length
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
```

Seq. No. 400311

[Oryza sativa]

NCBI GI

```
Seq. ID
                   LIB3431-033-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   q115787
BLAST score
                   491
E value
                   1.0e-49
Match length
                   121
% identity
                   83
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   400312
Seq. No.
                   LIB3431-033-P1-K1-E7
Seq. ID
Method
                   BLASTX
                   q3126854
NCBI GI
BLAST score
                   634
                   2.0e-66
E value
                   124
Match length
                   97
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   400313
                   LIB3431-033-P1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   426
                   6.0e-42
E value
                   77
Match length
                   100
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4.\overline{1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   400314
Seq. No.
Seq. ID
                   LIB3431-033-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
                   9.0e-20
E value
                   44
Match length
                   100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   400315
Seq. No.
                   LIB3431-033-P1-K1-F1
Seq. ID
Method
                   BLASTX
```

g3249064

```
BLAST score
                  456
E value
                  7.0e-48
Match length
                  145
                  61
% identity
                   (AC004473) Strong similarity to trehalose-6-phosphate
NCBI Description
                  synthase homolog gb_2245136 from A. thaliana chromosome 4
                  contig gb Z97344. [Arabidopsis thaliana]
                  400316
Seq. No.
                  LIB3431-033-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407281
                  638
BLAST score
E value
                  8.0e-67
Match length
                  124
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  400317
Seq. No.
                  LIB3431-033-P1-K1-F11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2921158
BLAST score
                  383
                  4.0e-37
E value
Match length
                  102
                  75
%'identity
NCBI Description
                   (AF022909) ClpC [Arabidopsis thaliana]
                  400318
Seq. No.
                  LIB3431-033-P1-K1-F2
Seq. ID
                  BLASTX
Method
                  g6056372
NCBI GI
BLAST score
                  224
                  2.0e-18
E value
                  75
Match length
                  59
% identity
                   (AC009894) Very similar to receptor-like serine/threonine
NCBI Description
                  kinase [Arabidopsis thaliana]
                  400319
Seq. No.
                  LIB3431-033-P1-K1-F4
Seq. ID
                  BLASTN
Method
                  q3273244
NCBI GI
                  56
BLAST score
                  2.0e-22
E value
                  132
Match length
                  86
% identity
                  Oryza sativa DNA for NLS receptor, complete cds
NCBI Description
                  400320
Seq. No.
                  LIB3431-033-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  277
                  2.0e-24
E value
```

70

Match length

```
% identity
                  73
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
                  400321
Seq. No.
                  LIB3431-033-P1-K1-F8
Seq. ID
Method
                  BLASTX
                  g320618
NCBI GI
                  380
BLAST score
                 4.0e-44
E value
                  108
Match length
                  86
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  400322
Seq. No.
                  LIB3431-033-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  595
                  9.0e-62
E value
                  129
Match length
                  87
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf __1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400323
                  LIB3431-033-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662310
BLAST score
                  173
E value
                  3.0e-12
Match length
                  34
                  100
% identity
NCBI Description
                  (AB009307) bpwl [Hordeum vulgare]
                  400324
Seq. No.
                  LIB3431-033-P1-K1-G10
Seq. ID
                  BLASTX
Method
                  g5824418
NCBI GI
BLAST score
                  284
                  2.0e-25
E value
Match length
                  111
% identity
                  49
                  (Z36948) similar to polypyrimidine tract binding protein
NCBI Description
                  [Caenorhabditis elegans]
```

400325

Seq. No.

Match length

51

```
Seq. ID
                   LIB3431-033-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   q3075488
BLAST score
                   592
                   2.0e-61
E value
Match length
                   115
% identity
                   96
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   400326
Seq. ID
                   LIB3431-033-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   q4678927
BLAST score
                   188
E value
                   5.0e-14
Match length
                   140
                   37
% identity
NCBI Description
                   (AL049711) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   400327
Seq. ID
                   LIB3431-033-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g4079798
BLAST score
                   359
E value
                   4.0e-34
Match length
                   112
% identity
                   67
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
Seq. No.
                   400328
Seq. ID
                   LIB3431-033-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g2306981
BLAST score
                   482
                   2.0e-48
E value
Match length
                  86
% identity
                   98
NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]
                   400329
Seq. No.
                  LIB3431-033-P1-K1-G4
Seq. ID
Method.
                  BLASTX
NCBI GI
                  q4836892
BLAST score
                   427
E value
                   3.0e-46
                  136
Match length
% identity
NCBI Description
                  (AC007369) Putative RNA helicase [Arabidopsis thaliana]
Seq. No.
                  400330
Seq. ID
                  LIB3431-033-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g1710551
BLAST score
                  277
                  2.0e-24
E value
```

```
98
% identity
                   60S RIBOSOMAL PROTEIN L39 >gi 1177369_emb_CAA64728.1_
NCBI Description
                   (X95458) ribosomal protein L39 [Zea mays]
                   400331
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-G7
Method
                  BLASTX
NCBI GI
                   g733454
BLAST score
                   448
                   1.0e-44
E value
                   107
Match length
                   80
% identity
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                   400332
Seq. No.
                  LIB3431-033-P1-K1-G9
Seq. ID
Method
                  BLASTX
                   q3184098
NCBI GI
BLAST score
                   393
                   4.0e-38
E value
                   143
Match length
% identity
                   51
                   (AL023777) coenzyme a synthetase [Schizosaccharomyces
NCBI Description
                   400333
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-H1
Method
                  BLASTX
                   g584741
NCBI GI
                   377
BLAST score
                   3.0e-36
E value
                   107
Match length
% identity
                   69
                  ANKYRIN REPEAT PROTEIN (AKRP) >gi_322461_pir__JQ1729
NCBI Description
                   ankyrin-repeat protein - Arabidopsis thaliana >gi_166744
                   (M82883) ankyrin repeat-containing protein [Arabidopsis
                   thaliana]
                   400334
Seq. No.
                  LIB3431-033-P1-K1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1617197
                   286
BLAST score
E value
                   2.0e-25
                  76
Match length
                  74
% identity
                   (Z72488) CP12 [Nicotiana tabacum]
NCBI Description
                   400335
Seq. No.
                  LIB3431-033-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170745
BLAST score
                  384
E value
                   4.0e-37
Match length
                  116
```

57

% identity

Seq. ID Method

```
NCBI Description LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >gi_167326
                  (M88321) Group 4 late embryogenesis-abundant protein
                  [Gossypium hirsutum] >gi_167328 (M88322) Group 4 late
                  embryogenesis-abundant protein [Gossypium hirsutum]
Seq. No.
                  400336
                  LIB3431-033-P1-K1-H2
Seq. ID
Method
                  BLASTX
                  g2570511
NCBI GI
                  580
BLAST score
                  4.0e-60
E value
Match length
                  111
                  98
% identity
NCBI Description
                  (AF022738) chlorophyll a-b binding protein [Oryza sativa]
Seq. No.
                  400337
                  LIB3431-033-P1-K1-H4
Seq. ID
Method
                  BLASTN
                  q2072554
NCBI GI
BLAST score
                  173
                  1.0e-92
E value
Match length
                  249
% identity
                  92
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  400338
Seq. No.
Seq. ID
                  LIB3431-033-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  582
                  3.0e-60
E value
Match length
                  125
% identity
                  87
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400339
                  LIB3431-033-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g170131
BLAST score
                  383
E value
                  6.0e-37
Match length
                  98
% identity
NCBI Description
                  (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
Seq. No.
                  400340
```

LIB3431-033-P1-N1-A1

BLASTX

NCBI GI

```
q3789948
NCBI GI
BLAST score
                  167
E value
                  1.0e-11
Match length
                  34
% identity
                  97
                  (AF094773) translation initiation factor 5A [Oryza sativa] .
NCBI Description
                  400341
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-A11-----
Method
                  BLASTX
                  g115784
NCBI GI
BLAST score
                  145
E value
                  4.0e-09
                  26
Match length
                  100
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I (CAB)
                  (LHCP) >gi 167525 (M16058) chlorophyll a/b-binding protein
                   [Cucumis sativus]
                  400342
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-A12
Method
                  BLASTX
                  g548603
NCBI GI
                  294
BLAST score
                  1.0e-26
E value
Match length
                  57
% identity
                  96
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi 478404 pir JQ2247 photosystem I chain D precursor -
                  barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                  400343
                  LIB3431-033-P1-N1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2306980
BLAST score
                  229
E value
                  1.0e-126
                  254
Match length
% identity
                  Oryza sativa photosystem I antenna protein (Lhca) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  400344
                  LIB3431-033-P1-N1-A4
Seq. ID
                  BLASTX
Method
                  g2286153
NCBI GI
BLAST score
                  249
                  2.0e-21
E value
                  50
Match length
                  94
% identity
NCBI Description
                  (AF007581) cytoplasmic malate dehydrogenase [Zea mays]
Seq. No.
                  400345
                  LIB3431-033-P1-N1-A5
Seq. ID
Method
                  BLASTN
```

g2570514

```
BLAST score
                  141
                  2.0e-73
E value
                  227
Match length
% identity
NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
                  400346
Seq. No.
                  LIB3431-033-P1-N1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g728629
BLAST score
                  269
E value
                  1.0e-149
Match length
                  288
                  99
% identity
NCBI Description O.sativa mRNA for PCR clone D
                  400347
Seq. No.
                  LIB3431-033-P1-N1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g710308
BLAST score
                  209
E value
                  1.0e-16
Match length
                  43
                  88
% identity
                  (U11693) victorin binding protein [Avena sativa]
NCBI Description
                  400348
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-A8
Method
                  BLASTX
NCBI GI
                  g5733866
BLAST score
                  142
                  5.0e-09
E value
Match length
                  34
% identity
                  74
                  (AC007932) Contains similarity to gb_M73488
NCBI Description
                  1-aminocyclopropane-1-carboxylate deaminase from
                  Pseudomonas sp. ESTs gb_Z18033 and gb_Z34214 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  400349
                  LIB3431-033-P1-N1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  250
                  1.0e-138
E value
                  250
Match length
                  100
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS1139
Seq. No.
                  400350
Seq. ID
                  LIB3431-033-P1-N1-B1
Method
                  BLASTN
NCBI GI
                  g20177
BLAST score
                  299
```

1.0e-167

E value

```
Match length
                   321
                   99
% identity
                  Rice cab1R gene for light harvesting chlorophyll
NCBI Description
                   a/b-binding protein
                   400351
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-B5
Method
                  BLASTX
                   q1421730
NCBI GI
BLAST score
                  201
E value
                   1.0e-15
Match length
                   40
% identity
                   95
NCBI Description
                   (U43082) RF2 [Zea mays]
                   400352
Seq. No.
Seq. ID
                   LIB3431-033-P1-N1-C11
Method
                   BLASTX
NCBI GI
                   q3281853
BLAST score
                   200
                   1.0e-15
E value
                   70
Match length
% identity
                   59
                   (AL031004) putative protein [Arabidopsis thaliana]
NCBI Description
                   400353.
Seq. No.
                   LIB3431-033-P1-N1-C2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g6006355
BLAST score
                   221
                   1.0e-121
E value
                   331
Match length
                   100
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
NCBI Description
                   400354
Seq. No.
                   LIB3431-033-P1-N1-C4
Seq. ID
Method
                   BLASTX
                   g551047
NCBI GI
BLAST score
                   209
                   1.0e-16
E value
Match length
                   42
                   93
% identity
                   (X79277) type II LHCI [Lolium temulentum]
NCBI Description
                   400355
Seq. No.
                   LIB3431-033-P1-N1-C5
Seq. ID
                   BLASTN
Method
NCBI GI
                   g218171
BLAST score
                   72
                   2.0e-32
E value
Match length
                   112
% identity
                   Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                   a/b binding protein of photosystem II (LHCPII), complete
```

cds

```
400356
Seq. No.
                  LIB3431-033-P1-N1-C6
Seq. ID
                  BLASTN
Method
                  g5091597
NCBI GI
BLAST score
                  33
                  4.0e-09
E value
                  45
Match length
                  93
% identity
NCBI Description Oryza sativa chromosome 1 BAC 10A19I, complete sequence
                  400357
Seq. No.
                  LIB3431-033-P1-N1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q482311
BLAST score
                  171
                  3.0e-12
E value
                  33
Match length
                  100
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
Seq. No.
                  400358
                  LIB3431-033-P1-N1-C8
Seq. ID
Method
                  BLASTX
                  g482311
NCBI GI
BLAST score
                  315
E value
                   5.0e-29
Match length
                  63
                  100
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                   400359
Seq. No.
                  LIB3431-033-P1-N1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3789953
BLAST score
                  317
E value
                  1.0e-178
Match length
                  317
% identity
                   100
                  Oryza sativa chlorophyll a/b-binding protein precursor
NCBI Description
                   (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                   400360
Seq. No.
                  LIB3431-033-P1-N1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3885887
                  297
BLAST score
                   1.0e-166
E value
Match length
                   301
% identity
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
```

complete cds

```
400361
Seq. No.
                  LIB3431-033-P1-N1-D12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q218209
BLAST score
                  134
E value
                  3.0e-69
Match length
                  285
% identity
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
Seq. No.
                  400362
                  LIB3431-033-P1-N1-D2
Seq. ID
Method
                  BLASTN
                  g20262
NCBI GI
BLAST score
                  162
E value
                  5.0e-86
                  210
Match length
                  94
% identity
NCBI Description O.sativa light-induced mRNA
                  400363
Seq. No.
                  LIB3431-033-P1-N1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5729802
BLAST score
                  154
E value
                  3.0e-10
                  32
Match length
% identity
                  similar to S. pombe dim1+ >gi 2565275 (AF023611) Dim1p
NCBI Description
                  homolog [Homo sapiens]
                  400364
Seq. No.
                  LIB3431-033-P1-N1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169798
BLAST score
                  233
E value
                  2.0e-19
                  46
Match length
                  100
% identity
                  GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC B (GPI-B)
NCBI Description
                   (PHOSPHOGLUCOSE ISOMERASE B) (PGI-B) (PHOSPHOHEXOSE
                  ISOMERASE B) (PHI-B) >gi 639686 dbj BAA08149 (D45218)
                  phosphoglucose isomerase (Pgi-b) [Oryza sativa]
Seq. No.
                  400365
                  LIB3431-033-P1-N1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3345476
BLAST score
                  295
                  1.0e-165
E value
Match length
                  299
                  100
% identity
                  Oryza sativa gene for carbonic anhydrase, complete cds
NCBI Description
```

400366

Seq. No.

% identity

97

```
Seq. ID
                  LIB3431-033-P1-N1-D7
                  BLASTX
Method
NCBI GI
                  g5923670
BLAST score
                  177
                  7.0e-13
E value
Match length
                  70
                  50
% identity
                  (AC009326) unknown protein [Arabidopsis thaliana]
NCBI Description
                  400367
Seq. No.
                  LIB3431-033-P1-N1-E10
Seq. ID
Method
                  BLASTX
                  q3885892
NCBI GI
                  258
BLAST score
E value
                  2.0e-22
Match length
                  51
                  100
% identity
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
Seq. No.
                  400368
                  LIB3431-033-P1-N1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  186
E value
                  6.0e-14
Match length
                  35
                  100
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >qi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >qi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400369
Seq. ID
                  LIB3431-033-P1-N1-E12
Method
                  BLASTX
NCBI GI
                  g115813
BLAST score
                  176
E value
                  1.0e-12
Match length
                  41
                  80
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                  400370
Seq. ID
                  LIB3431-033-P1-N1-E3
Method
                  BLASTX
NCBI GI
                  q606817
BLAST score
                  182
E value
                  2.0e-13
Match length
                  34
```

% identity

```
NCBI Description
                  (U08404) carbonic anhydrase [Oryza sativa]
                  >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic
                  anhydrase 3 [Oryza sativa]
Seq. No.
                  400371
                  LIB3431-033-P1-N1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q20262
BLAST score
                  282
                  1.0e-157
E value
Match length
                  290
                  99
% identity
NCBI Description O.sativa light-induced mRNA
                  400372
Seq. No.
                  LIB3431-033-P1-N1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g421916
BLAST score
                  156
E value
                  2.0e-10
Match length
                  29 🗀
% identity
                  97
                  chlorophyll a/b-binding protein - English ivy (fragment)
NCBI Description
                  >gi_12582_emb_CAA48410_ (X68333) light harvesting
                  chlorophyll a /b binding protein [Hedera helix]
Seq. No.
                  400373
                  LIB3431-033-P1-N1-E6
Seq. ID
Method
                  BLASTN
                  g20181
NCBI GI
BLAST score
                  190
E value
                  1.0e-102
Match length
                  194
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
Seq. No.
                  400374
                  LIB3431-033-P1-N1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3126853
BLAST score
                  128
E value
                  1.0e-65
Match length
                  189
                  97
% identity
                  Oryza sativa chlorophyll a/b binding protein (RCABP89)
NCBI Description
                  mRNA, nuclear gene encoding chloroplast protein, complete
                  cds
Seq. No.
                  400375
                  LIB3431-033-P1-N1-E8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  205
                  1.0e-111
E value
                  240
Match length
                  97
```

```
Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
                  400376
Seq. No.
                  LIB3431-033-P1-N1-E9
Seq. ID
Method
                  BLASTN
                  g2072554
NCBI GI
                  157
BLAST score
                  4.0e-83
E value
                 . 185
Match length
% identity
                  96
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
Seq. No.
                  400377
                  LIB3431-033-P1-N1-F10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218209
BLAST score
                  34
E value
                  2.0e-09
Match length
                  50
                  92
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
                  400378
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-F8
Method
                  BLASTN
NCBI GI
                  q20177
BLAST score
                  346
                  0.0e + 00
E value
Match length
                  365
% identity
                  99
                  Rice cab1R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
Seq. No.
                  400379
                  LIB3431-033-P1-N1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  293
                  2.0e-26
E value
Match length
                  57
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

400380

Seq. No.

```
LIB3431-033-P1-N1-G1
Seq. ID
Method
                  BLASTN
                  g2662309
NCBI GI
BLAST score
                  53
E value
                  8.0e-21
                  61
Match length
                  97
% identity
                  Hordeum vulgare mRNA for bpwl, complete cds
NCBI Description
                  400381
Seq. No.
                  LIB3431-033-P1-N1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2326947
BLAST score
                  231
                   4.0e-19
E value
                   44
Match length
                   100
% identity
                   (Z50801) Chlorophyll a/b-binding protein CP29 precursor
NCBI Description
                   [Zea mays]
                   400382
Seq. No.
                  LIB3431-033-P1-N1-G2
Seq. ID
Method
                  BLASTN
                   g4079797
NCBI GI
                   129
BLAST score
                   3.0e-66
E value
                   251
Match length
% identity
                   100
                  Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
NCBI Description
                   complete cds
                   400383
Seq. No.
                   LIB3431-033-P1-N1-G3
Seq. ID
Method
                   BLASTX
                   g1076724
NCBI GI
                   268
BLAST score
                   2.0e-23
E value
                   52
Match length
% identity
                   96
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                   >gi 666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                   antenna protein [Hordeum vulgare]
                   400384
Seq. No.
                   LIB3431-033-P1-N1-G4
Seq. ID
                   BLASTX
Method
                   g2673917
NCBI GI
                   154
BLAST score
                   4.0e-10
E value
Match length
                   43
% identity
                   65
                   (AC002561) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                   thaliana]
                   400385
Seq. No.
                   LIB3431-033-P1-N1-G6
Seq. ID
```

BLASTX

Method

```
NCBI GI
                  q1710551
BLAST score
                  248
                   4.0e-21
E value
Match length
                  46
                  98
% identity
                   60S RIBOSOMAL PROTEIN L39 >gi 1177369 emb CAA64728.1
NCBI Description
                   (X95458) ribosomal protein L39 [Zea mays]
                  400386
Seq. No.
                  LIB3431-033-P1-N1-G7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2073379
BLAST score
                  88
                  8.0e-42
E value
                  88
Match length
                  100
% identity
NCBI Description Rice CP26 mRNA, partial sequence
                  400387
Seq. No.
                  LIB3431-033-P1-N1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g586339
                  207
BLAST score
                  3.0e-16
E value
                  71
Match length
% identity
NCBI Description
                  PEROXISOMAL-COENZYME A SYNTHETASE >gi 626794 pir S46098
                  probable AMP-binding protein - yeast (Saccharomyces
                  cerevisiae) >gi 536615 emb_CAA85185_ (Z36091) ORF YBR222c
                   [Saccharomyces cerevisiae]
                  400388
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-H10
Method
                  BLASTX
                  g1617197
NCBI GI
                  152
BLAST score
                  6.0e-10
E value
                  30
Match length
% identity
                  90
NCBI Description
                  (Z72488) CP12 [Nicotiana tabacum]
                  400389
Seq. No.
                  LIB3431-033-P1-N1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1170745
BLAST score
                  331
                  2.0e-33
E value
                  103
Match length
% identity
                  67
                  LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >gi_167326
NCBI Description
                   (M88321) Group 4 late embryogenesis-abundant protein
                   [Gossypium hirsutum] >gi 167328 (M88322) Group 4 late
                  embryogenesis-abundant protein [Gossypium hirsutum]
                  400390
Seq. No.
                  LIB3431-033-P1-N1-H2
Seq. ID
```

BLASTX

Method

NCBI Description

```
g4689380
NCBI GI
BLAST score
                  258
                  3.0e-22
E value
                  52
Match length
                  94
% identity
                  (AF139465) LHCII type III chlorophyll a/b binding protein
NCBI Description
                  [Vigna radiata]
                  400391
Seq. No.
                  LIB3431-033-P1-N1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2072554
                  290
BLAST score
                  1.0e-162
E value
Match length
                  294
                  100
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  cds
                  400392
Seq. No.
                  LIB3431-033-P1-N1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
                  301
BLAST score
                  2.0e-27
E value
                  57
Match length
% identity
                  100
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  400393
Seq. No.
Seq. ID
                  LIB3431-033-P1-N1-H9
Method
                  BLASTX
NCBI GI
                  g170131
BLAST score
                  152
E value
                  6.0e-10
Match length
                  47
% identity
                  64
                  (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
NCBI Description
Seq. No.
                  400394
                  LIB3431-034-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4469021
BLAST score
                  268
                  2.0e-23
E value
Match length
                  78
% identity
                  69
```

(AL035602) hypothetical protein [Arabidopsis thaliana]

Method

BLASTN

```
400395
Seq. No.
Seq. ID
                  LIB3431-034-P1-K1-A12
Method
                  BLASTX
NCBI GI
                   g1835731
BLAST score
                   310
E value
                   2.0e-28
Match length
                   71
% identity
                   83
NCBI Description
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                   400396
Seq. No.
                  LIB3431-034-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q548605
BLAST score
                   522
E value
                   3.0e-53
Match length
                   114
% identity
                   91
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir__A48527 photosystem I protein psaK precursor
                   - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
Seq. No.
                   400397
Seq. ID
                  LIB3431-034-P1-K1-A3
Method
                  BLASTX
NCBI GI
                   a3080375
BLAST score
                   386
                   3.0e-37
E value
Match length
                   118
% identity
                   (AL022580) putative protein [Arabidopsis thaliana]
NCBI Description
                   400398
Seq. No.
Seq. ID
                  LIB3431-034-P1-K1-A4
Method
                  BLASTN
NCBI GI
                   q6015437
BLAST score
                   36
                  1.0e-10
E value
                   47
Match length
                   65
% identity
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
Seq. No.
                  400399
                  LIB3431-034-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3420055
BLAST score
                  294
E value
                  2.0e-26
Match length
                  62
% identity
NCBI Description
                   (AC004680) cyclophilin [Arabidopsis thaliana]
                  400400
Seq. No.
                  LIB3431-034-P1-K1-A7
Seq. ID
```

```
NCBI GI
                  g5091597
BLAST score
                  141
E value
                  3.0e-73
Match length
                  225
% identity
                  26
                  Oryza sativa chromosome 1 BAC 10A19I, complete sequence
NCBI Description
Seq. No.
Seq. ID
                  LIB3431-034-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q3123270
BLAST score
                  643
E value
                  2.0e-67
Match length
                  130
% identity
                  95
                  40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620)
NCBI Description
                  >gi 2463335 emb CAA75242 (Y15009) ribosomal protein S4
                  [Oryza sativa]
Seq. No.
                  400402
                  LIB3431-034-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1532168
BLAST score
                  179
E value
                  4.0e-13
Match length
                  53
% identity
                  60
                   (U63815) localized according to blastn similarity to EST
NCBI Description
                  sequences; therefore, the coding span corresponds only to
                  an area of similarity since the initation codon and stop
                  codon could not be precisely determined [Arabidopsis
                  thaliana]
Seq. No.
                  400403
Seq. ID
                  LIB3431-034-P1-K1-B1
Method
                  BLASTN
                  g6015437
NCBI GI
BLAST score
                  39
E value
                  2.0e-12
Match length
                  39
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  400404
Seq. No.
                  LIB3431-034-P1-K1-B10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g320618
BLAST score
                  521
E value
                  4.0e-53
Match length
                  115
                  86
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
```

[Oryza sativa]

```
Seq. No.
                   400405
Seq. ID
                   LIB3431-034-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g2598589
BLAST score
                   250
E value
                   2.0e-21
Match length
                  94
% identity
                   51
                   (Y15367) MtN19 [Medicago truncatula]
NCBI Description
                   400406
Seq. No.
Seq. ID
                   LIB3431-034-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   q4079798
BLAST score
                   342
E value
                   3.0e-32
Match length
                   104
% identity
                   66
NCBI Description
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
Seq. No.
                   400407
Seq. ID
                  LIB3431-034-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   q129231
BLAST score
                   740
E value
                   9.0e-79
Match length
                   142
% identity
                   98
NCBI Description
                  ORYZAIN ALPHA CHAIN PRECURSOR >gi 67644 pir KHRZOA oryzain
                   (EC 3.4.22.-) alpha precursor - rice
                   >gi_218181_dbj_BAA14402_ (D90406) oryzain alpha precursor
                   [Oryza sativa]
Seq. No.
                   400408
Seq. ID
                  LIB3431-034-P1-K1-B5
Method
                  BLASTN
NCBI GI
                   q1815627
BLAST score
                   166
E value
                   3.0e-88
Match length
                   166
% identity
                   100
NCBI Description
                  Oryza sativa metallothionein-like type 2 (OsMT-2) mRNA,
                   complete cds
Seq. No.
                   400409
Seq. ID
                  LIB3431-034-P1-K1-B6
Method
                  BLASTX
NCBI GI
                   q480450
BLAST score
                   352
E value
                   3.0e-33
Match length
                  76
% identity
                  89
NCBI Description
                  ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
                   thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
```

reductoisomerase [Arabidopsis thaliana]

```
400410
Seq. No.
Seq. ID
                  LIB3431-034-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g4587571
BLAST score
                  148
                  2.0e-15
E value
Match length
                  82
% identity
                  (AC006550) Belongs to the PF_01027 Uncharacterized protein
NCBI Description
                  family UPF0005 with 7 transmembrane domains. [Arabidopsis
                  thaliana]
                  400411
Seq. No.
                  LIB3431-034-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2492514
BLAST score
                  672
                  7.0e-71
E value
Match length
                  141
% identity
                  94
                  CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
NCBI Description
                  >gi 1483215 emb CAA68141 (X99808) chloroplast FtsH
                  protease [Arabidopsis thaliana]
Seq. No.
                  400412
Seq. ID
                  LIB3431-034-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q5091509
BLAST score
                  509
E value
                  7.0e-52
Match length
                  115
                  88
% identity
                  (AB023482) EST AU065533(C2174) corresponds to a region of
NCBI Description
                  the predicted gene.; Similar to Homo sapiens splicing
                  factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa]
Seq. No.
                  400413
                  LIB3431-034-P1-K1-C455
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464705
BLAST score
                  594
                  1.0e-61
E value
Match length
                  122
% identity
                  97
                  40S RIBOSOMAL PROTEIN S13 >gi 419802 pir S30146 ribosomal
NCBI Description
                  protein S13.e - maize >gi_288059_emb_CAA44311_ (X62455)
                  cytoplasmatic ribosomal protein S13 [Zea mays]
Seq. No.
                  400414
                  LIB3431-034-P1-K1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q218218
BLAST score
                  67
E value
                  4.0e-29
                  95
Match length
% identity
                  93
```

NCBI Description Oryza sativa p-SINE1-r3 gene, repeat sequence

```
400415
Seq. No.
                  LIB3431-034-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g132096
BLAST score
                   461
E value
                   2.0e-50
Match length
                   125
                   84
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR
                   (RUBISCO SMALL SUBUNIT A) >gi_68095_pir__RKRZS6
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS2106) - rice >gi_218210_dbj_BAA00539_
                   (D00644) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa]
                   400416
Seq. No.
                  LIB3431-034-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   8.0e-20
                   44
Match length
                   100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   400417
Seq. No.
Seq. ID
                   LIB3431-034-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g439879
BLAST score
                   285
                   2.0e-25
E value
                  121
Match length
                   51
% identity
                   (L15194) [Golden delicious apple fruit expressed mRNA,
NCBI Description
                   complete cds.], gene product [Malus domestica]
                   400418
Seq. No.
Seq. ID
                   LIB3431-034-P1-K1-D3
Method
                   BLASTX
                   g4539335
NCBI GI
                   546
BLAST score
                   5.0e-56
E value
                   142
Match length
                   70
% identity
NCBI Description
                   (AL035539) putative protein [Arabidopsis thaliana]
                   400419
Seq. No.
Seq. ID
                   LIB3431-034-P1-K1-D4
Method
                   BLASTX
                   g671740
NCBI GI
BLAST score
                   647
                   7.0e-68
E value
                   119
Match length
```

100

% identity

Match length

120

```
(X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
Seq. No.
                   400420
Seq. ID
                   LIB3431-034-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   q461899
BLAST score
                   506
E value
                   2.0e-51
Match length
                   134
% identity
NCBI Description
                   PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR
                   (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING
                   PROTEIN) >gi_1076368_pir__B53422 peptidylprolyl isomerase
                   (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi_405131
                   (L14845) cyclophilin [Arabidopsis thaliana] >gi 1322278
                   (U42724) cyclophilin [Arabidopsis thaliana]
                   400421
Seq. No.
Seq. ID
                   LIB3431-034-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   q115787
BLAST score
                   535
E value
                   9.0e-55
Match length
                   122
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   400422
                   LIB3431-034-P1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   481
E value
                   2.0e-48
                   109
Match length
% identity
                   85
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   400423
                   LIB3431-034-P1-K1-E10
Seq. ID
Method
                   BLASTX
                   g320618
NCBI GI
BLAST score
                   551
                   1.0e-56
E value
```

Match length

141

```
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                  400424
Seq. No.
Seq. ID
                  LIB3431-034-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q3036951
                  333
BLAST score
                  4.0e-31
E value
Match length
                  64
                  100
% identity
                   (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                  400425
Seq. No.
Seq. ID
                  LIB3431-034-P1-K1-E2
Method
                  BLASTX
                  g505136
NCBI GI
BLAST score
                  564
                  4.0e-58
E value
Match length
                  108
                  98
% identity
                  (D30794) ferredoxin [Oryza sativa]
NCBI Description
                  400426
Seq. No.
                  LIB3431-034-P1-K1-E4
Seq. ID
Method
                  BLASTX
                  g4887618
NCBI GI
BLAST score
                  749
                  8.0e-80
E value
Match length
                  141
% identity
NCBI Description
                  (AB007628) homeobox gene [Oryza sativa]
                  400427
Seq. No.
                  LIB3431-034-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2492782
BLAST score
                  594
                  1.0e-61
E value
                  138
Match length
                   76
% identity
                  ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE)
NCBI Description
                   (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi_504489 (L27992)
                  alpha-galactosidase [Coffea arabica]
                   400428
Seq. No.
                  LIB3431-034-P1-K1-E6
Seq. ID
Method
                  BLASTX
                  g3250675
NCBI GI
BLAST score
                  367
                   5.0e-35
E value
```

```
% identity
NCBI Description
                  (AL024486) putative protein [Arabidopsis thaliana]
                  400429
Seq. No.
                  LIB3431-034-P1-K1-E7
Seq. ID
                                                             1
Method
                  BLASTX
NCBI GI
                  g2104959
BLAST score
                  188
E value
                  4.0e-14
Match length
                  42
% identity
                  81
NCBI Description
                  (U96925) immunophilin [Vicia faba]
                  400430
Seq. No.
Seq. ID
                  LIB3431-034-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g218171
BLAST score
                  159
E value
                  4.0e-84
Match length
                  279
                  89
% identity
NCBI Description
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
                  a/b binding protein of photosystem II (LHCPII), complete
Seq. No.
                  400431
                  LIB3431-034-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  435
E value
                  4.0e-43
Match length
                  89
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  400432
Seq. No.
Seq. ID
                  LIB3431-034-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g3913018
BLAST score
                  723
E value
                  8.0e-77
Match length
                  139
% identity
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
Seq. No.
                  400433
Seq. ID
                  LIB3431-034-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g283971
BLAST score
                  365
                  8.0e-35
E value
```

Seq. ID

```
137
Match length
% identity
                   51
                   aldehyde dehydrogenase (NAD(P)+) (EC 1.2.1.5) 3 - human
NCBI Description
                   >gi 178375 (M77477) aldehyde dehydrogenase [Homo sapiens]
                   >gi 300402 bbs 132241 (S61044) aldehyde dehydrogenase
                   isozyme 3, ALDH3 {EC 1.2.1.3} [human, stomach, Peptide, 453
                   aa] [Homo sapiens]
Seq. No.
                   400434
Seq. ID
                   LIB3431-034-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   q6013233
BLAST score
                   301
E value
                   3.0e-27
Match length
                   140
                   41
% identity
NCBI Description
                   (AF183932) ionotropic glutamate receptor homolog
                   [Arabidopsis thaliana]
Seq. No.
                   400435
Seq. ID
                   LIB3431-034-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   675
E value
                   4.0e-71
Match length
                   127
% identity
                   100
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   400436
Seq. ID
                   LIB3431-034-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   q115794
BLAST score
                   218
                   1.0e-17
E value
Match length
                   78
% identity
                   60
                   CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
NCBI Description
                   III CAB-13) >gi_72748_pir_CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato
                   >gi 19277 emb CAA42818 (X60275) LHCII type III
                   [Lycopersicon esculentum]
                   400437
Seq. No.
                   LIB3431-034-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q6006363
BLAST score
                   271
E value
                   7.0e-24
Match length
                   51
                   100
% identity
                   (AP000559) ESTs AU078183(C62904), C73912(E21020) correspond
NCBI Description
                   to a region of the predicted gene.; Similar to water stress
                   inducible protein (U74296) [Oryza sativa]
Seq. No.
```

LIB3431-034-P1-K1-F7

```
Method
                  BLASTX
                  q82080
NCBI GI
BLAST score
                  408
                  7.0e-40
E value
Match length
                  116
                  68
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  400439
Seq. No.
                  LIB3431-034-P1-K1-F8
Seq. ID
Method
                  BLASTX
                  g548605
NCBI GI
                  550
BLAST score
                  1.0e-56
E value
                  124
Match length
                  88
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055_pir__A48527 photosystem I protein psaK precursor
                  - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
                  400440
Seq. No.
                  LIB3431-034-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q733454
                  247
BLAST score
                  5.0e-21
E value
                  67
Match length
% identity
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                  400441
Seq. No.
Seq. ID
                  LIB3431-034-P1-K1-G10
Method
                  BLASTX
                  g2827533
NCBI GI
BLAST score
                  158
                  1.0e-10
E value
                  70
Match length
                  50
% identity
                   (AL021633) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  400442
Seq. No.
                  LIB3431-034-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2407281
BLAST score
                   641
                  3.0e-67
E value
                  121
Match length
                  98
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
```

400443

Seq. No.

```
LIB3431-034-P1-K1-G12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q6015437
BLAST score
                   34
E value
                   2.0e-10
Match length
                   38
                   97
% identity
NCBI Description
                  Homo sapiens PEX1 mRNA, complete cds
                   400444
Seq. No.
Seq. ID
                   LIB3431-034-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   q4079798
BLAST score
                   338
E value
                   1.0e-31
                   110
Match length
                   63
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   400445
Seq. No.
                   LIB3431-034-P1-K1-G4
Seq. ID
Method
                   BLASTX
                   g3319357
NCBI GI
                   374
BLAST score
E value
                   7.0e-36
Match length
                   118
                   67
% identity
                   (AF077407) contains similarity to phosphoenolpyruvate
NCBI Description
                   synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
Seq. No.
                   400446
                   LIB3431-034-P1-K1-G5
Seq. ID
Method
                   BLASTX
                   g3126854
NCBI GI
BLAST score
                   675
E value
                   4.0e-71
Match length
                   127
                   100
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   400447
Seq. No.
                   LIB3431-034-P1-K1-G7
Seq. ID
Method
                   BLASTN
                   g6015437
NCBI GI
                   35
BLAST score
E value
                   2.0e-10
Match length
                   35
% identity
                   100
                   Homo sapiens PEX1 mRNA, complete cds
NCBI Description
Seq. No.
                   400448
Seq. ID
                   LIB3431-034-P1-K1-H1
Method
                   BLASTX
                   g2288988
NCBI GI
                   170
BLAST score
```

6.0e-12

E value

```
66
Match length
                   47
% identity
NCBI Description
                   (AC002335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   400449
                   LIB3431-034-P1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g548605
BLAST score
                   594
E value
                   1.0e-61
Match length
                   130
                   91
% identity
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi_539055_pir__A48527 photosystem I protein psaK precursor
                   - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
                   400450
Seq. No.
Seq. ID
                   LIB3431-034-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q417482
BLAST score
                   397
E value
                   1.0e-38
Match length
                   140
                   58
% identity
                   PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (CAAX
NCBI Description
                   FARNESYLTRANSFERASE BETA SUBUNIT) (RAS PROTEINS
                   PRENYLTRANSFERASE) (FTASE-BETA) >gi_541966_pir__JQ2254
                   farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) beta
                   chain - garden pea >gi 169049 (L08664) farnesyl-protein
                   transferase beta-subunīt [Pisum sativum]
Seq. No.
                   400451
                   LIB3431-034-P1-K1-H5
Seq. ID
Method
                   BLASTX
                   q6006429
NCBI GI
                   298
BLAST score
E value
                   6.0e-27
Match length
                   118
% identity
                   49
                   (AJ242958) SPL1-Related3 protein [Arabidopsis thaliana]
NCBI Description
                   400452
Seq. No.
                  LIB3431-034-P1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   547
E value
                   4.0e-56
Match length
                   119
                   87
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
```

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa] Seq. No. 400453 LIB3431-034-P1-K1-H9 Seq. ID Method BLASTN NCBI GI g2073379 BLAST score 88 E value 5.0e-42Match length 92 99 % identity Rice CP26 mRNA, partial sequence NCBI Description 400454 Seq. No. LIB3431-034-P1-N1-A11 Seq. ID Method BLASTX NCBI GI q4469021

Method BLASTX
NCBI GI g4469021
BLAST score 292
E value 4.0e-26
Match length 76
% identity 74

NCBI Description (AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No. 400455 Seq. ID LIB3431-034-P1-N1-A12

Method BLASTX
NCBI GI g1835731
BLAST score 273
E value 4.0e-24
Match length 65
% identity 82

NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

 Seq. No.
 400456

 Seq. ID
 LIB3431-034-P1-N1-A2

 Method
 BLASTN

 NCBI GI
 g304219

 BLAST score
 49

 E value
 1.0e-18

 Match length
 71

Match length 71 % identity 92

NCBI Description Hordeum vulgare chloroplast photosystem I PSK-I subunit

mRNA, complete cds

Seq. No. 400457

Seq. ID LIB3431-034-P1-N1-A6

Method BLASTX
NCBI GI g3420055
BLAST score 260
E value 2.0e-22
Match length 55
% identity 89

NCBI Description (AC004680) cyclophilin [Arabidopsis thaliana]

Seq. No. 400458

Seq. ID LIB3431-034-P1-N1-A8

BLAST score

542

```
Method
                  BLASTX
NCBI GI
                   q3914899
BLAST score
                  199
E value
                   2.0e-15
Match length
                   41
% identity
                   93
                  40S RIBOSOMAL PROTEIN S4 >gi_2331301 (AF013487) ribosomal
NCBI Description
                  protein S4 type I [Zea mays]
                   400459
Seq. No.
Seq. ID
                  LIB3431-034-P1-N1-B10
Method
                  BLASTX
NCBI GI
                   q3036951
BLAST score
                   356
E value
                   8.0e-34
Match length
                   68
                   100
% identity
                   (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                   400460
Seq. No.
                  LIB3431-034-P1-N1-B2
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4079797
                   92
BLAST score
E value
                   2.0e-44
Match length
                  163
                   98
% identity
                  Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
NCBI Description
                   complete cds
Seq. No.
                   400461
                  LIB3431-034-P1-N1-B3
Seq. ID
Method
                  BLASTN
                   g218180
NCBI GI
BLAST score
                   294
E value
                   1.0e-164
Match length
                   390
                   93
% identity
                  Rice mRNA for oryzain alpha (EC 3.4.22)
NCBI Description
                   400462
Seq. No.
Seq. ID
                  LIB3431-034-P1-N1-B5
Method
                  BLASTN
                  g1815627
NCBI GI
BLAST score
                  116
E value
                   3.0e-58
Match length
                  151
                   97
% identity
                  Oryza sativa metallothionein-like type 2 (OsMT-2) mRNA,
NCBI Description
                  complete cds
                   400463
Seq. No.
                  LIB3431-034-P1-N1-B6
Seq. ID
Method
                  BLASTX
                  g480450
NCBI GI
```

NCBI GI

```
E value
                   2.0e-55
 Match length
                   150
 % identity
                   74
 NCBI Description
                   ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
                   thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                   reductoisomerase [Arabidopsis thaliana]
 Seq. No.
                   400464
 Seq. ID
                   LIB3431-034-P1-N1-B9
 Method
                   BLASTX
 NCBI GI
                   q5734790
 BLAST score
                   337
 E value
                   1.0e-31
 Match length
                   74
 % identity
 NCBI Description
                    (AC007980) ATP-dependent metalloprotease [Arabidopsis
                   thaliana]
                   400465
 Seq. No.
 Seq. ID
                   LIB3431-034-P1-N1-C1
 Method
                   BLASTN
 NCBI GI
                   q3789951
 BLAST score
                   96
 E value
                   1.0e-46
 Match length
                   211
% identity
 NCBI Description
                   Oryza sativa chlorophyll a/b-binding protein presursor
                    (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
 Seq. No.
                   400466
                   LIB3431-034-P1-N1-C10
 Seq. ID
 Method
                   BLASTX
                   g671740
 NCBI GI
 BLAST score
                   431
 E value
                   1.0e-42
 Match length
                   79
 % identity
 NCBI Description
                    (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
                                                                     • *-.
 Seq. No.
                   400467
 Seq. ID
                   LIB3431-034-P1-N1-C11
 Method
                   BLASTX
                   g5091509
 NCBI GI
 BLAST score
                   262
 E value
                   8.0e-23
Match length
                   47
                   100
 % identity
 NCBI Description
                   (AB023482) EST AU065533(C2174) corresponds to a region of
                   the predicted gene.; Similar to Homo sapiens splicing
                   factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa]
 Seq. No.
                   400468
 Seq. ID
                   LIB3431-034-P1-N1-C3
Method
                   BLASTX
```

g3123295

% identity

```
BLAST score
                   231
E value
                   4.0e-19
Match length
                   57
                   70
% identity
                  CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi_2583169
NCBI Description
                   (AF026473) calmodulin-related protein [Arabidopsis
                   thaliana]
                   400469
Seq. No.
                   LIB3431-034-P1-N1-C5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1296955
BLAST score
                   300
                   3.0e-27
E value
Match length
                   54
% identity
                   46
                   (X95402) duplicated domain structure protein [Oryza sativa]
NCBI Description
                   400470
Seq. No.
                   LIB3431-034-P1-N1-C7
Seq. ID
                   BLASTN
Method
NCBI GI
                   g1661159
                   157
BLAST score
                   5.0e-83
E value
                   237
Match length
                   92
% identity
                   Oryza sativa chlorophyll a/b binding protein (kcd1895)
NCBI Description
                   mRNA, complete cds
                   400471
Seq. No.
                   LIB3431-034-P1-N1-C8
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2072726
BLAST score
                   461
                   0.0e + 00
E value
                   503
Match length
                   98
% identity
                   O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2
NCBI Description
                   400472
Seq. No.
                   LIB3431-034-P1-N1-C9
Seq. ID
                   BLASTX
Method
                   q3345477
NCBI GI
                   211
BLAST score
E value
                   9.0e-17
Match length
                   44
                   91
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                   400473
Seq. No.
                   LIB3431-034-P1-N1-D10
Seq. ID
                   BLASTN
Method
NCBI GI
                   g218218
                   85
BLAST score
                   6.0e-40
E value
                   112
Match length
                   95
```

NCBI GI

g992633

```
NCBI Description Oryza sativa p-SINE1-r3 gene, repeat sequence
 Seq. No.
                   400474
                   LIB3431-034-P1-N1-D11
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   g132105
 BLAST score
                   451
 E value
                    6.0e-45
Match length
                   93
                   89
 % identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                   ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   400475
 Seq. No.
                   LIB3431-034-P1-N1-D12
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   q2072554
 BLAST score
                   277
 E value
                   1.0e-154
                   293
Match length
 % identity
                   Oryza sativa metallothionein-like protein mRNA, complete
 NCBI Description
                    400476
 Seq. No.
                   LIB3431-034-P1-N1-D3
 Seq. ID
 Method
                   BLASTX
NCBI GI
                    q3786007
 BLAST score
                    160
 E value
                    7.0e-11
                    43
Match length
                    53
 % identity
                    (AC005499) hypothetical protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    400477
                   LIB3431-034-P1-N1-D4
 Seq. ID
                   BLASTN
 Method
 NCBI GI
                    g218209
 BLAST score
                   74
 E value
                    1.0e-33
 Match length
                    143
 % identity
                    97
                   Oryza sativa mRNA for the small subunit of
 NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS2106
                    400478
 Seq. No.
                   LIB3431-034-P1-N1-D6
 Seq. ID
 Method
                   BLASTX
```

```
BLAST score
                   217
                   1.0e-17
E value
                   59
Match length
                   66
% identity
                   (U30874) cyclophilin B [Schistosoma mansoni]
NCBI Description
                   >qi 1588493 prf 2208425A B-like cyclophilin [Schistosoma
                   mansoni]
                   400479
Seq. No.
                   LIB3431-034-P1-N1-D7
Seq. ID
                   BLASTN
Method
NCBI GI
                   q20181
BLAST score
                   128
                   1.0e-65
E value
Match length
                   215
% identity
                   91
                   Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                   a/b-binding protein
                   400480
Seq. No.
Seq. ID
                   LIB3431-034-P1-N1-D8
Method
                   BLASTN
NCBI GI
                   g3819197
BLAST score
                   47
E value
                   3.0e-17
Match length
                   103
% identity
                   86
NCBI Description
                   Hordeum vulgare partial mRNA; clone cMWG0676.uni
Seq. No.
                   400481
                   LIB3431-034-P1-N1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   179
E value
                   4.0e-13
Match length
                   34
% identity
                   100
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   400482
Seq. ID
                   LIB3431-034-P1-N1-E10
Method
                   BLASTN
NCBI GI
                   q20177
BLAST score
                   35
E value
                   4.0e-10
Match length
                   67
% identity
                   88
                   Rice cab1R gene for light harvesting chlorophyll
NCBI Description
```

a/b-binding protein

```
Seq. No.
                   400483
Seq. ID
                   LIB3431-034-P1-N1-E11
Method
                  BLASTX
NCBI GI
                   g1181599
BLAST score
                   144
                   5.0e-09
E value
Match length
                   39
% identity
                   72
                  (D83007) subunit of photosystem I [Cucumis sativus]
NCBI Description
Seq. No.
                   400484
                   LIB3431-034-P1-N1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q5902389
BLAST score
                   170
E value
                   5.0e-12
Match length
                   49
                   55
% identity
NCBI Description
                  (AC008148) Unknown protein [Arabidopsis thaliana]
                   400485
Seq. No.
Seq. ID
                  LIB3431-034-P1-N1-E2
Method
                  BLASTN
NCBI GI
                   q1209384
BLAST score
                   337
                   0.0e + 00
E value
Match length
                   341
                   100
% identity
NCBI Description Oryza sativa mRNA for root ferredoxin, partial cds
                   400486
Seq. No.
                  LIB3431-034-P1-N1-E4
Seq. ID
Method
                  BLASTN
                  q4887617
NCBI GI
BLAST score
                   434
E value
                   0.0e + 00
Match length
                   449
                   99
% identity
NCBI Description Oryza sativa HOS59 mRNA, partial cds
Seq. No.
                   400487
                  LIB3431-034-P1-N1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2204226
BLAST score
                  255
E value
                   6.0e-22
Match length
                  55
% identity
                  82
NCBI Description (Y13848) alpha-galactosidase [Hordeum vulgare]
                   400488
Seq. No.
Seq. ID
                  LIB3431-034-P1-N1-F1
Method
                  BLASTX
                  g3036949
NCBI GI
BLAST score
                  234
                  1.0e-19
E value
```

E value

```
Match length
                  49
                  92
% identity
                   (AB012638) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
Seq. No.
                  400489
Seq. ID
                  LIB3431-034-P1-N1-F11
Method
                  BLASTX
NCBI GI
                  q2407279
BLAST score
                  176
                  1.0e-12
E value
Match length
                  37
% identity
NCBI Description
                  (AF017362) aldolase [Oryza sativa]
Seq. No.
                  400490
Seq. ID
                  LIB3431-034-P1-N1-F12
Method
                  BLASTX
NCBI GI
                  g4455169
BLAST score
                  233
E value
                  3.0e-19
Match length
                  77
% identity
NCBI Description
                  (AL035521) putative aldehyde dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  400491
                  LIB3431-034-P1-N1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  317
E value
                  3.0e-29
Match length
                  71
                  87
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir__A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
Seq. No.
                  400492
Seq. ID
                  LIB3431-034-P1-N1-F3
Method
                  BLASTX
NCBI GI
                  q3036951
BLAST score
                  347
                  9.0e-33
E value
Match length
                  68
% identity
NCBI Description
                  (AB012639) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
                  400493
Seq. No.
Seq. ID
                  LIB3431-034-P1-N1-F5
Method
                  BLASTN
NCBI GI
                  q2570510
BLAST score
                  255
```

1.0e-141

% identity

97

```
Match length
                    279
% identity
                    98
                   Oryza sativa chlorophyll a-b binding protein mRNA, complete
NCBI Description
                   cds
                    400494
Seq. No.
Seq. ID
                   LIB3431-034-P1-N1-F6
Method
                   BLASTN
NCBI GI
                   q6006355
BLAST score
                    374
E value
                    0.0e + 00
Match length
                    380
                    99
% identity
NCBI Description
                   Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
                    400495
Seq. No.
Seq. ID
                   LIB3431-034-P1-N1-F7
Method
                   BLASTX
NCBI GI
                   g115813
BLAST score
                   215
E value
                    3.0e-17
Match length
                    48
% identity
                    85
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                   CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                    400496
                   LIB3431-034-P1-N1-F8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g304219
BLAST score
                    40
E value
                    3.0e-13
Match length
                    68
% identity
                    90
NCBI Description
                   Hordeum vulgare chloroplast photosystem I PSK-I subunit
                   mRNA, complete cds
                    400497
Seq. No.
Seq. ID
                   LIB3431-034-P1-N1-F9
Method
                   BLASTX
NCBI GI
                   g733456
BLAST score
                   371
                   2.0e-35
E value
Match length
                   76
% identity
NCBI Description
                    (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
                    [Zea mays]
Seq. No.
                   400498
Seq. ID
                   LIB3431-034-P1-N1-G11
Method
                   BLASTN
NCBI GI
                   g218209
BLAST score
                   149
E value
                   4.0e-78
                   328
Match length
```

Match length

91

```
NCBI Description Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS2106
                  400499
Seq. No.
Seq. ID
                  LIB3431-034-P1-N1-G3
Method
                  BLASTN
NCBI GI
                  q1398998
BLAST score
                  110
E value
                   4.0e-55
Match length
                  185
                  96
% identity
                  Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II,
NCBI Description
                  complete cds
                  400500
Seq. No.
Seq. ID
                  LIB3431-034-P1-N1-G4
Method
                  BLASTX
NCBI GI
                  g3319357
BLAST score
                  237
E value
                   6.0e-20
Match length
                  61
% identity
                  70
NCBI Description
                   (AF077407) contains similarity to phosphoenolpyruvate
                  synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]
Seg. No.
                  400501
                  LIB3431-034-P1-N1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  345
E value
                  1.0e-32
Match length
                  65
% identity
NCBI Description
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  400502
Seq. ID
                  LIB3431-034-P1-N1-H11
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  234
E value
                  9.0e-20
Match length
                  48
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir__A48527 photosystem I protein psaK precursor
                  barley >gi_304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
Seq. No.
                  400503
Seq. ID
                  LIB3431-034-P1-N1-H3
Method
                  BLASTX
NCBI GI
                  g417482
BLAST score
                  371
E value
                  1.0e-35
```

Method

BLASTX

```
% identity
NCBI Description
                   PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (CAAX
                   FARNESYLTRANSFERASE BETA SUBUNIT) (RAS PROTEINS
                   PRENYLTRANSFERASE) (FTASE-BETA) >gi_541966_pir__JQ2254 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) beta
                   chain - garden pea >gi_169049 (L08664) farnesyl-protein
                   transferase beta-subunīt [Pisum sativum]
Seq. No.
                   400504
Seq. ID
                   LIB3431-034-P1-N1-H4
Method
                   BLASTN
NCBI GI
                   q3819197
BLAST score
                   47
E value
                   4.0e-17
Match length
                   103
% identity
                   86
                   Hordeum vulgare partial mRNA; clone cMWG0676.uni
NCBI Description
Seq. No.
                   400505
                   LIB3431-034-P1-N1-H7
Seq. ID
Method
                   BLASTN
NCBI GI
                   q218207
BLAST score
                   295
E value
                   1.0e-165
Match length
                   307
% identity
                   99
NCBI Description
                   Oryza sativa mRNA for the small subunit of
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   p0SSS1139
Seq. No.
                   400506
Seq. ID
                   LIB3431-035-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   q548605
BLAST score
                   471
E value
                   3.0e-47
Match length
                   98
% identity
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi_539055_pir__A48527 photosystem I protein psaK precursor
                   - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
Seq. No.
                   400507
Seq. ID
                   LIB3431-035-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   q1171579
BLAST score
                   239
E value
                   5.0e-20
Match length
                   91
% identity
                   48
                   (X95342) cytochrome P450 [Nicotiana tabacum]
NCBI Description
                   400508
Seq. No.
                   LIB3431-035-P1-K1-A2
Seq. ID
```

```
q2582822
NCBI GI
BLAST score
                    172
                    3.0e-12
E value
Match length
                    39
                    82
% identity
                    (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
NCBI Description
                    Protein of 32kDa) [Solanum tuberosum]
Seq. No.
                    400509
                    LIB3431-035-P1-K1-A3
Seq. ID
Method
                    BLASTX
NCBI GI
                    g728744
BLAST score
                    271
E value
                    2.0e-46
Match length
                    132
% identity
                    80
                    AUXIN-INDUCED PROTEIN PCNT115 >gi 100305 pir S16390
NCBI Description
                    auxin-induced protein - common tobacco >gi_19799_emb_CAA39708_ (X56267) auxin-induced protein
                    [Nicotiana tabacum]
Seq. No.
                    400510
Seq. ID
                    LIB3431-035-P1-K1-A7
Method
                    BLASTX
NCBI GI
                    q5912299
BLAST score
                    464
E value
                    8.0e-55
Match length
                    123
% identity
NCBI Description
                    (AJ133787) gigantea homologue [Oryza sativa]
Seq. No.
                    400511
Seq. ID
                    LIB3431-035-P1-K1-B11
Method
                    BLASTX
NCBI GI
                    q1076724
BLAST score
                    665
E value
                    6.0e-70
Match length
                    141
                    85
% identity
                    LHCI-680, photosystem I antenna protein - barley
NCBI Description
                    >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                    antenna protein [Hordeum vulgare]
Seq. No.
                    400512
                    LIB3431-035-P1-K1-B3
Seq. ID
Method
                    BLASTX
NCBI GI
                    g320618
BLAST score
                    578
E value
                    1.0e-59
Match length
                    127
% identity
                    87
NCBI Description
                    chlorophyll a/b-binding protein I precursor - rice
                    >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
```

[Oryza sativa]

>gi_227611_prf__1707316A chlorophyll a/b binding protein 1

```
400513
Seq. No.
Seq. ID
                   LIB3431-035-P1-K1-B4
                   BLASTX
Method
NCBI GI
                   g3386621
BLAST score
                   513
E value
                   4.0e-52
Match length
                   119
% identity
                   83
                   (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                   400514
Seq. No.
                   LIB3431-035-P1-K1-B5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3273202
BLAST score
                   394
E value
                   4.0e-38
Match length
                   115
% identity
                   74
NCBI Description
                   (AB010918) responce reactor4 [Arabidopsis thaliana]
                   400515
Seq. No.
Seq. ID
                   LIB3431-035-P1-K1-B7
Method
                   BLASTN
NCBI GI
                   q20181
BLAST score
                   92
E value
                   6.0e-44
Match length
                   243
% identity
                   Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                   a/b-binding protein
                   400516
Seq. No.
Seq. ID
                   LIB3431-035-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   q417488
BLAST score
                   608
E value
                   3.0e-63
Match length
                   152
                   75
% identity
                   ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
NCBI Description
                   H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1)
                   H - potato >gi_169473 (M69038) alpha-glucan phosphorylase
                   type H isozyme [Solanum tuberosum]
                   400517
Seq. No.
                   LIB3431-035-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q115787
BLAST score
                   600
                   3.0e-62
E value
                   135
Match length
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
```

[Oryza sativa]

```
400518
Seq. No.
Seq. ID
                  LIB3431-035-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  758
E value
                  7.0e-81
Match length
                  149
% identity
                  95
NCBI Description
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
                  400519
Seq. No.
Seq. ID
                  LIB3431-035-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q100454
BLAST score
                  664
                  7.0e-70
E value
                  146
Match length
% identity
                  photosystem II oxygen-evolving complex protein 1 - potato
NCBI Description
                  >gi_809113_emb_CAA35601_ (X17578) 33kDa precursor protein
                  of oxygen-evolving complex [Solanum tuberosum]
Seq. No.
                  400520
Seq. ID
                  LIB3431-035-P1-K1-C3
Method
                  BLASTX
                  g544437
NCBI GI
BLAST score
                  339
E value
                  1.0e-31
Match length
                  73
% identity
NCBI Description
                  GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN)
                  >gi_296358_emb_CAA47018_ (X66377) CIT-SAP [Citrus sinensis]
                  400521
Seq. No.
Seq. ID
                  LIB3431-035-P1-K1-C4
Method
                  BLASTN
                  g473980
NCBI GI
BLAST score
                  76
                  9.0e-35
E value
Match length
                  113
% identity
                  90
NCBI Description Rice mRNA, partial homologous to glycine-rich protein gene
                  400522
Seq. No.
                  LIB3431-035-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82080
BLAST score
                  415
                  1.0e-40
E value
                  141
Match length
```

[Lycopersicon esculentum]

chlorophyll a/b-binding protein type III precursor - tomato >gi 226872 prf 1609235A chlorophyll a/b binding protein

62

% identity

NCBI Description

```
400523
Seq. No.
Seq. ID
                  LIB3431-035-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q3345477
BLAST score
                  662
E value
                  1.0e-69
Match length
                  127
% identity
                  (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                  400524
Seq. No.
                  LIB3431-035-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5042462
BLAST score
                  450
E value
                  9.0e-45
                  114
Match length
                  80
% identity
                  (AC007789) putative negatively light-regulated protein
NCBI Description
                  [Oryza sativa]
                  400525
Seq. No.
                  LIB3431-035-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  676
E value
                  3.0e-71
Match length
                  144
                  89
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_ 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400526
                  LIB3431-035-P1-K1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1173347
                  793
BLAST score
                  6.0e-85
E value
                  153
Match length
                  95
% identity
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7) P2ASE)
                  >gi 100803 pir S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
                  400527
Seq. No.
                  LIB3431-035-P1-K1-D10
Seq. ID
```

BLASTX

Method

E value

4.0e-52

```
q82080
NCBI GI
BLAST score
                   483
E value
                   1.0e-48
Match length
                  134
% identity
                   69
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                  400528
Seq. ID
                  LIB3431-035-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q170131
BLAST score
                  263
E value
                  8.0e-23
Match length
                  67
                   67
% identity
                   (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
NCBI Description
Seq. No.
                  400529
                  LIB3431-035-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2773154
BLAST score
                  242
E value
                  2.0e-20
Match length
                  118
% identity
                  47
NCBI Description
                   (AF039573) abscisic acid- and stress-inducible protein
                   [Oryza sativa]
Seq. No.
                  400530
                  LIB3431-035-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  744
E value
                  3.0e-79
Match length
                  141
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  400531
Seq. No.
Seq. ID
                  LIB3431-035-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g6014904
                  372
BLAST score
E value
                  1.0e-35
Match length
                  70
% identity
                  97
NCBI Description
                  DAG PROTEIN, CHLOROPLAST PRECURSOR
                  >gi_1200205_emb_CAA65064_ (X95753) DAG [Antirrhinum majus]
                  400532
Seq. No.
Seq. ID
                  LIB3431-035-P1-K1-D4
Method
                  BLASTX
                  g3789952
NCBI GI
BLAST score
                  512
```

```
108
Match length
% identity
                    94
NCBI Description
                    (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                   sativa]
                   400533
Seq. No.
Seq. ID
                   LIB3431-035-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   q543711
BLAST score
                   367
E value
                    5.0e-35
Match length
                   71
                   99
% identity
                   14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)
NCBI Description
                   brain specific protein [Oryza sativa]
Seq. No.
                   400534
                   LIB3431-035-P1-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1172874
BLAST score
                   204
E value
                   7.0e-16
Match length
                   135
% identity
                   38
NCBI Description
                   DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR
                   >gi_479589_pir__S34823 dehydration-induced protein RD22 -
                   Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22
                    [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene
                    [Arabidopsis thaliana]
Seq. No.
                   400535
Seq. ID
                   LIB3431-035-P1-K1-D8
                   BLASTX
Method
                   g132105
NCBI GI
BLAST score
                   673
E value
                   7.0e-71
Match length
                   124
% identity
                   100
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4\overline{.1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   400536
Seq. ID
                   LIB3431-035-P1-K1-E1
                   BLASTX
Method
NCBI GI
                   g320618
BLAST score
                   544
E value
                   1.0e-55
Match length
                   128
% identity
                   84
```

```
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf_1707316A chlorophyll a/b binding protein 1
                   [Oryza satīva]
Seq. No.
                   400537
Seq. ID
                   LIB3431-035-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   q1617197
BLAST score
                   304
                   1.0e-27
E value
Match length
                   76
                   76
% identity
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                   400538
                   LIB3431-035-P1-K1-E11
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2306980
                   98
BLAST score
                   7.0e-48
E value
Match length
                   122
% identity
NCBI Description
                   Oryza sativa photosystem I antenna protein (Lhca) mRNA,
                   complete cds
                   400539
Seq. No.
Seq. ID
                   LIB3431-035-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   q2464852
BLAST score
                   205
E value
                   5.0e-16
Match length
                   100
                   46
% identity
NCBI Description
                   (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                   400540
                   LIB3431-035-P1-K1-E3
Seq. ID
Method
                   BLASTN
                   g6015437
NCBI GI
BLAST score
                   38
E value
                   9.0e-12
Match length
                   38
                   100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                   400541
Seq. No.
                   LIB3431-035-P1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115794
BLAST score
                   374
E value
                   7.0e-36
Match length
                   77
                   91
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
                   III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding
```

```
400542
Seq. No.
                  LIB3431-035-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q320618
BLAST score
                  724
                  8.0e-77
E value
Match length
                  156
% identity
                  89
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  400543
Seq. No.
                  LIB3431-035-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3355476
                  246
BLAST score
                  8.0e-21
E value
Match length
                  72
                  60
% identity
                  (AC004218) unknown protein [Arabidopsis thaliana]
NCBI Description
                  400544
Seq. No.
                  LIB3431-035-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115787
                  423
BLAST score
                  5.0e-42
E value
                  116
Match length
                  83
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                  400545
Seq. No.
                  LIB3431-035-P1-K1-F10
Seq. ID
                  BLASTX
Method
                  g4585882
NCBI GI
BLAST score
                  522
                  4.0e-53
E value
Match length
                  143
% identity
                  (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                  400546
Seq. No.
                  LIB3431-035-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5441881
```

protein type III precursor (cab-13) - tomato
>gi 19277_emb_CAA42818_ (X60275) LHCII type III

[Lycopersicon esculentum]

Match length

127

```
BLAST score
                   175
E value
                   2.0e-12
Match length
                   115
% identity
                   39
                   (APO00367) Similar to putative receptor kinase. (AC002332)
NCBI Description
                   [Oryza sativa]
Seq. No.
                   400547
Seq. ID
                  LIB3431-035-P1-K1-F6
Method
                  BLASTX
NCBI GI
                   g4049341
BLAST score
                   285
E value
                   2.0e-25
Match length
                   87
% identity
NCBI Description
                   (AL034567) putative protein [Arabidopsis thaliana].
                   400548
Seq. No.
Seq. ID
                  LIB3431-035-P1-K1-F8
Method
                  BLASTN
NCBI GI
                   q6015437
BLAST score
                   36
E value
                   1.0e-10
Match length
                   47
% identity
                   65
NCBI Description
                  Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  400549
                  LIB3431-035-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4079798
BLAST score
                   499
E value
                   1.0e-50
Match length
                  126
% identity
                   78
NCBI Description
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                  sativa]
                  400550
Seq. No.
                  LIB3431-035-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g482311
BLAST score
                  771
E value
                  2.0e-82
Match length
                  149
% identity
NCBI Description
                  photosystem II oxygen-evolving complex protein 1 - rice
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
Seq. No.
                  400551
Seq. ID
                  LIB3431-035-P1-K1-G10
Method
                  BLASTX
                  q115787
NCBI GI
BLAST score
                  565
E value
                  3.0e-58
```

Match length

146

```
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                  400552
Seq. ID
                  LIB3431-035-P1-K1-G11
Method
                  BLASTX
                  q3789954
NCBI GI
BLAST score
                  507
E value
                  1.0e-51
                  95
Match length
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
Seq. No.
                  400553
                  LIB3431-035-P1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2407282
BLAST score
                  111
E value
                  2.0e-55
Match length
                  111
% identity
                  100
                  Oryza sativa ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
Seq. No.
                   400554
                  LIB3431-035-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q733454
BLAST score
                  300
E value
                   4.0e-27
Match length
                  69
% identity
                  88
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
Seq. No.
                   400555
                  LIB3431-035-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352461
BLAST score
                  358
E value
                   4.0e-34
Match length
                  87
% identity
                  79
NCBI Description
                  IN2-2 PROTEIN
Seq. No.
                  400556
Seq. ID
                  LIB3431-035-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q1616659
BLAST score
                  512
E value
                  1.0e-56
```

```
% identity
NCBI Description
                  (U49387) adenylosuccinate synthetase [Triticum aestivum]
                  400557
Seq. No.
Seq. ID
                  LIB3431-035-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g5031281
BLAST score
                  314
E value
                  9.0e-29
                  98
Match length
% identity
                  62
                  (AF139499) unknown [Prunus armeniaca]
NCBI Description
Seq. No.
                  400558
Seq. ID
                  LIB3431-035-P1-K1-G6
                  BLASTN
Method
NCBI GI
                  g1245938
BLAST score
                  35
E value
                  6.0e-10
Match length
                  35
                  100
% identity
NCBI Description
                  rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
                  heart atrium, mRNA, 2998 nt]
Seq. No.
                  400559
                  LIB3431-035-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3885888
BLAST score
                  347
E value
                  1.0e-32
Match length
                  70
% identity
NCBI Description
                  (AF093632) high mobility group protein [Oryza sativa]
Seq. No.
                  400560
Seq. ID
                  LIB3431-035-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q422029
BLAST score
                  542
E value
                  2.0e-55
Match length
                  150
% identity
                  73
NCBI Description
                  transcription factor OBF3.2, ocs element-binding - maize
                  >gi_297018_emb_CAA48904_ (X69152) ocs-element binding
                  factor 3.2 [Zea mays]
Seq. No.
                  400561
Seq. ID
                  LIB3431-035-P1-K1-H1
Method
                  BLASTX
                  g2407281
NCBI GI
BLAST score
                  705
E value
                  1.0e-74
Match length
                  132
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
```

subunit [Oryza sativa]

Seq. No.

400566

```
Seq. No.
                  400562
Seq. ID
                  LIB3431-035-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  595
E value
                  9.0e-62
Match length
                  128
% identity
                  ጸጸ
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400563
Seq. ID
                  LIB3431-035-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q3914603
BLAST score
                  699
E value
                  5.0e-74
Match length
                  134
% identity
                  99
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
Seq. No.
                  400564
Seq. ID
                  LIB3431-035-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q6063542
BLAST score
                  351
E value
                  2.0e-33
Match length
                  109
% identity
                  72
                  (AP000615) EST C74302(E30840) corresponds to a region of
NCBI Description
                  the predicted gene.; similar to glyceraldehyde-3-phosphate
                  dehydrogenase. (M64118) [Oryza sativa]
Seq. No.
                  400565
Seq. ID
                  LIB3431-035-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q1172813
BLAST score
                  563
E value
                  5.0e-58
Match length
                  108
% identity
                  99
NCBI Description
                  60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPRESSOR SG12)
                  >gi 1076752 pir S49596 ribosomal protein L10.e, cytosolic
                  - rice >gi_575357_emb_CAA57340_ (X81692) putative tumor
                  supressor [Oryza sativa]
```

```
LIB3431-035-P1-K1-H4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g417260
BLAST score
                   421
E value
                   2.0e-41
                   128
Match length
% identity
                   66
NCBI Description
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
                   lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                   light-regulated gene [Oryza sativa]
                   400567
Seq. No.
                   LIB3431-035-P1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4585882
BLAST score
                   628
E value
                   1.0e-65
Match length
                   157
                   72
% identity
NCBI Description
                   (AC005850) PSI type III chlorophyll a/b-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                   400568
Seq. ID
                   LIB3431-035-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   a4454459
BLAST score
                   433
                   1.0e-42
E value
Match length
                   112
                   76
% identity
NCBI Description
                   (AC006234) unknown protein [Arabidopsis thaliana]
                   400569
Seq. No.
                   LIB3431-035-P1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3402713
BLAST score
                   219
                   1.0e-17
E value
                   62
Match length
% identity
                   (AC004261) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   400570
Seq. No.
                   LIB3431-035-P1-N1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q548605
BLAST score
                   320
E value
                   1.0e-29
Match length
                   67
% identity
                   93
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi 539055 pir__A48527 photosystem I protein psaK precursor
                   - \overline{\text{barley}} > \overline{\text{gi}} 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
```

400571

Seq. No.

```
LIB3431-035-P1-N1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2582822
BLAST score
                  169
                  6.0e-12
E value
Match length
                  39
% identity
                  (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
NCBI Description
                  Protein of 32kDa) [Solanum tuberosum]
                  400572
Seq. No.
                  LIB3431-035-P1-N1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  368
                  3.0e-35 `
E value
                  73
Match length
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  400573
Seq. No.
Seq. ID
                  LIB3431-035-P1-N1-B8
Method
                  BLASTX
NCBI GI
                  q417488
                  184
BLAST score
                  9.0e-19
E value
Match length
                  60
% identity
                  ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
NCBI Description
                  H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1)
                  H - potato >gi_169473 (M69038) alpha-glucan phosphorylase
                  type H isozyme [Solanum tuberosum]
Seq. No.
                  400574
                  LIB3431-035-P1-N1-B9
Seq. ID
                  BLASTX
Method
                  g1085987
NCBI GI
BLAST score
                  179
E value
                  4.0e-13
                  34
Match length
% identity
                  light harvesting chlorophyll a protein precursor - Norway
NCBI Description
                  spruce >gi_607148_emb_CAA57407_ (X81808) light harvesting
                  chlorophyll a /b-binding protein Lhcb1*1 [Picea abies]
Seq. No.
                  400575
                  LIB3431-035-P1-N1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q671740
BLAST score
                  406
                  1.0e-39
E value
                  79
Match length
                  96
% identity
```

```
(X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
Seq. No.
                   400576
                  LIB3431-035-P1-N1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q482311
BLAST score
                   171
E value
                   4.0e-12
                   33
Match length
% identity
                   100
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                   400577
Seq. No.
                  LIB3431-035-P1-N1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1362150
BLAST score
                   290
E value
                   1.0e-33
                   84
Match length
                   88
% identity
                  hypothetical protein (clone AFN3) - wild oat (fragment)
NCBI Description
                   >gi_726478 (U20000) putative ORF1 [Avena fatua]
Seq. No.
                   400578
                  LIB3431-035-P1-N1-C4
Seq. ID
Method
                   BLASTN
                   g2331130
NCBI GI
BLAST score
                   227
                   1.0e-125
E value
                   251
Match length
                   98
% identity
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
                   cds
Seq. No.
                   400579
                   LIB3431-035-P1-N1-C7
Seq. ID
Method
                   BLASTN
                   g218209
NCBI GI
BLAST score
                   57
E value
                   3.0e-23
Match length
                   172
                   90
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS2106
                   400580
Seq. No.
Seq. ID
                   LIB3431-035-P1-N1-C8
                   BLASTN
Method
                   g5042437
NCBI GI
BLAST score
                   325
E value
                  0.0e + 00
Match length
                   389
```

100

% identity

Match length

388

```
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
                  400581
Seq. No.
Seq. ID
                  LIB3431-035-P1-N1-C9
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                  237
E value
                  7.0e-20
                  47
Match length
% identity
                  98
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  satival
                  400582
Seq. No.
Seq. ID
                  LIB3431-035-P1-N1-D1
Method
                  BLASTX
NCBI GI
                  g1173347
BLAST score
                  190
E value
                  2.0e-14
Match length
                  41
% identity
                  95
NCBI Description
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi 14265 emb CAA46507
                  (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivuml
Seq. No.
                  400583
Seq. ID
                  LIB3431-035-P1-N1-D10
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  256
E value
                  3.0e-25
Match length
                  76
% identity
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
Seq. No.
                  400584
                  LIB3431-035-P1-N1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q170131
BLAST score
                  152
                  6.0e-10
E value
Match length
                  47
% identity
                  (M55322) ribosomal protein 30S subunit [Spinacia oleracea]
NCBI Description
                  400585
Seq. No.
Seq. ID
                  LIB3431-035-P1-N1-D12
Method
                  BLASTN
NCBI GI
                  q2773153
BLAST score
                  364
                  0.0e + 00
E value
```

· Serve

E value

2.0e-20

```
% identity
                   Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                    (Asr1) mRNA, complete cds
                   400586
Seq. No.
Seq. ID
                   LIB3431-035-P1-N1-D2
Method
                   BLASTN
NCBI GI
                   g3126853
BLAST score
                   160
                   1.0e-84
E value
                   210
Match length
                   99
% identity
                   Oryza sativa chlorophyll a/b binding protein (RCABP89)
NCBI Description
                   mRNA, nuclear gene encoding chloroplast protein, complete
                   cds
                   400587
Seq. No.
Seq. ID
                   LIB3431-035-P1-N1-D4
Method
                   BLASTX
NCBI GI
                   q3789952
BLAST score
                   168
E value
                   1.0e-11
Match length
                   30
                   100
% identity
NCBI Description
                    (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                   sativa]
                   400588
Seq. No.
                   LIB3431-035-P1-N1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g543711
                   367
BLAST score
E value
                    6.0e-35
Match length
                   71
% identity
                   99
                   14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140)
NCBI Description
                   brain specific protein [Oryza satīva]
Seq. No.
                   400589
Seq. ID
                   LIB3431-035-P1-N1-D8
Method
                   BLASTN
NCBI GI
                   g218209
BLAST score
                   34
E value
                   2.0e-09
Match length
                   50
% identity
                   92
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS2106
Seq. No.
                   400590
Seq. ID
                   LIB3431-035-P1-N1-D9
Method
                   BLASTX
NCBI GI
                   g259138
BLAST score
                   242
```

```
Match length
                   45
                   100
% identity
                   oryzacystatin=cysteine protease inhibitor [Oryza=rice,
NCBI Description
                   Peptide Recombinant, 90 aa]
                   400591
Seq. No.
Seq. ID
                   LIB3431-035-P1-N1-E1
Method
                   BLASTX
NCBI GI
                   g115787
                   410
BLAST score
                   4.0e-40
E value
                   77
Match length
                   100
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   400592
Seq. ID
                   LIB3431-035-P1-N1-E10
Method
                   BLASTX
NCBI GI
                   q1617197
BLAST score
                   286
E value
                   2.0e-25
Match length
                   71
                   73
% identity
NCBI Description
                   (Z72488) CP12 [Nicotiana tabacum]
                   400593
Seq. No.
Seq. ID
                   LIB3431-035-P1-N1-E11
Method
                   BLASTX
NCBI GI
                   q1076724
BLAST score
                   263
                   6.0e-23
E value
Match length
                   51
% identity
                   96
                   LHCI-680, photosystem I antenna protein - barley
NCBI Description
                   >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                   antenna protein [Hordeum vulgare]
Seq. No.
                   400594
Seq. ID
                   LIB3431-035-P1-N1-E2
Method
                   BLASTX
NCBI GI
                   q2464852
BLAST score
                   171
E value
                   5.0e-12
Match length
                   80
% identity
                   49
                   (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   400595
Seq. ID
                   LIB3431-035-P1-N1-E4
                   BLASTX
Method
NCBI GI
                   q115794
BLAST score
                   467
```

1.0e-46

E value

Seq. ID

```
Match length
                  94
% identity
                  91
                  CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
NCBI Description
                  III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding
                  protein type III precursor (cab-13) - tomato
                  >gi_19277_emb_CAA42818_ (X60275) LHCII type III
                  [Lycopersicon esculentum]
                  400596
Seq. No.
Seq. ID
                  LIB3431-035-P1-N1-E6
Method
                  BLASTX
NCBI GI
                  q115768
BLAST score
                  223
E value
                  4.0e-18
                  43
Match length
                  98
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB) (LHCP) >gi_72743_pir__CDKV chlorophyll a/b-binding
                  protein precursor - cucumber (fragment) >gi 167523 (M16057)
                  chlorophyll a/b-binding protein [Cucumis sativus]
Seq. No.
                  400597
Seq. ID
                  LIB3431-035-P1-N1-E9
Method
                  BLASTX
NCBI GI
                  q2582822
BLAST score
                  362
E value
                  2.0e-34
Match length
                  79
% identity
                  85
NCBI Description
                  (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
                  Protein of 32kDa) [Solanum tuberosum]
Seq. No.
                  400598
Seq. ID
                  LIB3431-035-P1-N1-F1
Method
                  BLASTX
NCBI GI
                  q671737
BLAST score
                  199
E value
                  2.0e-15
Match length
                  37
% identity
NCBI Description
                  (X74731) Chloropyll a/b binding protein [Amaranthus
                  hypochondriacus]
Seq. No.
                  400599
Seq. ID
                  LIB3431-035-P1-N1-F10
Method
                  BLASTX
NCBI GI
                  q115813
BLAST score
                  230
E value
                  6.0e-19
Match length
                  55
% identity
                  82
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
```

LIB3431-035-P1-N1-F7

NCBI GI

q733454

```
BLASTX
Method
NCBI GI
                  g2262116
                  152
BLAST score
                   6.0e-10
E value
Match length
                  92
% identity
                   39
NCBI Description
                   (AC002343) cellulose synthase isolog [Arabidopsis thaliana]
Seq. No.
                   400601
                  LIB3431-035-P1-N1-F9
Seq. ID
                  BLASTX
Method
                   q4079798
NCBI GI
BLAST score
                   322
                   5.0e-34
E value
                  81
Match length
                   96
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   400602
Seq. No.
                  LIB3431-035-P1-N1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q482311
BLAST score
                   303
E value
                   2.0e-27
Match length
                   64
                   95
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                   complex protein 1 [Oryza sativa]
Seq. No.
                   400603
Seq. ID
                   LIB3431-035-P1-N1-G10
Method
                  BLASTX
NCBI GI
                   q289920
BLAST score
                   154
E value
                   4.0e-10
Match length
                   29
                   97
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                   400604
Seq. No.
                   LIB3431-035-P1-N1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3789954 .
BLAST score
                   410
E value
                   5.0e-40
                   78
Match length
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   satival
                   400605
Seq. No.
                  LIB3431-035-P1-N1-G2
Seq. ID
Method
                  BLASTX
```

E value

2.0e-36

```
289
BLAST score
                   6.0e-26
E value
Match length
                   62
                   92
% identity
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
Seq. No.
                   400606
Seq. ID
                   LIB3431-035-P1-N1-G3
Method
                   BLASTX
NCBI GI
                   g2462750
BLAST score
                   184
E value
                   1.0e-13
Match length
                   53
% identity
                   68
NCBI Description
                   (AC002292) Highly similar to auxin-induced protein
                   (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                   400607
Seq. ID
                   LIB3431-035-P1-N1-G4
Method
                   BLASTX
NCBI GI
                   q1616659
BLAST score
                   343
E value
                   4.0e-32
                   75
Match length
% identity
                   88
                   (U49387) adenylosuccinate synthetase [Triticum aestivum]
NCBI Description
                   400608
Seq. No.
                   LIB3431-035-P1-N1-G8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3885887
BLAST score
                   304
E value
                   1.0e-170
Match length
                   315
% identity
NCBI Description
                   Oryza sativa high mobility group protein (HMG) mRNA,
                   complete cds
                   400609
Seq. No.
                   LIB3431-035-P1-N1-H1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g218209
BLAST score
                   152
E value
                   7.0e-80
Match length
                   343
                   97
% identity
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS2106
                   400610
Seq. No.
Seq. ID
                   LIB3431-035-P1-N1-H10
Method
                   BLASTX
NCBI GI
                   q347451
BLAST score
                   380
```

```
69
Match length
                  100
% identity
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa]
                  400611
Seq. No.
Seq. ID
                  LIB3431-035-P1-N1-H11
Method
                  BLASTN
NCBI GI
                  g3377792
BLAST score
                  263
E value
                  1.0e-146
Match length
                  334
                  95
% identity
NCBI Description
                  Oryza sativa ribulose-1,5-bisphosphate
                  carboxylase/oxygenase activase (rca) mRNA, complete cds
                  400612
Seq. No.
Seq. ID
                  LIB3431-035-P1-N1-H12
Method
                  BLASTN
NCBI GI
                  q6063530
BLAST score
                  364
                  0.0e+00
E value
Match length
                  389
% identity
                  98
                  Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
NCBI Description
                  400613
Seq. No.
                  LIB3431-035-P1-N1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1172813
BLAST score
                  450
                  1.0e-44
E value
                  88
Match length
% identity
                  60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPRESSOR SG12)
NCBI Description
                  >gi 1076752 pir S49596 ribosomal protein L10.e, cytosolic
                  - rice >gi_575357_emb_CAA57340_ (X81692) putative tumor
                  supressor [Oryza sativa]
Seq. No.
                  400614
                  LIB3431-035-P1-N1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q417260
BLAST score
                  300
                  3.0e-27
E value
                  81
Match length
% identity
                  70
NCBI Description
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
                  lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
Seq. No.
                  400615
Seq. ID
                  LIB3431-035-P1-N1-H5
Method
                  BLASTX
NCBI GI
                  g115813
BLAST score
                  171
```

4.0e-12

E value

E value

```
Match length
                   42
% identity
                   79
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                   CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
                   400616
Seq. No.
Seq. ID
                   LIB3431-036-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g2997684
BLAST score
                   245
E value
                   1.0e-20
Match length
                   85
% identity
                   56
NCBI Description
                   (AF053302) putative transcriptional co-activator
                   [Arabidopsis thaliana]
Seq. No.
                   400617
Seq. ID
                   LIB3431-036-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   9.0e-20
Match length
                   44
% identity
                   100
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   400618
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-A12
Method
                  BLASTX
NCBI GI
                   g871931
BLAST score
                   399
E value
                   7.0e-39
Match length
                   95
% identity
                   86
NCBI Description
                  (D30763) ferredoxin [Oryza sativa]
                   400619
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-A4
Method
                  BLASTX
                  g1709846
NCBI GI
BLAST score
                  180
E value
                   4.0e-13
Match length
                  122
                   47
% identity
NCBI Description
                  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi 706853 (U04336)
                  22 kDa component of photosystem II [Lycopersicon
                  esculentum]
Seq. No.
                  400620
Seq. ID
                  LIB3431-036-P1-K1-A5
Method
                  BLASTN
                  g6016845
NCBI GI
BLAST score
                  301
```

1.0e-168

Seq. ID

```
Match length
                   426
% identity
                   93
                   Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
NCBI Description
Seq. No.
                   400621
Seq. ID
                   LIB3431-036-P1-K1-A6
Method
                   BLASTN
NCBI GI
                   q218207
BLAST score
                   227
E value
                   1.0e-124
Match length
                   259
% identity
                   97
NCBI Description
                   Oryza sativa mRNA for the small subunit of
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   p0SSS1139
Seq. No.
                   400622
                   LIB3431-036-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   470
E value
                   3.0e-47
Match length
                   107
% identity
                   85
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf _1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   400623
Seq. ID
                   LIB3431-036-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g730456
BLAST score
                   663
E value
                   9.0e-70
Match length
                   128
% identity
                   98
NCBI Description 40S RIBOSOMAL PROTEIN S19
Seq. No.
                   400624
Seq. ID
                  LIB3431-036-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q2407281
BLAST score
                   556
                  3.0e-57
E value
Match length
                  108
% identity
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  400625
```

LIB3431-036-P1-K1-B2

NCBI Description

```
Method
                  BLASTN
NCBI GI
                  q19094
BLAST score
                  52
                  4.0e-20
E value
Match length
                  64
% identity
                  95
                  H.vulgare mRNA PsaN for photosystem I subunit N
NCBI Description
                  400626
Seq. No.
                  LIB3431-036-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
                  9.0e-20
E value
Match length
                  44
% identity
                  100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  400627
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g2306981
BLAST score
                  385
                  4.0e-37
E value
Match length
                  68
% identity
                  99
                  (AF010321) photosystem I antenna protein [Oryza sativa]
NCBI Description
Seq. No.
                  400628
                  LIB3431-036-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
                  567
BLAST score
E value
                  2.0e-58
Match length
                  122
                  87
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400629
                  LIB3431-036-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4760553.
BLAST score
                  703
E value
                  2.0e-74
Match length
                  142
% identity
                  96
```

(AB019533) Nad-dependent formate dehydrogenase [Oryza

```
sativa]
                  400630
Seq. No.
                  LIB3431-036-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                  637
                  1.0e-66
E value
                  123
Match length
                  98
% identity
                  (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                  400631
Seq. No.
                  LIB3431-036-P1-K1-B9
Seq. ID
                  BLASTX
Method
                  g320618
NCBI GI
BLAST score
                  486
                  5.0e-49
E value
                  111
Match length
                  84
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  400632
Seq. No.
                  LIB3431-036-P1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1835731
                  378
BLAST score
                  3.0e-36
E value
                  122
Match length
% identity
                  67
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                  400633
Seq. No.
                  LIB3431-036-P1-K1-C11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3126854
BLAST score
                  715
                  7.0e-76
E value
                  136
Match length
% identity
                  99
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   400634
                  LIB3431-036-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82080
                   425
BLAST score
E value
                  7.0e-42
                  121
Match length
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi 226872 prf _1609235A chlorophyll a/b binding protein
```

[Lycopersicon esculentum]

BLAST score

356

```
Seq. No.
                  400635
                  LIB3431-036-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914468
BLAST score
                  536
                  7.0e-55
E value
                  142
Match length
                  75
% identity
                  26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
NCBI Description
                  >gi_478411_pir__JQ2257 nuclear antigen 21D7 - carrot
                  >gi 217911 dbj BAA02696 (D13434) 21D7 antigen [Daucus
                  carota]
                  400636
Seq. No.
                  LIB3431-036-P1-K1-C5
Seq. ID
Method
                  BLASTX
                  g119784
NCBI GI
                  221
BLAST score
                  6.0e-18
E value
                  92
Match length
                  55
% identity
                  3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR
NCBI Description
                  (BETA-KETOACYL-ACP SYNTHASE I) (KAS I)
                  >gi_100555_pir__A39356 3-oxoacyl-[acyl-carrier-protein]
                  synthase (EC 2.3.1.41) I beta chain precursor, chloroplast
                  - barley >gi 167065 (M60410) beta-ketoacyl-ACP synthase I
                  [Hordeum vulgare]
                  400637
Seq. No.
                  LIB3431-036-P1-K1-C6
Seq. ID
Method
                  BLASTX
                  g131225
NCBI GI
BLAST score
                  663
                  1.0e-69
E value
                  147
Match length
% identity
                  85
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  400638
                  LIB3431-036-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4097547
BLAST score
                  261
                  1.0e-22
E value
                  124
Match length
% identity
                  (U64906) ATFP3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  400639
                  LIB3431-036-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024440
```

```
7.0e-34
E value
Match length
                  75
                  88
% identity
                  PROTEASOME DELTA CHAIN PRECURSOR (MULTICATALYTIC
NCBI Description
                  ENDOPEPTIDASE COMPLEX DELTA CHAIN)
                  >gi 1743356 emb CAA70699 (Y09505) proteasome delta subunit
                  [Nicotiana tabacum]
                  400640
Seq. No.
                  LIB3431-036-P1-K1-D1
Seq. ID
                  BLASTX
Method
                  g4105561
NCBI GI
                  186
BLAST score
                  8.0e-14
E value
                  80
Match length
% identity
                  54
                  (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
NCBI Description
                  400641
Seq. No.
                  LIB3431-036-P1-K1-D10
Seq. ID
                  BLASTX
Method
                  g115787
NCBI GI
BLAST score
                  592
                  5.0e-64
E value
                  133
Match length
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -2\overline{8} to 235)
                  [Oryza sativa]
                  400642
Seq. No.
                  LIB3431-036-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131388
BLAST score
                  283
                  3.0e-25
E value
Match length
                  107
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408)
                  33kDa oxygen evolving protein of photosystem II [Triticum
                  aestivum]
Seq. No.
                  400643
Seq. ID
                  LIB3431-036-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g4759278
BLAST score
                  301
                  3.0e-27
E value
Match length
                  144
                  43
% identity
                  prp28, U5 snRNP 100 kd protein >gi 2655202 (AF026402) U5
NCBI Description
```

snRNP 100 kD protein [Homo sapiens] 400644 Seq. No. LIB3431-036-P1-K1-D4 Seq. ID BLASTX Method g2529682 NCBI GI 238 BLAST score 6.0e-20 E value 143 Match length 42 % identity NCBI Description (AC002535) unknown protein [Arabidopsis thaliana] 400645 Seq. No. LIB3431-036-P1-K1-D5 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g4519936
BLAST score 481
E value 2.0e-48
Match length 136
% identity 71

NCBI Description (AB019186) RPR1 [Oryza sativa]

 Seq. No.
 400646

 Seq. ID
 LIB3431-036-P1-K1-D6

 Method
 BLASTX

Method BLASIX
NCBI GI g4678279
BLAST score 311
E value 2.0e-28
Match length 97
% identity 67

NCBI Description (AL049660) carboxyl terminal protease-like protein

[Arabidopsis thaliana]

Seq. No. 400647

Seq. ID LIB3431-036-P1-K1-D7

Method BLASTX
NCBI GI g3789954
BLAST score 582
E value 3.0e-60
Match length 109
% identity 100

NCBI Description (AF094776) chlorophyll a/b-binding protein precursor [Oryza

sativa]

Seq. No. 400648

Seq. ID LIB3431-036-P1-K1-D8

Method BLASTX
NCBI GI g3126854
BLAST score 662
E value 1.0e-69
Match length 124
% identity 100

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

Seq. No. 400649

Seq. ID LIB3431-036-P1-K1-E1

Method BLASTX

```
NCBI GI
                  q115787
BLAST score
                  531
                  3.0e-54
E value
Match length
                  121
% identity
                  88
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                  400650
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g4263714
BLAST score
                  536
                  7.0e-55
E value
Match length
                  142
                  77
% identity
                   (AC006223) putative integral membrane protein [Arabidopsis
NCBI Description
                  thaliana]
                   400651
Seq. No.
                  LIB3431-036-P1-K1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q6006310
                  751
BLAST score
                   5.0e-80
E value
                  144
Match length
% identity
NCBI Description
                   (AB018443) nonphototrophic hypocotyl 1b [Oryza sativa]
                   400652
Seq. No.
                  LIB3431-036-P1-K1-E12
Seq. ID
                  BLASTX
Method
                  q1421751
NCBI GI
BLAST score
                  175
                   2.0e-12
E value
                   36
Match length
% identity
                   (U60592) putative ORF; conserved in 5' leaders of plant
NCBI Description
                   SAMdC [Pisum sativum]
                   400653
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-E3
Method
                  BLASTX
NCBI GI
                   q3047090
BLAST score
                   419
E value
                   4.0e-41
                   138
Match length
% identity
                   55
                   (AF058826) T26D22.18 gene product [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   400654
                   LIB3431-036-P1-K1-E4
Seq. ID
                   BLASTX
Method
```

g2944180

NCBI GI

NCBI GI

```
454
BLAST score
E value
                  3.0e-45
Match length
                  114
% identity
NCBI Description
                  (AF007779) trehalose-6-phosphate phosphatase [Arabidopsis
                  thaliana]
                  400655
Seq. No.
                  LIB3431-036-P1-K1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1835730
BLAST score
                  274
                  1.0e-152
E value
Match length
                  290
                  99
% identity
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
NCBI Description
                  complete cds
Seq. No.
                  400656
Seq. ID
                  LIB3431-036-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g3461848
                  210
BLAST score
                  1.0e-16
E value
Match length
                  75
% identity
                  (AC005315) putative ATPase [Arabidopsis thaliana]
NCBI Description
                  400657
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g1071913
BLAST score
                  490
                  2.0e-49
E value
                  127
Match length
                  73
% identity
                  cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
NCBI Description
                  - spinach >gi 1066153 dbj BAA07177 (D37963) cysteine
                  synthase [Spinacia oleracea]
                  400658
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-F10
Method.
                  BLASTX
NCBI GI
                  q461595
BLAST score
                  262
                  8.0e-23
E value
Match length
                  94
                  55
% identity
                  ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II)
NCBI Description
                  >gi 479533 pir S34473 H+-transporting ATP synthase (EC
                  3.6.1.34) chain 9 - spinach >gi 394755 emb CAA50520
                  (X71397) CF(o) II ATP synthase subunit 9 [Spinacia oleracea]
Seq. No.
                  400659
Seq. ID
                  LIB3431-036-P1-K1-F11
Method
                  BLASTX
```

q2072555

```
237
BLAST score
                  9.0e-20
E value
                  44
Match length
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >qi 6103441 gb AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  400660
Seq. No.
                  LIB3431-036-P1-K1-F12
Seq. ID
                  BLASTN
Method
                  q1245938
NCBI GI
                  36
BLAST score
                  1.0e-10
E value
                  36
Match length
                  100
% identity
                  rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
NCBI Description
                  heart atrium, mRNA, 2998 nt]
Seq. No.
                  400661
                  LIB3431-036-P1-K1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g6017100
BLAST score
                  588
                  6.0e-61
E value
                  142
Match length
                  71
% identity
                  (AC009895) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  400662
                  LIB3431-036-P1-K1-F3
Seq. ID
                  BLASTX
Method
                  q131388
NCBI GI
                   383
BLAST score
E value
                   6.0e-37
                  127
Match length
                   66
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi_100831_pir__S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
                   33kDa oxygen evolving protein of photosystem II [Triticum
                   aestivum]
                   400663
Seq. No.
                  LIB3431-036-P1-K1-F4
Seq. ID
                   BLASTX
Method
                   q3789952
NCBI GI
BLAST score
                   275
                   3.0e-24
E value
                   55
Match length
                   96
% identity
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
```

400664

Seq. No.

```
Seq. ID
                  LIB3431-036-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g4558549
BLAST score
                  627
                  2.0e-65
E value
Match length
                  144
% identity
                  83
                   (AC007138) putative SecA-type chloroplast protein transport
NCBI Description
                  factor [Arabidopsis thaliana]
                  400665
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g2191152
BLAST score
                  149
E value
                  2.0e-09
Match length
                  105
% identity
NCBI Description
                   (AF007269) A IG002N01.31 gene product [Arabidopsis
                  thaliana]
                  400666
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-F8
Method
                  BLASTX
                  g2407281
NCBI GI
BLAST score
                  682
                  6.0e-72
E value
Match length
                  127
% identity
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
                  400667
Seq. No.
                  LIB3431-036-P1-K1-G1
Seq. ID
Method
                  BLASTX
                  g2130052
NCBI GI
                  451
BLAST score
                  7.0e-45
E value
                  99
Match length
% identity
NCBI Description
                  xylose isomerase (EC 5.3.1.5) - barley
                  >gi_1296809_emb_CAA64545_ (X95257) xylose isomerase
                  [Hordeum vulgare]
                  400668
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  237
E value
                  9.0e-20
Match length
                  44
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
```

400669

Seq. No.

NCBI GI

```
LIB3431-036-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3913808
BLAST score
                  590
E value
                  4.0e-61
                  132
Match length
                  89
% identity
                  FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME
NCBI Description
                  SYNTHETASE) >qi 2429618 dbj BAA22284 (AB007120)
                  ferrochelatase [Oryza sativa]
                  400670
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-G4
                  BLASTX
Method
                  q4079798
NCBI GI
                   496
BLAST score
                   4.0e-50
E value
Match length
                  127
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   400671
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-G5
Method
                  BLASTX
                   g3126854
NCBI GI
                   511
BLAST score
                   6.0e-52
E value
                   99
Match length
                   97
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   400672
Seq. No.
Seq. ID
                   LIB3431-036-P1-K1-G6
                   BLASTX
Method
NCBI GI
                   q4895205
BLAST score
                   248
                   4.0e-21
E value
Match length
                   61
% identity
                   (AC007661) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   400673
                   LIB3431-036-P1-K1-G7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2695931
BLAST score
                   350
                   5.0e-33
E value
                   141
Match length
                   53
% identity
                  (AJ222779) hypothetical protein [Hordeum vulgare]
NCBI Description
                   400674
Seq. No.
Seq. ID
                   LIB3431-036-P1-K1-G8
Method
                   BLASTN
```

ğ6015437

```
BLAST score
                  36
                  1.0e-10
E value
Match length
                  36
% identity
                  100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  400675
                  LIB3431-036-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3789952
BLAST score
                  578
E value
                  8.0e-60
Match length
                  116
% identity
NCBI Description
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                  sativa]
                  400676
Seq. No.
Seq. ID
                  LIB3431-036-P1-K1-H6
                  BLASTX
Method
NCBI GI
                  q132105
BLAST score
                  591
                  3.0e-61
E value
Match length
                  127
% identity
                  87
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208 dbj BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  400677
Seq. No.
                  LIB3431-036-P1-K1-H7
Seq. ID
                  BLASTN
Method
                  g5917782
NCBI GI
BLAST score
                  36
E value
                  5.0e-11
Match length
                  120
% identity
                  82
NCBI Description Oryza sativa carbonic anhydrase 3 mRNA, complete cds
Seq. No.
                  400678
                  LIB3431-036-P1-K1-H8
Seq. ID
Method
                  BLASTX
                  g548605
NCBI GI
                  561
BLAST score
E value
                  8.0e-58
                  127
Match length
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
```

- barley >qi 304220 (L12707) photosystem I PSI-K subunit

% identity

NCBI Description

[Hordeum vulgare] 400679 Seq. No. LIB3431-036-P1-K1-H9 Seq. ID BLASTX Method q1709846 NCBI GI BLAST score 164 3.0e-11 E value 121 Match length % identity 44 PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336) NCBI Description 22 kDa component of photosystem II [Lycopersicon esculentum] 400680 Seq. No. Seq. ID LIB3431-036-P1-N1-A1 Method BLASTN NCBI GI g576770 BLAST score 280 1.0e-156 E value Match length 304 98 % identity Oryza sativa clone ST1 sucrose-regulated mRNA, 3'-end NCBI Description sequence 400681 Seq. No. LIB3431-036-P1-N1-A11 Seq. ID BLASTX Method NCBI GI q2072555 BLAST score 237 1.0e-19 E value 44 Match length 100 % identity (AF001396) metallothionein-like protein [Oryza sativa] NCBI Description >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like protein [Oryza sativa] 400682 Seq. No. Seq. ID LIB3431-036-P1-N1-A4 Method BLASTX NCBI GI q6103011 BLAST score 515 2.0e-52 E value 115 Match length 48 % identity (X84225) precursor of photosystem II subunit (22KDa) NCBI Description [Nicotiana tabacum] 400683 Seq. No. LIB3431-036-P1-N1-A5 Seq. ID Method BLASTN q6016845 NCBI GI BLAST score 206 E value 1.0e-112 Match length 347

Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

BLAST score

237

```
Seq. No.
                  400684
                  LIB3431-036-P1-N1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  402
                  4.0e-39
E value
                  73
Match length
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  400685
Seq. No.
                  LIB3431-036-P1-N1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g730456
BLAST score
                  335
E value
                  3.0e-31
Match length
                  65
                  100
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S19
Seq. No.
                  400686
                  LIB3431-036-P1-N1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  532
E value
                  2.0e-54
Match length
                  103
                  95
% identity
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                  400687
                  LIB3431-036-P1-N1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914466
BLAST score
                  369
E value
                  3.0e-35
Match length
                  67
                  99
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                  (PSI-N) >qi 2981214 (AF052429) photosystem I complex PsaN
                  subunit precursor [Zea mays]
Seq. No.
                  400688
Seq. ID
                  LIB3431-036-P1-N1-B3
Method
                  BLASTX
NCBI GI
                  g2072555
```

```
E value
                  1.0e-19
Match length
                  44
% identity
                  100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >qi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  400689
Seq. No.
                  LIB3431-036-P1-N1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2306981
BLAST score
                  236
E value
                  1.0e-19
Match length
                  52
                  87
% identity
                  (AF010321) photosystem I antenna protein [Oryza sativa]
NCBI Description
                  400690
Seq. No.
Seq. ID
                  LIB3431-036-P1-N1-B5
                  BLASTX
Method
                  q132105
NCBI GI
                  443
BLAST score
                  7.0e-44
E value
Match length
                  80
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400691
                  LIB3431-036-P1-N1-B6
Seq. ID
Method
                  BLASTX
                  g4760553
NCBI GI
BLAST score
                  429
E value
                  3.0e-42
Match length
                  82
% identity
                  (AB019533) Nad-dependent formate dehydrogenase [Oryza
NCBI Description
                  sativa]
                  400692
Seq. No.
                  LIB3431-036-P1-N1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115794
BLAST score
                  550
E value
                  2.0e-56
Match length
                  111
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
NCBI Description
                  III CAB-13) >gi 72748 pir CDTO33 chlorophyll a/b-binding
                  protein type III precursor (cab-13) - tomato
```

```
[Lycopersicon esculentum]
                   400693
Seq. No.
                   LIB3431-036-P1-N1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   501
E value
                   1.0e-50
Match length
                   97
                   99
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
Seq. No.
                   400694
Seq. ID
                   LIB3431-036-P1-N1-C1
Method
                   BLASTN
NCBI GI
                   q1835730
BLAST score
                   197
E value
                   1.0e-106
Match length
                   277
                   93
% identity
NCBI Description
                   Oryza sativa photosystem II 10 kDa polypeptide mRNA,
                   complete cds
Seq. No.
                   400695
Seq. ID
                   LIB3431-036-P1-N1-C11
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   190
                   3.0e-14
E value
                   71
Match length
% identity
NCBI Description
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
         4
                   400696
Seq. No.
                   LIB3431-036-P1-N1-C12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q115813
BLAST score
                   209
                   2.0e-16
E value
                   69
Match length
% identity
                   67
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                   CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
                   400697
Seq. No.
                   LIB3431-036-P1-N1-C5
Seq. ID
Method
                   BLASTX
                   q119784
NCBI GI
BLAST score
                   312
                   2.0e-28
E value
```

>gi 19277 emb CAA42818 (X60275) LHCII type III

62

Match length

```
% identity
                    3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR
NCBI Description
                    (BETA-KETOACYL-ACP SYNTHASE I) (KAS I)
                    >gi_100555_pir__A39356 3-oxoacyl-[acyl-carrier-protein]
synthase (EC 2.3.1.41) I beta chain precursor, chloroplast
                    - barley >gi 167065 (M60410) beta-ketoacyl-ACP synthase I
                    [Hordeum vulgare]
Seq. No.
                    400698
Seq. ID
                    LIB3431-036-P1-N1-C9
Method
                    BLASTX
NCBI GI
                    q2511594
BLAST score
                    326
E value
                    4.0e-30
Match length
                    95
% identity
NCBI Description
                    (Y13694) multicatalytic endopeptidase complex, proteasome
                    precursor, beta subunit [Arabidopsis thaliana]
                    >gi_2827525_emb_CAA16533.1_ (AL021633) multicatalytic
                    endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S
                    proteasome subunit PBA1 [Arabidopsis thaliana]
Seq. No.
                    400699
                    LIB3431-036-P1-N1-D1
Seq. ID
Method
                    BLASTX
                    a4105561
NCBI GI
BLAST score
                    391
                    9.0e-38
E value
Match length
                    85
% identity
NCBI Description
                    (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
                    400700
Seq. No.
                    LIB3431-036-P1-N1-D10
Seq. ID
Method
                    BLASTX
NCBI GI
                    q3036942
BLAST score
                    363
E value
                    2.0e-34
Match length
                    71
% identity
                    (AB012636) light harvesting chlorophyll a/b-binding protein
NCBI Description
                    [Nicotiana sylvestris]
                    400701
Seq. No.
                    LIB3431-036-P1-N1-D11
Seq. ID
Method
                    BLASTX
NCBI GI
                    q482311
BLAST score
                    428
                    4.0e-42
E value
Match length
                    86
% identity
NCBI Description
                   photosystem II oxygen-evolving complex protein 1 - rice
                    (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                    complex protein 1 [Oryza sativa]
```

400702

Seq. No.

```
LIB3431-036-P1-N1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2529682
BLAST score
                  202
E value
                  1.0e-15
Match length
                  104
                  38
% identity
NCBI Description
                   (AC002535) unknown protein [Arabidopsis thaliana]
                  400703
Seq. No.
Seq. ID
                  LIB3431-036-P1-N1-D7
Method
                  BLASTX
NCBI GI
                  q3789954
BLAST score
                  181
E value
                  4.0e-13
Match length
                  32
                  100
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  400704
Seq. No.
                  LIB3431-036-P1-N1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  405
E value
                  1.0e-39
Match length
                  78
                  97
% identity
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  400705
                  LIB3431-036-P1-N1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3036946
BLAST score
                  321
E value
                  1.0e-29
Match length
                 .. 63
% identity
                  97
NCBI Description
                   (AB012637) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
Seq. No.
                  400706
                  LIB3431-036-P1-N1-E11
Seq. ID
Method
                  BLASTX
                  g6006310
NCBI GI
BLAST score
                  454
E value
                  4.0e-45
Match length
                  86
                  100
% identity
                  (AB018443) nonphototrophic hypocotyl 1b [Oryza sativa]
NCBI Description
                  400707
Seq. No.
Seq. ID
                  LIB3431-036-P1-N1-E2
Method
                  BLASTX
                  g4966372
NCBI GI
BLAST score
                  277
```

2.0e-24

E value

```
Match length
                  83
% identity
                  67
                  (AC006341) ESTs gb_N38586 and gb_N38613 come from this
NCBI Description
                  gene. [Arabidopsis thaliana]
                  400708
Seq. No.
Seq. ID
                  LIB3431-036-P1-N1-E5
Method
                  BLASTX
NCBI GI
                  q3047125
BLAST score
                  205
E value
                  6.0e-16
Match length
                  75
% identity
                  (AF058919) No definition line found [Arabidopsis thaliana]
NCBI Description
                  400709
Seq. No.
                  LIB3431-036-P1-N1-E8
Seq. ID
Method
                  BLASTX
                  q3461848
NCBI GI
BLAST score
                  210
                  1.0e-16
E value
                  75
Match length
                  64
% identity
                  (AC005315) putative ATPase [Arabidopsis thaliana]
NCBI Description
                  400710
Seq. No.
                  LIB3431-036-P1-N1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1071913
BLAST score
                  365
E value
                  1.0e-34
Match length
                  103
                  70
% identity
                  cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
NCBI Description
                  - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine
                  synthase [Spinacia oleracea]
Seq. No.
                  400711
                  LIB3431-036-P1-N1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q461595
BLAST score
                  220
E value
                  9.0e-18
                  98
Match length
                  49
% identity
                  ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II)
NCBI Description
                  >gi_479533_pir__S34473 H+-transporting ATP synthase (EC
                  3.6.1.34) chain 9 - spinach >gi_394755_emb_CAA50520
                  (X71397) CF(o)II ATP synthase subunit 9 [Spinacia oleracea]
                  400712
Seq. No.
                  LIB3431-036-P1-N1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2072555
                  237
BLAST score
                  1.0e-19
E value
Match length
```

E value

1.0e-36

```
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                   400713
Seq. No.
                  LIB3431-036-P1-N1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q482311
BLAST score
                   302
E value
                   2.0e-27
Match length
                   60
                   100
% identity
NCBI Description
                  photosystem II oxygen-evolving complex protein 1 - rice
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                   complex protein 1 [Oryza sativa]
                   400714
Seq. No.
                  LIB3431-036-P1-N1-F4
Seq. ID
Method
                  BLASTX
                   g3789952
NCBI GI
BLAST score
                   273
E value
                   6.0e-24
Match length
                  52
% identity
                  100
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
                   400715
Seq. No.
Seq. ID
                  LIB3431-036-P1-N1-F5
Method
                  BLASTN
                  g2662340
NCBI GI
BLAST score
                  71
E value
                  1.0e-31
Match length
                  215
                  83
% identity
NCBI Description
                  Oryza sativa mRNA for EF-1 alpha, complete cds
                  400716
Seq. No.
Seq. ID
                  LIB3431-036-P1-N1-F6
Method
                  BLASTX
NCBI GI
                  q2500724
BLAST score
                  182
                  3.0e-13
E value
Match length
                  39
                  87
% identity
                  PREPROTEIN TRANSLOCASE SECA SUBUNIT PRECURSOR
NCBI Description
                  >gi_2129894_pir__S72453 secA protein precursor - garden pea
                  >gi 1122325 emb CAA57798 (X82404) chloroplast SecA protein
                   [Pisum sativum]
                  400717
Seq. No.
Seq. ID
                  LIB3431-036-P1-N1-F8
                  BLASTX
Method
                  g671740
NCBI GI
BLAST score
                  382
```

Match length

95

```
70
Match length
                   99
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                   400718
Seq. No.
                  LIB3431-036-P1-N1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4314378
                  175
BLAST score
E value
                   2.0e-12
                  57
Match length
% identity
                   60
                   (AC006232) putative lipase [Arabidopsis thaliana]
NCBI Description
                  >gi 5306262 gb AAD41994.1 AC006233_5 (AC006233) putative
                  lipase [Arabidopsis thaliana]
                   400719
Seq. No.
                  LIB3431-036-P1-N1-G10
Seq. ID
                  BLASTX
Method
                  g2072555
NCBI GI
BLAST score
                  237
                   1.0e-19
E value
                   44
Match length
                   100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                   400720
Seq. No.
                  LIB3431-036-P1-N1-G4
Seq. ID
Method
                  BLASTX
                   g4079798
NCBI GI
BLAST score
                   354
                   2.0e-33
E value
                   68
Match length
                   100
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   400721
Seq. No.
                  LIB3431-036-P1-N1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3126854
BLAST score
                   520
                   6.0e-53
E value
                   99
Match length
                   98
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   400722
Seq. No.
                   LIB3431-036-P1-N1-G6
Seq. ID
Method
                   BLASTX
                   g3378650
NCBI GI
BLAST score
                   335
                   3.0e-31
E value
```

% identity

83

```
% identity
NCBI Description
                    (X97606) abscisic acid activated [Medicago sativa]
                    400723
Seq. No.
Seq. ID
                    LIB3431-036-P1-N1-G7
Method
                    BLASTX
NCBI GI
                    q2695931
BLAST score
                    504
                    5.0e-51
E value
                    106
Match length
                    89
% identity
NCBI Description
                    (AJ222779) hypothetical protein [Hordeum vulgare]
                    400724
Seq. No.
                    LIB3431-036-P1-N1-G9
Seq. ID
                    BLASTX
Method
NCBI GI
                    q6063542
BLAST score
                    390
E value
                    1.0e-37
Match length
                    71
                    100
% identity
                    (AP000615) EST C74302(E30840) corresponds to a region of
NCBI Description
                    the predicted gene.; similar to glyceraldehyde-3-phosphate
                    dehydrogenase. (M64118) [Oryza sativa]
                    400725
Seq. No.
                    LIB3431-036-P1-N1-H11
Seq. ID
Method
                    BLASTX
NCBI GI
                    g115774
BLAST score
                    189
E value
                    4.0e-14
Match length
                    65
% identity
                    57
                    CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE I
NCBI Description
                    CAB-13) (LHCP) >gi_72731_pir__CDPJ13 chlorophyll a/b-binding protein 13 precursor - petunia
                    >gi_20471_emb_CAA26210_ (X02357) cab 13 precursor
polypeptide (aa -33 to 233) [Petunia sp.]
                    400726
Seq. No.
Seq. ID
                    LIB3431-036-P1-N1-H12
Method
                    BLASTX
NCBI GI
                    q552740
BLAST score
                    197
E value
                    2.0e-15
Match length
                    56
% identity
                    75
NCBI Description
                    (M17841) ribosomal protein S7 [Zea mays]
                    400727
Seq. No.
                                                                            195
Seq. ID
                    LIB3431-036-P1-N1-H2
Method
                    BLASTX
NCBI GI
                    q6016428
BLAST score
                    301
E value
                    3.0e-27
Match length
                    63
```

```
NCBI Description
                  PUTATIVE CASEIN KINASE II BETA-4 CHAIN (CK II) >gi 3341688
                   (AC003672) putative casein kinase II beta subunit
                   [Arabidopsis thaliana]
                   400728
Seq. No.
Seq. ID
                   LIB3431-036-P1-N1-H3
Method
                   BLASTX
NCBI GI
                   g2582822
                   393
BLAST score
                   5.0e-38
E value
                   83
Match length
                   86
% identity
                   (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
NCBI Description
                   Protein of 32kDa) [Solanum tuberosum]
                   400729
Seq. No.
                   LIB3431-036-P1-N1-H4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3126854
BLAST score
                   287
                   1.0e-25
E value
Match length
                   54
% identity
                   100
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   400730
Seq. No.
                   LIB3431-036-P1-N1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3789954
BLAST score
                   431
E value
                   2.0e-42
Match length
                   81
% identity
NCBI Description
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                   sativa]
                   400731
Seq. No.
                   LIB3431-036-P1-N1-H6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q902200
BLAST score
                   44
E value
                   4.0e-16
Match length
                   48
% identity
                   49
NCBI Description
                  Z.mays complete chloroplast genome
Seq. No.
                   400732
                   LIB3431-036-P1-N1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q606817
BLAST score
                   491
E value
                   2.0e-49
Match length
                   92
% identity
                   (U08404) carbonic anhydrase [Oryza sativa]
NCBI Description
                   >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic
                   anhydrase 3 [Oryza sativa]
```

Seq. No.

```
Seq. No.
                   400733
Seq. ID
                  LIB3431-036-P1-N1-H8
Method
                  BLASTX
NCBI GI
                   g548605
BLAST score
                   473
E value
                   2.0e-47
Match length
                   113
                   85
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi 539055 pir A48527 photosystem I protein psaK precursor
                   - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
                   400734
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-A1
Method
                  BLASTX
NCBI GI
                   g671740
BLAST score
                   471
E value
                   2.0e-47
Match length
                  89
% identity
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
Seq. No.
                   400735
                   LIB3431-037-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g5262946
BLAST score
                   661
E value
                   2.0e-69
Match length
                  149
% identity
NCBI Description (Y19104) beta-alanine synthase [Lycopersicon esculentum]
                   400736
Seq. No.
                   LIB3431-037-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2984709
BLAST score
                  154
E value
                   1.0e-12
Match length
                  105
% identity
                   49
NCBI Description (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
Seq. No.
                   400737
                  LIB3431-037-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4996105
BLAST score
                  386
E value
                   3.0e-37
Match length
                  93
% identity
NCBI Description (AB014076) histidine decarboxylase [Brassica napus]
```

Method

BLASTX

```
LIB3431-037-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
                  290
BLAST score
E value
                  1.0e-40
Match length
                  138
% identity
                  71
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4.\overline{1}.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400739
Seq. ID
                  LIB3431-037-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g1076724
BLAST score
                  387
E value
                  2.0e-37
Match length
                  74
% identity
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                  >gi 666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                  400740
Seq. ID
                  LIB3431-037-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q3914603
BLAST score
                  735
E value
                  4.0e-78
Match length
                  142
                  99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
Seq. No.
                  400741
                  LIB3431-037-P1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q482311
BLAST score
                  320
E value
                  1.0e-29
Match length
                  64
% identity
                  100
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                  400742
Seq. No.
                  LIB3431-037-P1-K1-B10
Seq. ID
```

BLAST score

E value

388

2.0e-37

```
NCBI GI
                   g132105
BLAST score
                   614
                   6.0e-64
E value
                   132
Match length
                   88
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   400743
Seq. No.
Seq. ID
                   LIB3431-037-P1-K1-B12
Method
                   BLASTX
                   g3377815
NCBI GI
BLAST score
                   258
E value
                   3.0e-22
Match length
                   76
                   68
% identity
                   (AF076275) similar to protein kinases (Pfam: pkinase.hmm,
NCBI Description
                   score: 255.71) [Arabidopsis thaliana]
                   400744
Seq. No.
                   LIB3431-037-P1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   558
                   2.0e-57
E value
                   140
Match length
% identity
                   81
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   400745
Seq. ID
                   LIB3431-037-P1-K1-B3
Method
                   BLASTN
NCBI GI
                   g3885891
BLAST score
                   129
E value
                   2.0e-66
Match length
                   182
                   99
% identity
                   Oryza sativa photosystem-1 F subunit precursor (PSI-F)
NCBI Description
                   mRNA, complete cds
Seq. No.
                   400746
Seq. ID
                   LIB3431-037-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   q3789954
```

BLAST score

```
Match length
                   73
                   97
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
Seq. No.
                   400747
                   LIB3431-037-P1-K1-B5
Seq. ID
Method
                   BLASTX
                   q733454
NCBI GI
BLAST score
                   418
E value
                   5.0e-41
Match length
                   84
% identity
NCBI Description
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
Seq. No.
                   400748
Seq. ID
                   LIB3431-037-P1-K1-B7
Method
                   BLASTX
                   g100293
NCBI GI
BLAST score
                   320
                   2.0e-29
E value
Match length
                   80
% identity
                   40
                  ribonucleoprotein A, 29K - wood tobacco
NCBI Description
                  >gi_19754_emb_CAA43427_ (X61113) 29kD A ribonucleoprotein
[Nicotiana sylvestris]
Seq. No.
                   400749
Seq. ID
                   LIB3431-037-P1-K1-B9
Method
                  BLASTX
NCBI GI
                   g3913641
BLAST score
                   442
                   8.0e-44
E value
Match length
                   108
                   82
% identity
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                   >gi 3041777 dbj BAA25423 (AB007194)
                   fructose-1,6-bisphosphatase [Oryza sativa]
                   400750
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g2191138
BLAST score
                  148
E value
                   2.0e-09
Match length
                  56
% identity
                   (AF007269) A IG002N01.18 gene product [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                   400751
Seq. ID
                  LIB3431-037-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  q1617197
```

E value

3.0e-51

```
2.0e-09
E value
Match length
                  29
% identity
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
                  400752
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-C3
                  BLASTX
Method
NCBI GI
                  q5042409
BLAST score
                  425
                  9.0e-42
E value
Match length
                  139
% identity
                  61
NCBI Description
                  (ACO06193) Putative membrane related protein [Arabidopsis
                  thaliana]
                  400753
Seq. No.
                  LIB3431-037-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3776557
BLAST score
                  389
E value
                  1.0e-37
Match length
                  142
                  51
% identity
                  (ACO05388) Contains similarity to gi 2924495 hypothetical
NCBI Description
                  protein Rv1920 from Mycobacterium tuberculosis genome
                  gb AL022020. [Arabidopsis thaliana]
                  400754
Seq. No.
                  LIB3431-037-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3885892
BLAST score
                  284
E value
                  2.0e-35
Match length
                  104
% identity
                  72
NCBI Description (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
                  400755
Seq. No.
                  LIB3431-037-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5882720
BLAST score
                  294
                  2.0e-26
E value
                  99
Match length
% identity
NCBI Description
                  (AC008263) Similar to gb D86180 phosphoribosylanthranilate
                  transferase from Pisum sativum and contains 2 PF 00168 C2
                   (phospholipid binding) domains. ESTs gb H76726, gb T45544
                  and gb N96377 come from this gene. [Arab
Seq. No.
                  400756
                  LIB3431-037-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  506
```

```
Match length
                  143
% identity
                  70
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                  400757
Seq. ID
                  LIB3431-037-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q3789952
BLAST score
                  490
E value
                  2.0e-49
Match length
                  114
% identity
                  86
NCBI Description
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                  sativa]
                  400758
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  631
E value
                  6.0e-66
Match length
                  116
% identity
                  100
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400759
Seq. ID
                  LIB3431-037-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  q115796
BLAST score
                  785
E value
                  5.0e-84
Match length
                  148
% identity
                  98
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I
                  CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II
                  light-harvesting chlorophyll a/b-binding protein [Oryza
                  sativa]
Seq. No.
                  400760
Seq. ID
                  LIB3431-037-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  557
E value
                  3.0e-57
Match length
                  133
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
```

protein 2R precursor - rice >gi_20182 emb CAA32109

```
(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                  400761
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g5734758
                  321
BLAST score
E value
                  1.0e-29
Match length
                  155
% identity
                   41
                   (AC007651) Similar to tuftelin-interacting protein
NCBI Description
                   [Arabidopsis thaliana]
                  400762
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q3335335
                  190
BLAST score
E value
                  3.0e-14
Match length
                  61
% identity
                  62
                   (AC004512) ESTs gb F14113 and gb T42122 come from this
NCBI Description
                  region. [Arabidopsis thaliana]
                  400763
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-D7
                  BLASTX
Method
NCBI GI
                  g3435096
BLAST score
                  273
E value
                   6.0e-24
Match length
                  101
% identity
                  55
                  (AF033587) SRZ21 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  400764
Seq. ID
                  LIB3431-037-P1-K1-E1
                  BLASTX
Method
NCBI GI
                  g1653513
BLAST score
                  158
E value
                  2.0e-10
Match length
                  81
% identity
                  41
                  (D90914) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                  400765
Seq. ID
                  LIB3431-037-P1-K1-E10
                  BLASTN
Method
NCBI GI
                  g6015437
BLAST score
                  35
E value
                  6.0e-10
Match length
                  35
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  400766
Seq. ID
                  LIB3431-037-P1-K1-E11
```

% identity

```
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  748
                  1.0e-79
E value
Match length
                  157
                  90
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400767
Seq. ID
                  LIB3431-037-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g3894193
BLAST score
                  152
                  9.0e-10
E value
                  117
Match length
% identity
                  38
NCBI Description
                  (AC005662) putative strictosidine synthase [Arabidopsis
                  thaliana]
                  400768
Seq. No.
                  LIB3431-037-P1-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3075487
BLAST score
                  59
E value
                  2.0e-24
Match length
                  187
% identity
                  83
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
                  mRNA, complete cds
Seq. No.
                  400769
                  LIB3431-037-P1-K1-E3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2239152
BLAST score
                  290
E value
                  1.0e-162
Match length
                  306
% identity
                  99
NCBI Description
                  O.sativa mRNA for putative T3/T7-like RNA polymerase,
                  partial
Seq. No.
                  400770
Seq. ID
                  LIB3431-037-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  667
E value
                  4.0e-70
Match length
                  142
```

Match length

```
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4\overline{.1}.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  400771
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g132105
                  286
BLAST score
                  2.0e-25
E value
Match length
                  118
                  59
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                 - (RUBISCO SMALL SUBUNIT C) >gi 68094 pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400772
Seq. ID
                  LIB3431-037-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q1076724
BLAST score
                  410
E value
                  5.0e-40
Match length
                  78
% identity
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                  >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                  400773
Seq. ID
                  LIB3431-037-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q461999
BLAST score
                  708
E value
                  6.0e-75
Match length
                  154
% identity
                  90
NCBI Description ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)
Seq. No.
                  400774
Seq. ID
                  LIB3431-037-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g118170
BLAST score
                  429
                  3.0e-42
E value
```

Seq. No.

```
% identity
                    85
                    CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I)
NCBI Description
                    >gi_82491_pir__A28464 oryzacystatin - rice >gi 169784
                    (J0\overline{3}469) oryzacystatin [Oryza sativa] >gi_1698\overline{0}7 (M29259)
                    oryzastatin [Oryza sativa] >gi_259137_bbs_120195 (S49967)
                    oryzacystatin=cysteine protease inhibitor [Oryza=rice,
                    Peptide, 102 aa] [Oryza] >gi 1280613 (U54702) oryzacystatin
                    [Oryza sativa]
                    400775
Seq. No.
Seq. ID
                    LIB3431-037-P1-K1-F1
                    BLASTX
Method
NCBI GI
                    q1076724
                    548
BLAST score
                    3.0e-56
E value
                    102
Match length
                    96
% identity
                    LHCI-680, photosystem I antenna protein - barley
NCBI Description
                    >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
antenna protein [Hordeum vulgare]
Seq. No.
                    400776
                    LIB3431-037-P1-K1-F10
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2288969
BLAST score
                    390
E value
                    1.0e-37
Match length
                    118
% identity
                    65
NCBI Description
                    (Y12862) glutathione transferase [Zea mays]
Seq. No.
                    400777
                    LIB3431-037-P1-K1-F11
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4469020
BLAST score
                    314
E value
                    9.0e-29
                    72
Match length
% identity
                    (AL035602) putative protein (fragment) [Arabidopsis
NCBI Description
                    thaliana]
Seq. No.
                    400778
                    LIB3431-037-P1-K1-F2
Seq. ID
Method
                    BLASTX
NCBI GI
                    q115787
BLAST score
                    470
E value
                    4.0e-47
Match length
                    126
% identity
                    CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                    CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
```

```
LIB3431-037-P1-K1-F3
Seq. ID
Method
                  BLASTX
                  g1706260
NCBI GI
BLAST score
                   768
E value
                   5.0e-82
Match length
                  156
% identity
                   89
NCBI Description
                  CYSTEINE PROTEINASE 1 PRECURSOR >qi 2118131 pir S59597
                  cysteine proteinase 1 precursor - maize
                  >gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea
                  mays]
                   400780
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-F4
Method
                  BLASTN
NCBI GI
                  g11957
BLAST score
                   467
E value
                  0.0e + 00
Match length
                   475
                   100
% identity
NCBI Description
                  Rice complete chloroplast genome
                   400781
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                   472
                   3.0e-47
E value
Match length
                  125
                  78
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
Seq. No.
                  400782
Seq. ID
                  LIB3431-037-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g3738304
BLAST score
                  270
                  1.0e-23
E value
Match length
                  143
% identity
                   42
NCBI Description
                   (AC005309) hypothetical protein [Arabidopsis thaliana]
                  400783
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  237
                  1.0e-19
E value
Match length
                  44
                  100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa] .
NCBI Description
                  >gi 6103441 gb AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
```

```
400784
Seq. No.
                  LIB3431-037-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417260
BLAST score
                  421
E value
                  3.0e-41
Match length
                  128
% identity
                  66
NCBI Description
                  LIGHT REGULATED PROTEIN PRECURSÖR >gi 422003 pir S33632
                  lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                  light-regulated gene [Oryza sativa]
Seq. No.
                  400785
Seq. ID
                  LIB3431-037-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2347098
BLAST score
                  448
E value
                  2.0e-44
Match length
                  94
% identity
                  86
                  (U76845) ubiquitin-specific protease [Arabidopsis thaliana]
NCBI Description
                  >gi 4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific
                  protease (AtUBP3) [Arabidopsis thaliana]
                  400786
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-G12
                  BLASTX
Method
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  1.0e-19
Match length
                  44
% identity
                  100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  400787
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  520
E value
                  6.0e-53
Match length
                  138
% identity
                  76
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                  - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
                  400788
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g2565436
BLAST score
                  159
E value
                  1.0e-10
Match length
                  99
```

E value

6.0e-72

```
% identity
NCBI Description (AF028842) DegP protease precursor [Arabidopsis thaliana]
                  400789
                  LIB3431-037-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1708191
BLAST score
                  428
E value
                  4.0e-42
Match length
                  135
% identity
                  55
                  HEXOSE CARRIER PROTEIN HEX6 >gi 467319 (L08188) hexose
NCBI Description
                  carrier protein [Ricinus communis]
Seq. No.
                  400790
Seq. ID
                  LIB3431-037-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q548603
BLAST score
                  698
E value
                  2.0e-75
Match length
                  148
% identity
                  97
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                  barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]
                  400791
Seq. No.
                  LIB3431-037-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3603401
BLAST score
                  414
E value
                  2.0e-40
Match length
                  131
% identity
NCBI Description (AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]
Seq. No.
                  400792
Seq. ID
                  LIB3431-037-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  546
E value
                  6.0e-56
Match length
                  123
% identity
NCBI Description chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  400793
Seq. No.
Seq. ID
                  LIB3431-037-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g3294467
BLAST score
                  682
```

```
Match length
                    148
                    89
% identity
                    (U89341) phosphoglucomutase 1 [Zea mays]
NCBI Description
Seq. No.
                    400794
Seq. ID
                    LIB3431-037-P1-K1-H11
Method
                    BLASTX
NCBI GI
                    q3126854
BLAST score
                    660
                    5.0e-75
E value
Match length
                    143
% identity
                    99
                    (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   400795
Seq. No.
                   LIB3431-037-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                    g733454
BLAST score
                    569
E value
                    1.0e-58
Match length
                    131
                    82
% identity
                    (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                    [Zea mays]
                    400796
Seq. No.
Seq. ID
                   LIB3431-037-P1-K1-H3
Method
                   BLASTX
NCBI GI
                    g131388
BLAST score
                    294
E value
                    1.0e-26
Match length
                    115
% identity
                    61
NCBI Description
                   OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                    SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                    THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260
                   photosystem II oxygen-evolving complex protein 1 - common
                   wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
33kDa oxygen evolving protein of photosystem II [Triticum
                    aestivum]
                    400797
Seq. No.
Seq. ID
                   LIB3431-037-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g1561774
                    733
BLAST score
E value
                    7.0e-78
Match length
                    161
% identity
                    81
NCBI Description
                    (U67426) malate dehydrogenase [Vitis vinifera]
                    400798
Seq. No.
Seq. ID
                   LIB3431-037-P1-K1-H7
                   BLASTX
Method
NCBI GI
                   g548605
BLAST score
                    485
```

6.0e-54

E value

```
133
 Match length
 % identity
                    87
                    PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 NCBI Description
                    (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                    >gi_539055_pir__A48527 photosystem I protein psaK precursor
                    - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                    [Hordeum vulgare]
                    400799
 Seq. No.
 Seq. ID
                    LIB3431-037-P1-K1-H8
 Method
                    BLASTX
 NCBI GI
                    q3757515
 BLAST score
                    536
                    8.0e-55
 E value
 Match length
                    130
                    75
 % identity
 NCBI Description
                    (AC005167) hypothetical protein [Arabidopsis thaliana]
                    >gi 4581130 gb AAD24620.1 AC005825 27 (AC005825)
                    hypothetical protein [Arabidopsis thaliana]
                    400800
 Seq. No.
                    LIB3431-037-P1-K1-H9
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q132105
                    604
 BLAST score
                    9.0e-63
 E value
                    130
 Match length
                    88
 % identity
 NCBI Description
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                    (RUBISCO SMALL SUBUNIT C) >gi_68094 pir RKRZS9
                    ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
                    400801
 Seq. No.
                    LIB3431-037-P1-N1-A1
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g347451
                    202
 BLAST score
 E value
                    8.0e-16
 Match length
                    38
 % identity
                    100
 NCBI Description
                    (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                    sativa]
                    400802
 Seq. No.
 Seq. ID
                    LIB3431-037-P1-N1-A12
 Method
                    BLASTN
 NCBI GI
                    g11957
 BLAST score
                    168
 E value
                    3.0e-89
 Match length
                    284
                    45
% identity
```

```
NCBI Description Rice complete chloroplast genome
Seq. No.
                  400803
Seq. ID
                  LIB3431-037-P1-N1-A4
Method
                  BLASTX
NCBI GI
                  q4996105
BLAST score
                  316
E value
                  5.0e-29
Match length
                  77
                  73
% identity
NCBI Description (AB014076) histidine decarboxylase [Brassica napus]
                  400804
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-A5
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  336
E value
                  3.0e - 31
Match length
                  84
                  80
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  400805
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-A8
Method
                  BLASTX
NCBI GI
                  g167097
BLAST score
                  151
E value
                  7.0e-22
                  70
Match length
                  79
% identity
NCBI Description
                  (M55449) ribulose 1,5-bisphosphate carboxylase activase
                  [Hordeum vulgare]
                  400806
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-B1
Method
                  BLASTX
NCBI GI
                  g482311
BLAST score
                  320
E value
                  2.0e-29
Match length
                  64
                  100
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                  (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                  400807
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-B10
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  397
E value
                  2.0e-38
Match length
                  72
                  100
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
```

NCBI GI

E value

BLAST score

g5042409

4.0e-09

147

```
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  400808
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-B2
Method
                  BLASTX
NCBI GI
                  q693920
BLAST score
                  374
                  9.0e-36
E value
Match length
                  71
% identity
                  100
NCBI Description
                  (U21113) chlorophyll a/b binding protein [Solanum
                  tuberosum]
Seq. No.
                  400809
                  LIB3431-037-P1-N1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3885891
BLAST score
                  262
                  1.0e-145
E value
                  330
Match length
                  95
% identity
NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                  mRNA, complete cds
                  400810
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-B5
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                  397
                  1.0e-38
E value
Match length
                  84
                  92
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
Seq. No.
                  400811
                  LIB3431-037-P1-N1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2191138
BLAST score
                  253
E value
                  1.0e-21
                  73
Match length
% identity
                  (AF007269) A IG002N01.18 gene product [Arabidopsis
NCBI Description
                  thaliana]
                  400812
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-C3
Method
                  BLASTX
```

precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)

(D00643) small subunit of ribulose-1,5-bisphosphate

```
Match length
                   41
% identity
                   66
                   (AC006193) Putative membrane related protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  400813
                  LIB3431-037-P1-N1-C6
Seq. ID
Method
                  BLASTX
                  q3885892
NCBI GI
BLAST score
                  471
E value
                   4.0e-47
                  89
Match length
% identity
                  100
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
                  400814
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-C8
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  182
                  2.0e-13
E value
Match length
                  34
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                  400815
Seq. No.
                  LIB3431-037-P1-N1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3885886
BLAST score
                  199
E value
                  3.0e-15
Match length
                  35
% identity
                  100
NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
                  400816
Seq. No.
                  LIB3431-037-P1-N1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3789952
BLAST score
                  203
                  1.0e-15
E value
                  37
Match length
                  100
% identity
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                  sativa]
                  400817
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-D10
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  263
E value
                  9.0e-23
                  51
Match length
                  100
% identity
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
```

```
400818
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-D11
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                   345
                   2.0e-32
E value
Match length
                   65
% identity
                   100
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                   400819
Seq. No.
                  LIB3431-037-P1-N1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3036942
BLAST score
                  216
                   2.0e-17
E value
Match length
                   45
                   89
% identity
                  (AB012636) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                   400820
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-D3
                  BLASTN
Method
NCBI GI
                  g342643
                  34
BLAST score
E value
                   2.0e-09
                  106
Match length
% identity
                   83
NCBI Description Maize mitochondrion with chloroplast insert containing
                  rRNAs
Seq. No.
                   400821
Seq. ID
                  LIB3431-037-P1-N1-D8
Method
                  BLASTX
NCBI GI
                  g2501190
BLAST score
                  202
E value
                   1.0e-15
Match length
                   60
% identity
                   72
                  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
NCBI Description
                   >gi 2130147 pir S61420 thiamine biosynthetic enzyme thi1-2
                   - maize >gi 596080 (U17351) thiamine biosynthetic enzyme
                   [Zea mays]
Seq. No.
                   400822
                  LIB3431-037-P1-N1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g132105
BLAST score
                   443
E value
                   7.0e-44
                  80
Match length
                   100
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{EC} 4.\overline{1}.1.39) small chain
```

23 mm - 1 - 1 - 1 - 1

precursor (clone pOSSS1139) - rice >gi 218208 dbj_BAA00538_

```
sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                   400823
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-E2
Method
                  BLASTN
NCBI GI
                  q3075487
BLAST score
                   60
                   5.0e-25
E value
                   92
Match length
                   91
% identity
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                  mRNA, complete cds
                   400824
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-E5
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                   637
E value
                  1.0e-66
                  117
Match length
                   100
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                   400825
Seq. ID
                  LIB3431-037-P1-N1-E6
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                   462
                   4.0e-46
E value
Match length
                  84
                   100
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                   400826
Seq. ID
                  LIB3431-037-P1-N1-E7
Method
                  BLASTX
NCBI GI
                  g1076724
BLAST score
                   405
E value
                   2.0e-39
Match length
                  78
                   94
% identity
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                  >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
                   400827
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-E8
Method
                  BLASTX
NCBI GI
                  g461999
```

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

169

6.0e-12

BLAST score

E value

```
44
Match length
                  75
% identity
NCBI Description ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)
                  400828
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-F1
Method
                  BLASTX
NCBI GI
                  g2306981
BLAST score
                  342
                  5.0e-32
E value
Match length
                  87
% identity
                  72
NCBI Description (AF010321) photosystem I antenna protein [Oryza sativa]
                  400829
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-F10
Method
                  BLASTX
NCBI GI
                  g2288969
BLAST score
                  281
                  7.0e-25
E value
                  127
Match length
                   47
% identity
                  (Y12862) glutathione transferase [Zea mays]
NCBI Description
                  400830
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-F11
Method
                  BLASTX
NCBI GI
                  g4469020
                  258
BLAST score
                   3.0e-22
E value
                  59
Match length
                  83
% identity
                   (AL035602) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                   400831
Seq. No.
                  LIB3431-037-P1-N1-F2
Seq. ID
                  BLASTN
Method
NCBI GI
                  q20181
BLAST score
                  87
E value
                   4.0e-41
Match length
                  167
% identity
                  88
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
Seq. No.
                  400832
Seq. ID
                  LIB3431-037-P1-N1-F3
Method
                  BLASTX
NCBI GI
                  g1706260
BLAST score
                  442
E value
                  9.0e-44
Match length
                  82
% identity
                  95
                  CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597
NCBI Description
                  cysteine proteinase 1 precursor - maize
                  >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
```

```
mays]
                   400833
Seq. No.
                   LIB3431-037-P1-N1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g128690
                   533
BLAST score
                   2.0e-54
E value
                   120
Match length
% identity
                   NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST
NCBI Description
                   >gi 66161 pir DERZN3 NADH dehydrogenase (ubiquinone) (EC
                   1.6.5.3) chain 3 - rice chloroplast >gi 11989 emb CAA34001
                   (X15901) ndhC; NADH dehydrogenase ND3 [Oryza sativa]
                   >gi 226610 prf 1603356AG NADH dehydrogenase ND3 [Oryza
                   satīva]
                   400834
Seq. No.
Seq. ID
                   LIB3431-037-P1-N1-F5
                   BLASTX
Method
NCBI GI
                   g131176
                   333
BLAST score
                   6.0e-31
E value
Match length
                   65
% identity
                   97
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                   >gi 72683 pir F1BH4 photosystem I chain IV precursor -
                  barley >gi 19087 emb CAA68782 (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi 226163 prf 1413233A
                   10.8kD photosystem I protein (Hordeum vulgare var.
                   distichum]
Seq. No.
                   400835
Seq. ID
                   LIB3431-037-P1-N1-F6
Method
                   BLASTX
NCBI GI
                   q548605
BLAST score
                   277
E value
                   2.0e-24
Match length
                   59
% identity
                   90
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi 539055 pir A48527 photosystem I protein psaK precursor
                   - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
                   400836
Seq. No.
                   LIB3431-037-P1-N1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   1.0e-19
Match length
                   44
% identity
                   100
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
```

```
protein [Oryza sativa]
Seq. No.
                   400837
Seq. ID
                   LIB3431-037-P1-N1-F9
Method
                   BLASTX
NCBI GI
                   g417260
BLAST score
                   400
                   7.0e-39
E value
Match length
                   120
                   68
% identity
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                   lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                   light-regulated gene [Oryza sativa]
                   400838
Seq. No.
Seq. ID
                   LIB3431-037-P1-N1-G1
Method
                   BLASTN
NCBI GI
                   g2950394
BLAST score
                   35
E value
                   5.0e-10
Match length
                   51
                   92
% identity
NCBI Description
                   Zea mays me gene, exons 1 to
                   400839
Seq. No.
Seq. ID
                   LIB3431-037-P1-N1-G10
Method
                   BLASTX
NCBI GI
                   g2347098
BLAST score
                   245
E value
                   1.0e-20
Match length
                   52
% identity
NCBI Description
                   (U76845) ubiquitin-specific protease [Arabidopsis thaliana]
                   >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific
                   protease (AtUBP3) [Arabidopsis thaliana]
                   400840
Seq. No.
Seq. ID
                   LIB3431-037-P1-N1-G12
Method
                   BLASTN
NCBI GI
                   g2072554
BLAST score
                   220
E value
                   1.0e-120
Match length
                   243
                   98
% identity
NCBI Description
                   Oryza sativa metallothionein-like protein mRNA, complete
                   cds
                   400841
Seq. No.
Seq. ID
                   LIB3431-037-P1-N1-G2
                   BLASTN
Method
NCBI GI
                   q596079
BLAST score
                   44
                   2.0e-15
E value
Match length
                   76
                   89
% identity
NCBI Description
                   Zea mays thiamine biosynthetic enzyme (thi1-2) mRNA,
```

complete cds

```
400842
Seq. No.
Seq. ID
                   LIB3431-037-P1-N1-G3
Method
                   BLASTX
NCBI GI
                   g2565436
BLAST score
                   158
E value
                   2.0e-10
                   91
Match length
% identity
                  (AF028842) DegP protease precursor [Arabidopsis thaliana]
NCBI Description
                   400843
Seq. No.
Seq. ID
                   LIB3431-037-P1-N1-G5
                   BLASTX
Method
NCBI GI
                   g1708191
BLAST score
                   396
                   2.0e-38
E value
Match length
                   104
                   68
% identity
                  HEXOSE CARRIER PROTEIN HEX6 >gi 467319 (L08188) hexose
NCBI Description
                   carrier protein [Ricinus communis]
                   400844
Seq. No.
Seq. ID
                   LIB3431-037-P1-N1-G7
Method
                   BLASTX
NCBI GI
                   q548603
BLAST score
                   565
                   3.0e-58
E value
Match length
                   110
                   97
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                   >gi 478404_pir__JQ2247 photosystem I chain D precursor -
                   barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
                   400845
Seq. No.
Seq. ID
                   LIB3431-037-P1-N1-G8
                   BLASTX
Method
NCBI GI
                   g1168732
BLAST score
                   289
                   8.0e-26
E value
Match length
                   128
                   49
% identity
                  CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi 421914 pir S28045
NCBI Description
                  ELI3 protein - parsley (fragment) >gi_836638_emb_CAA48028_ (X67817) Eli3 [Petroselinum crispum]
                   400846
Seq. No.
Seq. ID
                   LIB3431-037-P1-N1-G9
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   513
E value
                   4.0e-52
                   98
Match length
                   100
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
```

```
protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                  400847
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-H1
Method
                  BLASTX
NCBI GI
                  g3294467
                  369
BLAST score
                  3.0e - 35
E value
                  78
Match length
% identity
NCBI Description (U89341) phosphoglucomutase 1 [Zea mays]
                  400848
Seq. No.
                  LIB3431-037-P1-N1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g517500
                  190
BLAST score
                  5.0e-23
E value
                  94
Match length
% identity
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
                  400849
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-H11
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  415
                  1.0e-40
E value
                  79
Match length
% identity
                  99
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  400850
Seq. No.
                  LIB3431-037-P1-N1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                  402
E value
                  3.0e-39
Match length
                  81
% identity
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
                  400851
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-H3
Method
                  BLASTX
NCBI GI
                  g482311
BLAST score
                  374
E value
                  8.0e-36
Match length
                  74
                  100
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                  (strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving
```

E value

8.0e-28

complex protein 1 [Oryza sativa]

```
400852
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-H4
Method
                  BLASTX
NCBI GI
                  q1708924
BLAST score
                  252
                  2.0e-21
E value
                  54
Match length
                  87
% identity
                  MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT
NCBI Description
                  MALIC ENZYME) (NADP-ME) >gi 515759 (L34836) malate
                  dehydrogenase (NADP+) [Vitis vinifera]
                  400853
Seq. No.
Seq. ID
                  LIB3431-037-P1-N1-H5
                  BLASTX
Method
NCBI GI
                  g671740
                                  13.7
BLAST score
                  202
E value
                  1.0e-15
Match length
                  38
% identity
                  100
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                  400854
Seq. ID
                  LIB3431-037-P1-N1-H6
                  BLASTX
Method
NCBI GI
                  g4206195
BLAST score
                  213
                  5.0e-17
E value
Match length
                  54
                  67
% identity
NCBI Description
                   (AF071527) hypothetical protein [Arabidopsis thaliana]
                  >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein
                  [Arabidopsis thaliana]
Seq. No.
                  400855
                  LIB3431-037-P1-N1-H7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q548605
BLAST score
                  493
                  8.0e-50
E value
Match length
                  109
                  90
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                  - barley >qi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
Seq. No.
                  400856
Seq. ID
                  LIB3431-037-P1-N1-H8
Method
                  BLASTX
NCBI GI
                  g3757515
BLAST score
                  305
```

```
Match length
                  73
                  77
% identity
                  (AC005167) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4581130 gb AAD24620.1 AC005825 27 (AC005825)
                  hypothetical protein [Arabidopsis thaliana]
                  400857
Seq. No.
                  LIB3431-037-P1-N1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  264
E value
                  5.0e-23
Match length
                  53
% identity
                  96
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  400858
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-A1
Method
                  BLASTX
                  g166410
NCBI GI
BLAST score
                  443
E value
                  6.0e-44
Match length
                  118
                  71
% identity
NCBI Description
                 (L07291) Alfin-1 [Medicago sativa]
                  400859
Seq. No.
                  LIB3431-038-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3075488
BLAST score
                  634
                  2.0e-66
E value
Match length
                  117
% identity
                  100
NCBI Description
                 (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                  400860
Seq. ID
                  LIB3431-038-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g3367596
BLAST score
                  394
E value
                  3.0e-38
Match length
                  121
% identity
NCBI Description (AL031135) putative protein [Arabidopsis thaliana]
Seq. No.
                  400861
Seq. ID
                  LIB3431-038-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g729535
BLAST score
                  223
E value
                  4.0e-18
Match length
                  76
                  58
% identity
NCBI Description
                  FERREDOXIN-THIOREDOXIN REDUCTASE, CATALYTIC CHAIN PRECURSOR
```

(FTR-C) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT B)

Seq. ID

```
(FTR-B)
                  400862
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  g5852170
BLAST score
                  79
                  3.0e-36
E value
                  150
Match length
                  34
% identity
NCBI Description Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                  clone:t17804
                  400863
Seq. No.
                  LIB3431-038-P1-K1-A3
Seq. ID
                  BLASTX
Method
                  g3548808
NCBI GI
                  322
BLAST score
                  8.0e-30
E value
Match length
                  81
                  67
% identity
                  (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
                  400864
Seq. No.
                  LIB3431-038-P1-K1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5031281
BLAST score
                  274
                  4.0e-24
E value
Match length
                  71
                  75
% identity
NCBI Description
                  (AF139499) unknown [Prunus armeniaca]
Seq. No.
                  400865
Seq. ID
                  LIB3431-038-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g2293480
BLAST score
                  431
E value
                  2.0e-42
                  85
Match length
% identity
                  98
NCBI Description (AF011331) glycine-rich protein [Oryza sativa]
                  400866
Seq. No.
                  LIB3431-038-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g282882
BLAST score
                  175
E value
                  2.0e-12
Match length
                  105
% identity
                  37
NCBI Description
                  receptor-like protein kinase precursor - Arabidopsis
                  thaliana >qi 166848 (M84659) receptor-like protein kinase
                  [Arabidopsis thaliana]
                  400867
Seq. No.
                  LIB3431-038-P1-K1-A8
```

Match length

```
Method
                   BLASTX
NCBI GI
                   g3822223
BLAST score
                   444
                   4.0e-44
E value
                   123
Match length
                   61
% identity
NCBI Description
                   (AF077955) branched-chain alpha keto-acid dehydrogenase E1
                   alpha subunit [Arabidopsis thaliana]
                   400868
Seq. No.
Seq. ID
                   LIB3431-038-P1-K1-B1
Method
                   BLASTX
                   g2293480
NCBI GI
BLAST score
                   431
                   1.0e-42
E value
                   85
Match length
% identity
NCBI Description
                   (AF011331) glycine-rich protein [Oryza sativa]
                   400869
Seq. No.
Seq. ID
                   LIB3431-038-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g4689384
BLAST score
                   231
E value
                   4.0e-19
                   43
Match length
                   100
% identity
                   (AF139467) LHCII type I chlorophyll a/b binding protein
NCBI Description
                   [Vigna radiata]
                   400870
Seq. No.
                   LIB3431-038-P1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5734748
BLAST score
                   206
E value
                   4.0e-16
                   129
Match length
                   36
% identity
                   (AC007651) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   400871
                   LIB3431-038-P1-K1-B3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4959460
BLAST score
                   35
E value
                   5.0e-10
Match length
                   35
% identity
                   100
                   Zea mays RACB small GTP binding protein mRNA, complete cds
NCBI Description
                   400872
Seq. No.
Seq. ID
                   LIB3431-038-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g2501190
BLAST score
                   602
                   1.0e-62
E value
```

Match length

```
85
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
NCBI Description
                  >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
                  - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  400873
Seq. ID
                  LIB3431-038-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q448445
                  229
BLAST score
                  7.0e-19
E value
Match length
                  62
% identity
                  69
NCBI Description CFO ATP synthase:SUBUNIT=9 [Spinacia oleracea]
                  400874
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g710308
BLAST score
                  732
                  8.0e-78
E value
                  143
Match length
% identity
                  97
NCBI Description
                  (U11693) victorin binding protein [Avena sativa]
Seq. No.
                  400875
                  LIB3431-038-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g400879
BLAST score
                  383
                  6.0e-37
E value
                  135
Match length
% identity
                  60
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                   (PSI-N) >gi_479690_pir__S35159 photosystem I chain psaN -
                  barley >gi 19095 emb CAA47056 (X66428) photosystem I
                  subunit N [Hordeum vulgare]
Seq. No.
                  400876
Seq. ID
                  LIB3431-038-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g4115918
BLAST score
                  213
E value
                  6.0e-17
Match length
                  50
% identity
                  82
                   (AF118222) similar to nascent polypeptide associated
NCBI Description
                  complex alpha chain [Arabidopsis thaliana]
                  400877
Seq. No.
                  LIB3431-038-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  759
                  5.0e-81
E value
```

```
100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  400878
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g167097
BLAST score
                  188
E value
                  9.0e-27
                  76
Match length
% identity
                  82
                  (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                  [Hordeum vulgare]
                  400879
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q4204263
BLAST score
                  349
E value
                  6.0e-33
Match length
                  113
% identity
                  60
NCBI Description
                  (AC005223) 40409 [Arabidopsis thaliana]
Seq. No.
                  400880
Seq. ID
                  LIB3431-038-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  8.0e-20
Match length
                  44
% identity
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  400881
Seq. ID
                  LIB3431-038-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  333
E value
                  4.0e-31
Match length
                  92
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
```

[Oryza sativa]

>gi_227611_prf__1707316A chlorophyll a/b binding protein 1

```
400882
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                  191
E value
                  2.0e-14
Match length
                  38
                  97
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
                  400883
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-C4
                  BLASTX
Method
                  g417260
NCBI GI
BLAST score
                  176
                  7.0e-13
E value
                  38
Match length
% identity
                  84
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                  lir1 protein - rice >gi 20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
Seq. No.
                  400884
Seq. ID
                  LIB3431-038-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  508
E value
                  1.0e-51
Match length
                  135
                  73
% identity
NCBI Description
                 (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                  400885
                  LIB3431-038-P1-K1-C6
Seq. ID
Method
                  BLASTX
                  q4678364
NCBI GI
BLAST score
                  220
E value
                  8.0e-18
Match length
                  71
% identity
NCBI Description
                 (AL049659) putative protein [Arabidopsis thaliana]
                  400886
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g130274
BLAST score
                  337
E value
                  1.0e-31
Match length
                  63
% identity
                  100
                  PLASTOCYANIN >qi 82500 pir S06105 plastocyanin - rice
NCBI Description
                  400887
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-D1
Method
                  BLASTX
```

```
g4056488
NCBI GI
BLAST score
                   477
E value
                   6.0e-48
                  105
Match length
% identity
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]
                  400888
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  q3063523
BLAST score
                  50
                   6.0e-19
E value
Match length
                  138
                  84
% identity
                  Oryza sativa ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
                  400889
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3075488
BLAST score
                  483
E value
                  1.0e-48
Match length
                  93
                  100
% identity
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                  400890
Seq. ID
                  LIB3431-038-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  552
E value
                   9.0e-57
Match length
                  117
% identity
                   90
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4\overline{.1}.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  400891
Seq. ID
                  LIB3431-038-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q3914587
BLAST score
                  254
                  9.0e-22
E value
Match length
                  112
                  50
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT) >gi_1076711_pir__S49992
```

ribulose-1,5-bisphosphate carboxylase/oxygenase - Aegilops

```
squarrosa >gi 599620 emb_CAA58150_ (X83095) rbcS gene
                   [Aegilops squarrosa]
                  400892
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  586
                  1.0e-60
E value
                  144
Match length
                  78
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  400893
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-D7
                  BLASTX
Method
NCBI GI
                  g4582445
BLAST score
                  269
                  2.0e-23
E value
                  64
Match length
                  70
% identity
                   (AC007071) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4589952 gb AAD26470.1 AC007169 2 (AC007169) unknown
                  protein [Arabidopsis thaliana]
                  400894
Seq. No.
                  LIB3431-038-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2760334
BLAST score
                  294
                  2.0e-26
E value
Match length
                  76
% identity
                   (AC002130) F1N21.5 [Arabidopsis thaliana]
NCBI Description
                  400895
Seq. No.
                  LIB3431-038-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1001532
BLAST score
                  251
E value
                  2.0e-21
                  93
Match length
% identity
                  (D64000) hypothetical protein [Synechocystis sp.]
NCBI Description
                  400896
Seq. No.
                  LIB3431-038-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g82080
BLAST score
                  638
                  8.0e-67
E value
                  140
Match length
% identity
                  81
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
```

```
400897
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  580
E value
                  5.0e-60
Match length
                  130
                  88
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  400898
Seq. ID
                  LIB3431-038-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g3075488
BLAST score
                  518
                  9.0e-53
E value
Match length
                  117
% identity
                  85
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                  400899
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-E5
                  BLASTX
Method
NCBI GI
                  g1617197
BLAST score
                  304
E value
                  1.0e-27
Match length
                  76
% identity
                  76
NCBI Description (272488) CP12 [Nicotiana tabacum]
                  400900
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g4544399
BLAST score
                  597
E value
                  5.0e-62
Match length
                  128
% identity
                  84
                  (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  400901
Seq. ID
                  LIB3431-038-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g1777312
BLAST score
                  196
                  5.0e-15
E value
                  122
Match length
                  37
% identity
NCBI Description (D30622) novel serine/threonine protein kinase [Arabidopsis
```

>gi 226872 prf 1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

thaliana]

```
400902
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g542200
BLAST score
                  431
E value
                  1.0e-42
                  138
Match length
% identity
                  hypothetical protein - garden asparagus
NCBI Description
                  >gi 452714 emb CAA54526 (X77320) unknown [Asparagus
                  officinalis]
                  400903
Seq. No.
                  LIB3431-038-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
                  591
BLAST score
E value
                  3.0e-61
Match length
                  127
                  87
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  400904
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q224293
                  409
BLAST score
E value
                  6.0e-40
                  82
Match length
                  100
% identity
NCBI Description histone H4 [Triticum aestivum]
                  400905
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  q132105
                  322
BLAST score
E value
                  4.0e-46
Match length
                  110
                  87
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
```

```
carboxylase S [Oryza sativa]
                   400906
Seq. No.
Seq. ID
                   LIB3431-038-P1-K1-F2
Method
                   BLASTN
NCBI GI
                   q6015437
                   35
BLAST score
E value
                   5.0e-10
                   35
Match length
                   100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                   400907
Seq. No.
Seq. ID
                   LIB3431-038-P1-K1-F3
                   BLASTX
Method
NCBI GI
                   g2497903
BLAST score
                   220
E value
                   8.0e-18
Match length
                   59
                   68
% identity
                   METALLOTHIONEIN-LIKE PROTEIN TYPE 2
NCBI Description
                   >gi_1752831_dbj_BAA14038.1_ (D89931) metallothionein-like
protein [Oryza sativa] >gi_1815628 (U43530)
                   metallothionein-like type \overline{2} [Oryza sativa]
                   400908
Seq. No.
                   LIB3431-038-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3928097
BLAST score
                   213
E value
                   6.0e-17
                   94
Match length
% identity
                   47
NCBI Description
                    (AC005770) unknown protein, 5' partial [Arabidopsis
                   thaliana]
                   400909
Seq. No.
                   LIB3431-038-P1-K1-F5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2407281
BLAST score
                   653
E value
                   1.0e-68
                   127
Match length
                   94
% identity
NCBI Description
                    (AF017363) ribulose 1,5-bisphosphate carboxylase small
                   subunit [Oryza sativa]
                   400910
Seq. No.
                   LIB3431-038-P1-K1-F6
Seq. ID
                   BLASTX
Method
                   g548603
NCBI GI
BLAST score
                   407
E value
                   1.0e-39
Match length
                   118
% identity
                   71
NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
```

sativa] >gi 226375 prf 1508256A ribulose bisphosphate

Seq. ID

```
>gi 478404 pir__JQ2247 photosystem I chain D precursor -
                   barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
                   400911
Seq. No.
Seq. ID
                   LIB3431-038-P1-K1-F9
Method
                   BLASTX
NCBI ĠI
                   g5360953
                   519
BLAST score
                   7.0e-53
E value
                   137
Match length
                   79
% identity
                  (AJ225059) v-ATPase subunit D [Arabidopsis thaliana]
NCBI Description
                   400912
Seq. No.
Seq. ID
                   LIB3431-038-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g1362150
BLAST score
                   546
E value
                   5.0e-56
Match length
                   112
% identity
                   89
                   hypothetical protein (clone AFN3) - wild oat (fragment)
NCBI Description
                   >gi 726478 (U20000) putative ORF1 [Avena fatua]
Seq. No.
                   LIB3431-038-P1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5734640
BLAST score
                   550
E value
                   2.0e-56
Match length
                   145
% identity
                   81
NCBI Description
                   (AP000391) Similar to Arabidopsis thaliana chromosome II
                   BAC F17K2 genomic sequence; hypothetical protein (AC003680)
                   [Oryza sativa]
                   400914
Seq. No.
                   LIB3431-038-P1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   595
                   9.0e-62
E value
                   128
Match length
% identity
                   88
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   400915
```

(PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)

LIB3431-038-P1-K1-G2

Seq. ID

```
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  38
                  8.0e-12
E value
                  38
Match length
% identity
                  100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  400916
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  476
                  8.0e-48
E value
                  137
Match length
                  69
% identity
                 (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                  400917
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                  604
E value
                  8.0e-63
                  138
Match length
                  83
% identity
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
Seq. No.
                  400918
Seq. ID
                  LIB3431-038-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g3024440
BLAST score
                  368
E value
                  3.0e-35
Match length
                  77
                  88
% identity
                  PROTEASOME DELTA CHAIN PRECURSOR (MULTICATALYTIC
NCBI Description
                  ENDOPEPTIDASE COMPLEX DELTA CHAIN)
                  >gi 1743356 emb CAA70699 (Y09505) proteasome delta subunit
                  [Nicotiana tabacum]
                  400919
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q1170937
BLAST score
                  760
E value
                  4.0e-81
Match length
                  144
                  100
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine
                  synthetase [Oryza sativa]
                  400920
Seq. No.
```

LIB3431-038-P1-K1-H12

Seq. No.

```
BLASTX
Method
NCBI GI
                    g2245109
BLAST score
                    361
E value
                    2.0e-34
Match length
                    117
                    60
% identity
NCBI Description
                    (Z97343) carboxyl-terminal proteinase like protein
                    [Arabidopsis thaliana]
                    400921
Seq. No.
Seq. ID
                    LIB3431-038-P1-K1-H2
                    BLASTN
Method
NCBI GI
                    q2062705
BLAST score
                    36
                    1.0e-10
E value
Match length
                    36
                    100
% identity
                    Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
                    400922
Seq. No.
                    LIB3431-038-P1-K1-H3
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3834310
BLAST score
                    530
E value
                    4.0e-54
Match length
                    103
% identity
                    98
                    (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
NCBI Description
                    gb D83004 from Homo sapiens. ESTs gb T88233, gb Z24464,
                    gb_N37265, gb_H36151, gb_Z34711, gb_AA040983, and gb_T22122 come from this gene. [Arabidopsis thaliana]
Seq. No.
                    400923
                    LIB3431-038-P1-K1-H4
Seq. ID
Method
                    BLASTX
NCBI GI
                    g115787
BLAST score
                    745
E value
                    2.0e-79
Match length
                    145
% identity
                    99
NCBI Description
                    CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                    CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
Seq. No.
                    400924
                    LIB3431-038-P1-K1-H5
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4335761
BLAST score
                    238
E value
                    7.0e-20
Match length
                    142
% identity
NCBI Description
                    (AC006284) unknown protein [Arabidopsis thaliana]
```

E value

5.0e-11

```
LIB3431-038-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  591
                  3.0e-61
E value
                  127
Match length
                  87
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  400926
Seq. No.
Seq. ID
                  LIB3431-038-P1-K1-H7
Method
                  BLASTN
NCBI GI
                  g1245938
BLAST score
                  36
E value
                  1.0e-10
Match length
                  36
% identity
                  100
NCBI Description
                  rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
                  heart atrium, mRNA, 2998 nt]
Seq. No.
                  400927
Seq. ID
                  LIB3431-038-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g5007084
BLAST score
                  729
E value
                  2.0e-77
Match length
                  137
% identity
                  100
NCBI Description
                  (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
                  sativa]
Seq. No.
                  400928
Seq. ID
                  LIB3431-038-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q6006363
BLAST score
                  267
E value
                  3.0e-23
Match length
                  50
% identity
                  100
NCBI Description
                  (AP000559) ESTs AU078183(C62904), C73912(E21020) correspond
                  to a region of the predicted gene.; Similar to water stress
                  inducible protein (U74296) [Oryza sativa]
Seq. No.
                  400929
Seq. ID
                  LIB3431-038-P1-N1-A10
Method
                  BLASTX
NCBI GI
                  g3153151
BLAST score
                  162
```

```
30
Match length
% identity
                   100
                   (AJ006296) chlorophyll a/b-binding protein [Hordeum
NCBI Description
                   vulgare]
                   400930
Seq. No.
Seq. ID
                   LIB3431-038-P1-N1-A12
Method
                   BLASTX
NCBI GI
                   g729535
BLAST score
                   416
E value
                   9.0e-41
Match length
                   80
                   91
% identity
NCBI Description
                   FERREDOXIN-THIOREDOXIN REDUCTASE, CATALYTIC CHAIN PRECURSOR
                   (FTR-C) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT B)
                   (FTR-B)
                   400931
Seq. No.
Seq. ID
                   LIB3431-038-P1-N1-A2
Method
                   BLASTX
NCBI GI
                   q6103011
BLAST score
                   394
E value
                   3.0e-38
Match length
                   84
% identity
                   48
NCBI Description
                   (X84225) precursor of photosystem II subunit (22KDa)
                   [Nicotiana tabacum]
Seq. No.
                   400932
Seq. ID
                   LIB3431-038-P1-N1-A3
Method
                   BLASTX
NCBI GI
                   q3548808
BLAST score
                   244
E value
                   1.0e-20
Match length
                   69
% identity
NCBI Description
                   (AC005313) unknown protein [Arabidopsis thaliana]
Seq. No.
                   400933
Seq. ID
                   LIB3431-038-P1-N1-A4
Method
                   BLASTX
NCBI GI
                   g5031281
BLAST score
                   181
E value
                   3.0e-13
Match length
                   41
% identity
NCBI Description
                   (AF139499) unknown [Prunus armeniaca]
Seq. No.
                   400934
Seq. ID
                   LIB3431-038-P1-N1-A5
Method
                   BLASTN
NCBI GI
                   q2331130
BLAST score
                   129
E value
                   3.0e-66
Match length
                   181
                   93
% identity
NCBI Description Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
```

NCBI Description

[Zea mays]

```
cds
                  400935
Seq. No.
Seq. ID
                  LIB3431-038-P1-N1-A8
                  BLASTX
Method
NCBI GI
                  g3822223
BLAST score
                  323
E value
                  6.0e-30
                  96
Match length
                  56
% identity
                  (AF077955) branched-chain alpha keto-acid dehydrogenase El
NCBI Description
                  alpha subunit [Arabidopsis thaliana]
Seq. No.
                  400936
                  LIB3431-038-P1-N1-B1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2331130
BLAST score
                  187
E value
                  1.0e-101
                  235
Match length
% identity
                  95
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
Seq. No.
                  400937
                  LIB3431-038-P1-N1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4689384
BLAST score
                  231
E value
                  4.0e-19
Match length
                  43
% identity
                  100
                  (AF139467) LHCII type I chlorophyll a/b binding protein
NCBI Description
                  [Vigna radiata]
Seq. No.
                  400938
Seq. ID
                  LIB3431-038-P1-N1-B3
Method
                  BLASTX ·
NCBI GI
                  q3192019
BLAST score
                  146
E value
                  4.0e-09
Match length
                  50
% identity
NCBI Description (AL023797) uridylate kinase [Streptomyces coelicolor]
                  400939
Seq. No.
Seq. ID
                  LIB3431-038-P1-N1-B4
Method
                  BLASTX
NCBI GI
                  g2501190
BLAST score
                  155
                 4.0e-10
E value
Match length
                  51
% identity
                  69
```

THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR

>gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme

g11957

```
400940
Seq. No.
Seq. ID
                   LIB3431-038-P1-N1-B5
Method
                   BLASTX
NCBI GI
                   q461595
BLAST score
                   188
E value
                   5.0e-14
Match length
                   98
                   44
% identity
                  ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II)
NCBI Description
                   >qi 479533 pir S34473 H+-transporting ATP synthase (EC
                   3.6.1.34) chain 9 - spinach >gi_394755_emb_CAA50520_
                   (X71397) CF(o)II ATP synthase subunit 9 [Spinacia oleracea]
                   400941
Seq. No.
Seq. ID
                   LIB3431-038-P1-N1-B6
Method
                   BLASTX
NCBI GI
                   g710308
BLAST score
                   338
                   1.0e-31
E value
Match length
                   63
% identity
                   95
                  (U11693) victorin binding protein [Avena sativa]
NCBI Description
Seq. No.
                   400942
                   LIB3431-038-P1-N1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1658271
BLAST score
                   147
E value
                   2.0e-09
                   40
Match length
                   78
% identity
                   (U74622) nascent polypeptide associated complex alpha chain
NCBI Description
                   [Nicotiana tabacum]
Seq. No.
                   400943
                  LIB3431-038-P1-N1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   354
E value
                   2.0e-33
Match length
                   65
% identity
                   100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4\overline{.1}.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                   400944
Seq. ID
                  LIB3431-038-P1-N1-C1
Method
                  BLASTN
```

g417260

```
BLAST score
                   319
E value
                   1.0e-179
Match length
                   391
                   98
% identity
                   Rice complete chloroplast genome
NCBI Description
Seq. No.
                   400945
Seq. ID
                   LIB3431-038-P1-N1-C10
Method
                   BLASTX
NCBI GI
                   g167097
                   151
BLAST score
                   1.0e-21
E value
Match length
                   63
                   86
% identity
                   (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                   [Hordeum vulgare]
                   400946
Seq. No.
                   LIB3431-038-P1-N1-C12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2072554
BLAST score
                   393
                   0.0e + 00
E value
                   393
Match length
% identity
                   100
                   Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   cds
                   400947
Seq. No.
Seq. ID
                   LIB3431-038-P1-N1-C2
Method
                   BLASTX
NCBI GI
                   g115787
                   409
BLAST score
E value
                   6.0e-40
Match length
                   77
% identity
                   100
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   400948
                   LIB3431-038-P1-N1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q733454
BLAST score
                   191
E value
                   2.0e-14
Match length
                   38
% identity
NCBI Description
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
Seq. No.
                   400949
Seq. ID
                   LIB3431-038-P1-N1-C4
Method
                   BLASTX
```

% identity

```
BLAST score
                   176
                   7.0e-13
E value
                   38
Match length
                   84
% identity
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003_pir__$33632
NCBI Description
                   lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                   light-regulated gene [Oryza sativa]
                   400950
Seq. No.
Seq. ID
                   LIB3431-038-P1-N1-C5
                   BLASTX
Method
NCBI GI
                   q3345477
BLAST score
                   188
                   4.0e-14
E value
Match length
                   34
                   100
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
Seq. No.
                   400951
                   LIB3431-038-P1-N1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4678364
                   221
BLAST score
E value
                   7.0e-18
Match length
                   91
% identity
NCBI Description
                   (AL049659) putative protein [Arabidopsis thaliana]
Seq. No.
                   400952
Seq. ID
                   LIB3431-038-P1-N1-C9
Method
                   BLASTX
NCBI GI
                   g130274
BLAST score
                   492
E value
                   1.0e-49
Match length
                   96
% identity
                  PLASTOCYANIN >gi 82500 pir S06105 plastocyanin - rice
NCBI Description
Seq. No.
                   400953
                   LIB3431-038-P1-N1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g671740
BLAST score
                   165
E value
                   2.0e-11
Match length
                   65
% identity
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
                   400954
Seq. No.
Seq. ID
                   LIB3431-038-P1-N1-D11
Method
                   BLASTX
NCBI GI
                   q3075488
BLAST score
                   198
E value
                   3.0e-15
Match length
                   44
```

```
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                  400955
Seq. No.
                  LIB3431-038-P1-N1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q347451
BLAST score
                  197
                  4.0e-15
E value
Match length
                  62
% identity
                  63
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
                  400956
Seq. No.
Seq. ID
                  LIB3431-038-P1-N1-D2
                  BLASTX
Method
NCBI GI
                  g347451
                  208
BLAST score
                  2.0e-16
E value
Match length
                  48
% identity
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
Seq. No.
                  400957
Seq. ID
                  LIB3431-038-P1-N1-D5
                  BLASTX
Method
NCBI GI
                  q131225
BLAST score
                  311
E value
                  2.0e-28
Match length
                  81
                  75
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >qi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  400958
Seq. No.
Seq. ID
                  LIB3431-038-P1-N1-D7
Method
                  BLASTX
NCBI GI
                  g4582445
BLAST score
                  269
E value
                  1.0e-23
Match length
                  64
% identity
                  70
NCBI Description
                   (AC007071) unknown protein [Arabidopsis thaliana]
                  >qi 4589952 qb AAD26470.1 AC007169 2 (AC007169) unknown
                  protein [Arabidopsis thaliana]
Seq. No.
                  400959
                  LIB3431-038-P1-N1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115813
BLAST score
                  248
E value
                  4.0e-21
Match length
                  56
% identity
                  86
```

Seq. No.

```
CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                   400960
Seq. No.
Seq. ID
                  LIB3431-038-P1-N1-E11
Method
                  BLASTX
NCBI GI
                  g3036946
BLAST score
                  287
                  1.0e-25
E value
Match length
                  54
                  100
% identity
                   (AB012637) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                  400961
Seq. No.
                  LIB3431-038-P1-N1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3075488
BLAST score
                  326
E value
                   3.0e-30
Match length
                  63
                  100
% identity
NCBI Description
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                  400962
Seq. No.
Seq. ID
                  LIB3431-038-P1-N1-E5
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  244
E value
                   1.0e-20
Match length
                  50
                   90
% identity
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                  400963
                  LIB3431-038-P1-N1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3256035
BLAST score
                  195
                  7.0e-15
E value
                  67
Match length
% identity
                  55
                   (Y14274) putative serine/threonine protein kinase [Sorghum
NCBI Description
                  bicolor]
Seq. No.
                  400964
                  LIB3431-038-P1-N1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2586153
BLAST score
                  179
E value
                  5.0e-13
Match length
                  48
% identity
NCBI Description (AF001530) ripening-associated protein [Musa acuminata]
```

```
LIB3431-038-P1-N1-F1
Seq. ID
Method
                   BLASTN
                   g3063523
NCBI GI
BLAST score
                   192
E value
                   1.0e-103
Match length
                   271
% identity
                   93
                  Oryza sativa ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   400966
Seq. No.
Seq. ID
                  LIB3431-038-P1-N1-F10
Method
                  BLASTX
NCBI GI
                   g70772
BLAST score
                   236
                   9.0e-20
E value
Match length
                   60
                   82
% identity
NCBI Description histone H4 - wheat >gi 70773 pir HSPM4 histone H4 - garden
                   400967
Seq. No.
Seq. ID
                   LIB3431-038-P1-N1-F11
Method
                  BLASTX
NCBI GI
                  q132105
                   331
BLAST score
E value
                   8.0e-31
Match length
                   62
                   100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4.\overline{1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   400968
Seq. No.
Seq. ID
                  LIB3431-038-P1-N1-F4
                  BLASTX
Method
                   g3928097
NCBI GI
BLAST score
                   207
E value
                   3.0e-16
Match length
                   66
% identity
                   (AC005770) unknown protein, 5' partial [Arabidopsis
NCBI Description
                  thaliana]
                   400969
Seq. No.
Seq. ID
                  LIB3431-038-P1-N1-F5
Method
                  BLASTX
NCBI GI
                   g347451
BLAST score
                  197
                   4.0e-15
E value
Match length
                   37
```

```
% identity
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa]
Seq. No.
                  400970
Seq. ID
                  LIB3431-038-P1-N1-F6
Method
                  BLASTX
NCBI GI
                  q548603
                  535
BLAST score
E value
                  1.0e-54
Match length
                  109
% identity
                  94
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                  barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                  400971
Seq. ID
                  LIB3431-038-P1-N1-G1
Method
                  BLASTX
NCBI GI
                  g1362150
                  388
BLAST score
E value
                  2.0e-37
Match length
                  81
                  89
% identity
NCBI Description
                  hypothetical protein (clone AFN3) - wild oat (fragment)
                  >gi_726478 (U20000) putative ORF1 [Avena fatua]
Seq. No.
                  400972
Seq. ID
                  LIB3431-038-P1-N1-G11
Method
                  BLASTN
NCBI GI
                  g5734616
                  397
BLAST score
                  0.0e + 00
E value
Match length
                  409
                  99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
                  400973
Seq. No.
                  LIB3431-038-P1-N1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  315
E value
                  6.0e-29
Match length
                  60
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375 prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

Seq. No. 400974

```
LIB3431-038-P1-N1-G3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3789951
                   174
BLAST score
E value
                   6.0e-93
Match length
                   407
% identity
                   95
                   Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
Seq. No.
                   400975
Seq. ID
                   LIB3431-038-P1-N1-G6
                   BLASTX
Method
NCBI GI
                   g3345477
BLAST score
                   249
E value
                   3.0e-21
Match length
                   47
                   100
% identity
NCBI Description
                   (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                   400976
Seq. ID
                   LIB3431-038-P1-N1-G8
Method
                   BLASTX
NCBI GI
                   q733456
BLAST score
                   352
E value
                   3.0e-33
Match length
                   73
                   95
% identity
NCBI Description
                   (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
                   400977
Seq. No.
Seq. ID
                   LIB3431-038-P1-N1-H1
Method
                   BLASTX
NCBI GI
                   g2511594
BLAST score
                   337
                   2.0e-31
E value 1
Match length
                   84
% identity
NCBI Description
                   (Y13694) multicatalytic endopeptidase complex, proteasome
                   precursor, beta subunit [Arabidopsis thaliana]
                   >gi_2827525_emb_CAA16533.1_ (AL021633) multicatalytic
                   endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S
                   proteasome subunit PBA1 [Arabidopsis thaliana]
Seq. No.
                   400978
Seq. ID
                   LIB3431-038-P1-N1-H11
Method
                   BLASTX
NCBI GI .
                   q1170937
BLAST score
                   290
E value
                   5.0e-26
Match length
                   52
% identity
                   100
                   S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
```

4.00

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

```
400979
Seq. No.
Seq. ID
                   LIB3431-038-P1-N1-H12
Method
                   BLASTX
NCBI GI
                   g5174741
BLAST score
                   165
                   2.0e-11
E value
Match length
                   64
% identity
NCBI Description
                   ubiquitin carboxyl-terminal esterase L3 (ubiquitin
                   thiolesterase) >gi_136682_sp_P15374_UBL3_HUMAN UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L3 (UCH-L3) (UBIQUITIN
                   THIOLESTERASE L3) >gi_108014_pir__A40085 ubiquitin
                   carboxyl-terminal proteinase (EC 3.4.-.-) L3 - human
                   >gi 2914274 pdb 1UCH Deubiquitinating Enzyme Uch-L3
                   (Human) At 1.8 Angstrom Resolution >gi 340074 (M30496)
                   ubiquitin carboxyl-terminal hydrolase [Homo sapiens]
Seq. No.
                   400980
Seq. ID
                   LIB3431-038-P1-N1-H3
                   BLASTX
Method
NCBI GI
                   q5381319
                   271
BLAST score
                   9.0e-24
E value
                   55
Match length
% identity
                   (AF091621) ubiquitin-conjugating enzyme E2 [Catharanthus
NCBI Description
                   roseus]
                   400981
Seq. No.
Seq. ID
                   LIB3431-038-P1-N1-H4
Method
                   BLASTX
NCBI GI
                   q289920
                   291
BLAST score
E value
                   4.0e-26
                   55
Match length
% identity
                   100
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   400982
Seq. No.
                   LIB3431-038-P1-N1-H6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3063523
BLAST score
                   58
                   9.0e-24
E value
                   146
Match length
% identity
                   Oryza sativa ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
Seq. No.
                   400983
Seq. ID
                   LIB3431-038-P1-N1-H8
Method
                   BLASTX
```

>qi 450549 emb CAA81481 (Z26867) S-adenosyl methionine

synthetase [Oryza sativa]

g5007084

```
190
BLAST score
E value
                  3.0e-14
Match length
                  39
                  100
% identity
                  (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
                  sativa]
                  400984
Seq. No.
                  LIB3431-038-P1-N1-H9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g6006355
BLAST score
                  198
                  1.0e-107
E value
                  391
Match length
                  99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                  400985
                  LIB3431-039-P1-K2-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885894
BLAST score
                  177
                  3.0e-24
E value
Match length
                  69
% identity
                  90
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
                  400986
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-A6
Method
                  BLASTN
NCBI GI
                  g1835730
BLAST score
                  75
E value
                  2.0e-34
Match length
                  93
% identity
                  97
NCBI Description
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
                  complete cds
Seq. No.
                  400987
Seq. ID
                  LIB3431-039-P1-K2-A7
Method
                  BLASTX
NCBI GI
                  g3808101
BLAST score
                  532
E value
                  2.0e-54
                  125
Match length
% identity
                  82
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]
                  400988
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-B1
Method
                  BLASTN
NCBI GI
                  g606816
BLAST score
                  53
E value
                  3.0e-21
Match length
                  57
                  98
% identity
NCBI Description Oryza sativa chloroplast carbonic anhydrase mRNA, complete
```

cds 400989 Seq. No. Seq. ID LIB3431-039-P1-K2-B10 Method BLASTN NCBI GI g11957 BLAST score 378 0.0e + 00E value Match length 411 98 % identity NCBI Description Rice complete chloroplast genome 400990 Seq. No. Seq. ID LIB3431-039-P1-K2-B11 BLASTN Method NCBI GI g11957 BLAST score 127 E value 4.0e-65 Match length 251 % identity 88 NCBI Description Rice complete chloroplast genome 400991 Seq. No. Seq. ID LIB3431-039-P1-K2-B2 Method BLASTX NCBI GI g115772 . 189 BLAST score E value 1.0e-25 Match length 62 % identity CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I NCBI Description CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108_ (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235) [Oryza sativa] 400992 Seq. No. Seq. ID LIB3431-039-P1-K2-B3 Method BLASTX NCBI GI g733454 483 BLAST score E value 9.0e-49 Match length 111 % identity 82 (U23188) chlorophyll a/b-binding apoprotein CP26 precursor NCBI Description [Zea mays]

 Seq. No.
 400993

 Seq. ID
 LIB3431-039-P1-K2-B6

 Method
 BLASTX

 NCBI GI
 g3126854

NCBI GI g3126854
BLAST score 149
E value 7.0e-10
Match length 30
% identity 100

NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]

```
400994
Seq. No.
Seq. ID
                    LIB3431-039-P1-K2-B7
Method
                    BLASTX
NCBI GI
                    g3345477
BLAST score
                    626
E value
                    2.0e-65
Match length
                    120
% identity
                    99
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                    400995
Seq. No.
Seq. ID
                    LIB3431-039-P1-K2-B8
Method
                    BLASTX
NCBI GI
                    g131166
                    503
BLAST score
E value
                    3.0e-51
                    97
Match length
                    96
% identity
                    PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                    (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi 82100 pir S00449
                    photosystem I chain II precursor - tomato >gi_170492
                    (M21344) photosystem I subunit II protein precursor [Lycopersicon esculentum] >gi_226544_prf__1601516A photosystem I reaction center II [Lycopersicon esculentum]
Seq. No.
                    400996
Seq. ID
                    LIB3431-039-P1-K2-C1
Method
                    BLASTX
NCBI GI
                    g541950
BLAST score
                    237
E value
                    8.0e-20
Match length
                    69
% identity
                    67
NCBI Description
                    SPCP1 protein - soybean >gi 310576 (L12257).nodulin-26
                    [Glycine max]
                                                            Seq. No.
                    400997
Seq. ID
                    LIB3431-039-P1-K2-C10
Method
                    BLASTX
NCBI GI
                    q289920
BLAST score
                    238
E value
                    5.0e-20
Match length
                    44
% identity
NCBI Description
                    (L07119) chlorophyll A/B binding protein [Gossypium
                    hirsutum]
Seq. No.
                    400998
Seq. ID
                    LIB3431-039-P1-K2-C3
Method
                    BLASTX
NCBI GI
                    q3868758
BLAST score
                    612
E value
                    8.0e-64
Match length
                    114
                    96
% identity
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
```

```
Seq. No.
                   400999
Seq. ID
                   LIB3431-039-P1-K2-C4
Method
                   BLASTX
NCBI GI
                   g1706260
BLAST score
                   363
E value
                   6.0e-35
Match length
                   81
% identity
                   85
                   CYSTEINE PROTEINASE 1 PRECURSOR >gi 2118131 pir S59597
NCBI Description
                   cysteine proteinase 1 precursor - maize
                   >gi 643597 dbj BAA08244 (D45402) cysteine proteinase [Zea
                   mays]
                   401000
Seq. No.
Seq. ID
                   LIB3431-039-P1-K2-C5
                   BLASTX
Method
NCBI GI
                   g3126854
BLAST score
                   772
                   2.0e-82
E value
Match length
                   144
                   99
% identity
NCBI Description
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   401001
Seq. ID
                   LIB3431-039-P1-K2-C6
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   464
                   2.0e-46
E value
Match length
                   107
                   82
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   401002
Seq. ID
                   LIB3431-039-P1-K2-C7
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   37
E value
                   2.0e-11
Match length
                   48
% identity
                   66
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   401003
                   LIB3431-039-P1-K2-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g733454
BLAST score
                   369
E value
                   2.0e-35
Match length
                   100
% identity
                   71
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
```

[Zea mays]

```
401004
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-C9
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  7.0e-20
Match length
                  44
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  401005
                  LIB3431-039-P1-K2-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  386
E value
                  1.0e-37
Match length
                  83
                  90
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  401006
                  LIB3431-039-P1-K2-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                  225
E value
                  2.0e-18
Match length
                  43
% identity
                  100
NCBI Description
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa]
Seq. No.
                  401007
Seq. ID
                  LIB3431-039-P1-K2-D4
Method
                  BLASTX
NCBI GI
                  g4680193
BLAST score
                  226
E value
                  4.0e-19
Match length
                  60
% identity
NCBI Description
                  (AF111710) putative farnesyl pyrophosphate synthase [Oryza
                  sativa subsp. indica]
Seq. No.
                  401008
Seq. ID
                  LIB3431-039-P1-K2-D6
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  237
E value
                  5.0e-20
Match length
                  44
% identity
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
```

```
protein [Oryza sativa]
                  401009
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-D7
Method
                  BLASTX
                  q320618
NCBI GI
                  254
BLAST score
                  8.0e-22
E value
                  72
Match length
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi 218172 dbj BAA00536 (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  401010
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-E2
Method
                  BLASTX
NCBI GI
                  q1235664
                  549
BLAST score
E value
                  9.0e-57
Match length
                  121
% identity
                  56
                  (U37936) novel calmodulin-like protein [Oryza sativa]
NCBI Description
                  >gi 3171148 (AF064456) calmodulin-like protein [Oryza
                  sativa subsp. indica]
                  401011
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-E6
Method
                  BLASTN
NCBI GI
                  g2570510
BLAST score
                  137
E value
                  3.0e-71
Match length
                  148
                  98
% identity
NCBI Description
                  Oryza sativa chlorophyll a-b binding protein mRNA, complete
                  cds
                  401012
Seq. No.
                  LIB3431-039-P1-K2-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  600
E value
                  2.0e-62
                  129
Match length
                  88
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

>gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like

Seq. ID

```
401013
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-E9
Method
                  BLASTX
NCBI GI
                  g1332579
BLAST score
                  239
E value
                  5.0e-20
Match length
                   47
% identity
                  10
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
                   401014
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-F1
Method
                  BLASTX
NCBI GI
                  g1729971
                  233
BLAST score
E value
                   9.0e-20
Match length
                  59
% identity
                   80
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                  rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                  sativa]
Seq. No.
                   401015
Seq. ID
                  LIB3431-039-P1-K2-F2
Method
                  BLASTX
NCBI GI
                  q3885886
BLAST score
                   665
E value
                   4.0e-70
Match length
                  123
% identity
                   99
NCBI Description
                  (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
Seq. No.
                   401016
Seq. ID
                  LIB3431-039-P1-K2-F4
Method
                  BLASTN
NCBI GI
                  q4519191
BLAST score
                  35
E value
                   3.0e-10
Match length
                  71
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K9P8, complete sequence
                   401017
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-F6
Method
                  BLASTX
NCBI GI
                  g2598589
BLAST score
                  227
E value
                   3.0e-21
Match length
                  82
% identity
NCBI Description
                  (Y15367) MtN19 [Medicago truncatula]
Seq. No.
```

LIB3431-039-P1-K2-F7

E value

4.0e-20

```
BLASTX
Method
NCBI GI
                   g5729704
BLAST score
                   249
                   3.0e-21
E value
Match length
                   102
                   45
% identity
NCBI Description
                   (AC007927) unknown protein, 5' partial [Arabidopsis
                   thaliana]
                   401019
Seq. No.
Seq. ID
                   LIB3431-039-P1-K2-F8
Method
                   BLASTX
NCBI GI
                   q1773330
                   636
BLAST score
                   2.0e-66
E value
Match length
                   148
% identity
                   84
NCBI Description
                   (U80071) glycolate oxidase [Mesembryanthemum crystallinum]
Seq. No.
                   401020
Seq. ID
                   LIB3431-039-P1-K2-F9
Method
                   BLASTN
NCBI GI
                   g2073379
BLAST score
                   228
E value
                   1.0e-125
Match length
                   243
% identity
                   98
NCBI Description
                  Rice CP26 mRNA, partial sequence
Seq. No.
                   401021
                   LIB3431-039-P1-K2-G10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   35
E value
                   5.0e-10
Match length
                   35
% identity
                   100
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
Seq. No.
                   401022
Seq. ID
                   LIB3431-039-P1-K2-G12
Method
                   BLASTX
NCBI GI
                   q82080
BLAST score
                   417
E value
                   6.0e-41
Match length
                   122
% identity
                   66
NCBI Description
                   chlorophyll a/b-binding protein type III precursor - tomato
                   >gi_226872_prf__1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                   401023
Seq. ID
                   LIB3431-039-P1-K2-G2
Method
                   BLASTX
NCBI GI
                   g1729971
BLAST score
                   238
```

Seq. ID

```
66
Match length
                   74
% identity
                   TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                   rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                   sativa]
Seq. No.
                   401024
                   LIB3431-039-P1-K2-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2462762
BLAST score
                   337
                   3.0e - 39
E value
Match length
                   121
% identity
                   69
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
                   401025
                   LIB3431-039-P1-K2-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3063524
BLAST score
                   184
E value
                   3.0e-14
Match length
                   51
% identity
NCBI Description
                   (AF052305) ribulose 1,5-bisphosphate carboxylase small
                   subunit [Oryza sativa]
                   401026
Seq. No.
Seq. ID
                   LIB3431-039-P1-K2-G5
Method
                   BLASTX
NCBI GI
                   g82080
BLAST score
                   364
E value
                   9.0e-35
Match length
                   113
% identity
NCBI Description
                   chlorophyll a/b-binding protein type III precursor - tomato
                   >gi_226872_prf__1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                   401027
Seq. ID
                   LIB3431-039-P1-K2-G6
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   199
E value
                   9.0e-16
Match length
                   57
% identity
                   72
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   401028
Seq. No.
```

LIB3431-039-P1-K2-G8

q132105

```
Method
                  BLASTX
NCBI GI
                  g2464852
BLAST score
                  206
E value
                   4.0e-16
Match length
                  104
                   45
% identity
NCBI Description
                  (Z99707) putative protein [Arabidopsis thaliana]
                   401029
Seq. No.
                  LIB3431-039-P1-K2-G9
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3789952
BLAST score
                  544
                   6.0e-56
E value
Match length
                  103
                   99
% identity
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
                   401030
Seq. No.
                  LIB3431-039-P1-K2-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3395440
                  229
BLAST score
E value
                   6.0e-19
Match length
                  76
% identity
                   (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   401031
Seq. No.
                  LIB3431-039-P1-K2-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3328122
BLAST score
                   245
E value
                   2.0e-21
Match length
                   95
% identity
NCBI Description
                   (AF073473) phosphoglycerate kinase precursor [Solanum
                   tuberosum]
Seq. No.
                   401032
                  LIB3431-039-P1-K2-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4835754
BLAST score
                  220
E value
                   4.0e-18
Match length
                  83
% identity
                   (AC007202) Is a member of the PF 00162 Phosphoglycerate
NCBI Description
                   kinase family. ESTs gb_N38721, gb_T22178, gb_R90345,
                  gb_R90715, gb_T21140, gb_T46295, gb_H37082, gb_T46076,
                  gb N37132, gb AA597649, gb AI100648 and gb Z48462 c
                   401033
Seq. No.
                  LIB3431-039-P1-K2-H6
Seq. ID
Method
                  BLASTX
```

q417744

```
BLAST score
                  349
                  4.0e-33
E value
Match length
                  87
                  80
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  401034
Seq. No.
Seq. ID
                  LIB3431-039-P1-K2-H8
Method
                  BLASTX
NCBI GI
                  g129915
BLAST score
                  562
E value
                  6.0e-58
Match length
                  122
% identity
                  89
                  PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 66912 pir TVWTGC phosphoglycerate kinase (EC 2.7.2.3)
                  precursor, chloroplast - wheat >gi 21833 emb CAA33303
                  (X15233) phosphoglycerate kinase (AA 1 - 480) [Triticum
                  aestivum] >gi 3293043 emb CAA51931 (X73528)
                  phosphoglycerate kinase [Triticum aestivum]
Seq. No.
                  401035
Seq. ID
                  LIB3431-039-P1-N1-A10
Method
                  BLASTN
NCBI GI
                  q3885893
BLAST score
                  216
E value
                  1.0e-118
Match length
                  259
                  96
% identity
                  Oryza sativa photosystem-1 H subunit GOS5 (PSI-H) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  401036
Seq. ID
                  LIB3431-039-P1-N1-A4
Method
                  BLASTX
NCBI GI
                  g3913641
BLAST score
                  358
E value
                  4.0e-34
Match length
                  69
% identity
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi_3041777_dbj_BAA25423 (AB007194)
                  fructose-1,6-bisphosphatase [Oryza sativa]
Seq. No.
                  401037
Seq. ID
                  LIB3431-039-P1-N1-A5
Method
                  BLASTX
```

% identity

```
BLAST score
                   287
                   1.0e-25
E value
                   56
Match length
                   96
% identity
                  ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE
NCBI Description
                  HYDROLASE) (ADOHCYASE) >gi_169663 (M81885)
                  S-adenosylhomocysteine hydrolase [Petroselinum crispum]
                   401038
Seq. No.
Seq. ID
                  LIB3431-039-P1-N1-A6
                  BLASTX
Method
NCBI GI
                  g1835731
                   403
BLAST score
                   3.0e-39
E value
                   89
Match length
                   88
% identity
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                   401039
Seq. ID
                  LIB3431-039-P1-N1-A7
Method
                  BLASTX
NCBI GI
                   g3808101
BLAST score
                   350
                   5.0e-33
E value
Match length
                   80
% identity
                   90
NCBI Description (AJ012165) chloroplast protease [Capsicum annuum]
Seq. No.
                   401040
Seq. ID
                  LIB3431-039-P1-N1-A9
Method
                  BLASTX
NCBI GI
                   g1707008
BLAST score
                   384
E value
                   4.0e-37
Match length
                   92
% identity
NCBI Description
                   (U78721) 30S ribosomal protein S5 isolog [Arabidopsis
                   thaliana]
Seq. No.
                   401041
Seq. ID
                  LIB3431-039-P1-N1-B10
Method
                  BLASTN
NCBI GI
                   g11957
BLAST score
                  256
E value
                   1.0e-142
Match length
                   464
% identity
                   97
NCBI Description
                  Rice complete chloroplast genome
                   401042
Seq. No.
Seq. ID
                  LIB3431-039-P1-N1-B2
Method
                  BLASTX
NCBI GI
                   q3036951
BLAST score
                   333
E value
                   4.0e-31
Match length
                   64
```

```
NCBI Description
                    (AB012639) light harvesting chlorophyll a/b-binding protein
                    [Nicotiana sylvestris]
                   401043
Seq. No.
Seq. ID
                   LIB3431-039-P1-N1-B3
Method
                   BLASTX
NCBI GI
                   g733454
                   383
BLAST score
                   6.0e-37
E value
                   78
Match length
% identity
                    (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                    [Zea mays]
                   401044
Seq. No.
                   LIB3431-039-P1-N1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g113170
BLAST score
                   239
                   5.0e-20
E value
Match length
                   66
% identity
                   71
                   ACYL CARRIER PROTEIN II PRECURSOR (ACP II)
NCBI Description
                   >gi_99531_pir__S12310 acyl carrier protein II - spinach
>gi_21232_emb_CAA36288_ (X52065) acyl carrier protein II
                    [Spinacia oleracea]
Seq. No.
                   401045
                   LIB3431-039-P1-N1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3126854
BLAST score
                   345
E value
                   2.0e-32
Match length
                   65
% identity
                   100
NCBI Description
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   401046
Seq. ID
                   LIB3431-039-P1-N1-B7
Method
                   BLASTX
NCBI GI
                   g3345477
BLAST score
                   226
E value
                   2.0e-18
Match length
                   42
% identity
                   100
NCBI Description
                   (AB016283) carbonic anhydrase [Oryza sativa]
Seq. No.
                   401047
Seq. ID
                   LIB3431-039-P1-N1-B8
Method
                   BLASTN
NCBI GI
                   q167084
BLAST score
                   35
E value
                   3.0e-10
Match length
                   47
% identity.
NCBI Description
                   Barley PSI-D subunit of photosystem I (PsaD) mRNA, complete
```

Seq. No.

```
Seq. No.
                  401048
Seq. ID
                  LIB3431-039-P1-N1-C1
Method
                  BLASTX
NCBI GI
                  g541951
BLAST score
                  421
E value
                  2.0e-41
Match length
                  95
% identity
                  80
                  SPCP2 protein - soybean >gi 310578 (L12258) nodulin-26
NCBI Description
                  [Glycine max]
                  401049
Seq. No.
Seq. ID
                  LIB3431-039-P1-N1-C10
Method
                  BLASTX
NCBI GI
                  g289920
BLAST score
                  177
E value
                  7.0e-13
Match length
                  34
% identity
NCBI Description
                  (L07119) chlorophyll A/B binding protein [Gossypium
                  hirsutum]
Seq. No.
                  401050
Seq. ID
                  LIB3431-039-P1-N1-C11
Method
                  BLASTX
NCBI GI
                  q2911043
BLAST score
                  143
E value
                  9.0e-09
Match length
                  59
% identity
                  47
NCBI Description (ALO21961) putative protein [Arabidopsis thaliana]
                  401051
Seq. No.
Seq. ID
                  LIB3431-039-P1-N1-C3
Method
                  BLASTX
NCBI GI
                  q3868758
BLAST score
                  552
E value
                  1.0e-56
Match length
                  112
                  91
% identity
NCBI Description (D89802) elongation factor 1B gamma [Oryza sativa]
                  401052
Seq. No.
Seq. ID
                  LIB3431-039-P1-N1-C4
Method
                  BLASTX
NCBI GI
                  q1706260
BLAST score
                  349
E value
                  7.0e-33
Match length
                  67
                  94
% identity
                  CYSTEINE PROTEINASE 1 PRECURSOR >qi 2118131 pir S59597
NCBI Description
                  cysteine proteinase 1 precursor - maize
                  >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea
                  mays]
```

```
LIB3431-039-P1-N1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3126854
                   299
BLAST score
E value
                   5.0e-27
                   58
Match length
                   98
% identity
NCBI Description
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   401054
                   LIB3431-039-P1-N1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3036946
BLAST score
                   313
E value
                   8.0e-29
Match length
                   61
% identity
                   98
NCBI Description
                   (AB012637) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
Seq. No.
                   401055
Seq. ID
                   LIB3431-039-P1-N1-C8
Method
                  BLASTN
NCBI GI
                   q2073379
BLAST score
                   71
E value
                   1.0e-31
Match length
                   139
                   86
% identity
                  Rice CP26 mRNA, partial sequence
NCBI Description
Seq. No.
                   401056
Seq. ID
                  LIB3431-039-P1-N1-C9
Method
                  BLASTN
NCBI GI
                   q2072554
BLAST score
                   277
E value
                   1.0e-154
Match length
                   341
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
Seq. No.
                   401057
                  LIB3431-039-P1-N1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218209
BLAST score
                  48
E value
                   8.0e-18
Match length
                  68
% identity
                   93
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS2106
                  401058
Seq. No.
                  LIB3431-039-P1-N1-D4
Seq. ID
Method
                  BLASTX
```

g4115416

Match length

```
BLAST score
                   185
E value
                   1.0e-13
Match length
                   60
                   55
% identity
NCBI Description
                   (AB021979) farnesyl diphosphate synthase [Oryza sativa]
Seq. No.
                   401059
Seq. ID
                   LIB3431-039-P1-N1-D5
Method
                   BLASTX
                   g3522941
NCBI GI
BLAST score
                   231
E value
                   5.0e-19
                   50
Match length
                   86
% identity
                   (AC004411) putative peptide chain release factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   401060
Seq. ID
                   LIB3431-039-P1-N1-D6
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   1.0e-19
Match length
                   44
% identity
                   100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   401061
Seq. ID
                   LIB3431-039-P1-N1-D7
Method
                   BLASTX
NCBI GI
                   q3036949
BLAST score
                   276
E value
                   2.0e-24
Match length
                   57
                   93
% identity
                   (AB012638) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
Seq. No.
                   401062
                   LIB3431-039-P1-N1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455174
BLAST score
                   256
E value
                   4.0e-22
Match length
                   77
% identity
                   62
NCBI Description
                   (AL035521) putative protein [Arabidopsis thaliana]
                   401063
Seq. No.
                   LIB3431-039-P1-N1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4689380
BLAST score
                   266
E value
                   3.0e-23
```

```
% identity
                   (AF139465) LHCII type III chlorophyll a/b binding protein
NCBI Description
                  [Vigna radiata]
                  401064
Seq. No.
Seq. ID
                  LIB3431-039-P1-N1-E7
Method
                  BLASTX
NCBI GI
                  g671740
                  433
BLAST score
E value
                  9.0e-43
                  78
Match length
                  100
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  401065
Seq. No.
                  LIB3431-039-P1-N1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q464980
BLAST score
                  415
E value
                  1.0e-40
Match length
                  80
% identity
                  96
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >qi 166422 (L06967)
                  ubiquitin carrier protein [Medicago sativa]
Seq. No.
                  401066
                  LIB3431-039-P1-N1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2598589
BLAST score
                  234
E value
                  2.0e-19
Match length
                  70
% identity
NCBI Description
                  (Y15367) MtN19 [Medicago truncatula]
                  401067
Seq. No.
Seq. ID
                  LIB3431-039-P1-N1-F7
Method
                  BLASTX
NCBI GI
                  g5729704
BLAST score
                  249
E value
                  3.0e-21
Match length
                  102
                  45
% identity
NCBI Description
                  (AC007927) unknown protein, 5' partial [Arabidopsis
                  thaliana]
Seq. No.
                  401068
Seq. ID
                  LIB3431-039-P1-N1-F8
Method
                  BLASTN
NCBI GI
                  q2570514
BLAST score
                  287
E value
                  1.0e-160
Match length
                  335
                  96
% identity
NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
```

Seq. No.

```
401069
Seq. No.
                   LIB3431-039-P1-N1-F9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2073379
BLAST score
                   168
                   2.0e-89
E value
Match length
                   243
** identity
                   92
NCBI Description Rice CP26 mRNA, partial sequence
                   401070
Seq. No.
                   LIB3431-039-P1-N1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1168587
                   200
BLAST score
E value
                   2.0e-15
Match length
                   45
                   87
% identity
                   ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi_1084467_pir__S43728 H+-transporting ATP synthase (EC
                   3.6.1.34) - sorghum >gi_311231_emb_CAA46803 (X66004)
                   H(+)-transporting ATP synthase [Sorghum bicolor]
Seq. No.
                   401071
                   LIB3431-039-P1-N1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1296955
BLAST score
                   396
E value
                   2.0e-38
Match length
                   76
% identity
                   (X95402) duplicated domain structure protein [Oryza sativa]
NCBI Description
                   401072
Seq. No.
Seq. ID
                   LIB3431-039-P1-N1-G11
Method
                   BLASTX
NCBI GI
                   q1296955
BLAST score
                   320
E value
                   2.0e-29
Match length
                   73
% identity
NCBI Description (X95402) duplicated domain structure protein [Oryza sativa]
                   401073
Seq. No.
                   LIB3431-039-P1-N1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115813
BLAST score
                   257
                   4.0e-22
E value
Match length
                   61
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                   CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
                   401074
```

q115787

```
LIB3431-039-P1-N1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1729971
BLAST score
                   296
E value
                   7.0e-27
Match length
                   54
% identity
NCBI Description
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                   (AQUAPORIN-TIP) >gi 1076745 pir S52004 gamma-Tip protein -
                   rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                   sativa]
                   401075
Seq. No.
Seq. ID
                   LIB3431-039-P1-N1-G3
                   BLASTX
Method
NCBI GI
                   g2462750
                   277
BLAST score
E value
                   2.0e-24
Match length
                   72
% identity
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   LIB3431-039-P1-N1-G4
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   416
E value
                   1.0e-40
Match length
                   75
% identity
                   100
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   401077
Seq. ID
                   LIB3431-039-P1-N1-G5
Method
                   BLASTX
NCBI GI
                   q115813
BLAST score
                   257
E value
                   4.0e-22
Match length
                   61
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                   CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
                   401078
Seq. No.
Seq. ID
                   LIB3431-039-P1-N1-G6
Method
                   BLASTX
```

NCBI GI

```
BLAST score
                   409
E value
                   6.0e-40
Match length
                   77
                   100
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
                   401079
Seq. No.
Seq. ID
                   LIB3431-039-P1-N1-G7
Method
                   BLASTX
NCBI GI
                   g4206765
BLAST score
                   180
E value
                   5.0e-13
                   77
Match length
% identity
                   52
NCBI Description
                   (AF104329) putative type 1 membrane protein [Arabidopsis
                   thaliana]
Seq. No.
                   401080
Seq. ID
                   LIB3431-039-P1-N1-G8
Method
                   BLASTX
NCBI GI
                   q2464852
BLAST score
                   171
E value
                   5.0e-12
Match length
                   80
                   49
% identity
NCBI Description
                   (Z99707) putative protein [Arabidopsis thaliana]
Seq. No.
                   401081
Seq. ID
                   LIB3431-039-P1-N1-H3
Method
                   BLASTX
NCBI GI
                   q1708424
BLAST score
                   267
E value
                   3.0e-23
Match length
                   61
                   74
% identity
                   ISOFLAVONE REDUCTASE HOMOLOG >gi 1230614 (U48590)
NCBI Description
                   isoflavone reductase-like protein [Lupinus albus]
Seq. No.
                   401082
Seq. ID
                   LIB3431-039-P1-N1-H6
Method
                   BLASTX
NCBI GI
                   q671740
BLAST score
                   380
E value
                   2.0e-36
Match length
                   69
% identity
                   100
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   401083
Seq. No.
                   LIB3431-039-P1-N1-H8
Seq. ID
Method
                   BLASTX
```

q3738261

```
BLAST score
                   261
                   1.0e-22
E value
Match length
                   62
% identity
                   89
                   (AB018412) chloroplast phosphoglycerate kinase [Populus
NCBI Description
Seq. No.
                   401084
Seq. ID
                   LIB3431-040-P1-K2-A1
Method
                   BLASTX
NCBI GI
                   g2959781
BLAST score
                   193
E value
                   3.0e-15
Match length
                   60
% identity
                   (AJ223508) Zwille protein [Arabidopsis thaliana]
NCBI Description
                   401085
Seq. No.
Seq. ID
                   LIB3431-040-P1-K2-A7
Method
                   BLASTX
NCBI GI
                   g1370198
BLAST score
                   295
E value
                   8.0e-27
Match length
                   87
                   67
% identity
NCBI Description
                  (Z73948) RAB8E [Lotus japonicus]
                   401086
Seq. No.
                   LIB3431-040-P1-K2-A8
Seq. ID
Method
                   BLASTN
NCBI GI
                   q218184
BLAST score
                   59
E value
                   5.0e-25
Match length
                   80
                   91
% identity
NCBI Description Rice mRNA for oryzain gamma (EC 3.4.22)
                   401087
Seq. No.
Seq. ID
                   LIB3431-040-P1-K2-A9
Method
                   BLASTN
NCBI GI
                   q4138289
BLAST score
                   118
E value
                   9.0e-60
Match length
                   138
                   96
% identity
NCBI Description Oryza sativa mRNA for thioredoxin M
Seq. No.
                   401088
Seq. ID
                   LIB3431-040-P1-K2-B11
Method
                   BLASTX
NCBI GI
                   q3288821
BLAST score
                   436
E value
                   4.0e-43
Match length
                   109
                   76
% identity
                   (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
```

transaminase [Arabidopsis thaliana]

```
401089
Seq. No.
Seq. ID
                  LIB3431-040-P1-K2-B3
Method
                   BLASTX
NCBI GI
                   g871931
BLAST score
                   415
                   1.0e-40
E value
                   104
Match length
                   84
% identity
                   (D30763) ferredoxin [Oryza sativa]
NCBI Description
Seq. No.
                   401090
                  LIB3431-040-P1-K2-B4
Seq. ID
Method
                   BLASTX
                   g2244847
NCBI GI
BLAST score
                   152
E value
                   3.0e-10
Match length
                   79
% identity
                   44
                   (Z97337) hydroxyproline-rich glycoprotein homolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   401091
                   LIB3431-040-P1-K2-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   342
E value
                   2.0e-32
                   70
Match length
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094_pir RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{EC} 4\overline{.1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   401092
                   LIB3431-040-P1-K2-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   339
E value
                   8.0e-32
Match length
                   133
% identity
                   47
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094_pir__RKRZS9
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
```

>gi 4733989 gb AAD28669.1 AC007209 5 (AC007209)

alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

NCBI GI

BLAST score

g218207

165

```
carboxylase S [Oryza sativa]
                     401093
Seq. No.
                     LIB3431-040-P1-K2-B7
Seq. ID
Method
                     BLASTX
NCBI GI
                     g1353352
BLAST score
                     302
E value
                     2.0e-27
Match length
                     94
% identity
                     (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                     reinhardtiil
Seq. No.
                     401094
                     LIB3431-040-P1-K2-C1
Seq. ID
Method
                     BLASTX
NCBI GI
                     g114521
BLAST score
                     520
E value
                     6.0e-53
Match length
                     127
                     86
% identity
                     ATP SYNTHASE ALPHA CHAIN >gi_67827_pir__PWRZA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain -
NCBI Description
                     rice chloroplast >gi_11979_emb_CAA33993_ (X15901) ATPase alpha subunit [Oryza sativa] >gi_226696_prf__1603356X
                     ATPase alpha [Oryza sativa]
Seq. No.
                     401095
Seq. ID
                     LIB3431-040-P1-K2-C11
Method
                     BLASTX
NCBI GI
                     q3126854
BLAST score
                     520
E value
                     7.0e-53
Match length
                     104
% identity
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                     401096
Seq. No.
Seq. ID
                     LIB3431-040-P1-K2-C12
Method
                     BLASTX
NCBI GI
                     g231610
BLAST score
                     193
                     5.0e-15
E value
Match length
                     54
% identity
NCBI Description
                     ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR
                     >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC
                     3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase
                     (gamma subunit) [Nicotiana tabacum]
Seq. No.
                     401097
Seq. ID
                     LIB3431-040-P1-K2-C2
Method
                     BLASTN
```

sativa] >gi 226375 prf 1508256A ribulose bisphosphate

```
1.0e-87
E value
                  253
Match length
% identity
                  91
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
Seq. No.
                  401098
Seq. ID
                  LIB3431-040-P1-K2-C3
Method
                  BLASTX
NCBI GI
                  g2130042
BLAST score
                  486
E value
                  6.0e-56
Match length
                  126
% identity
                  92
                  Mg-chelatase chain Xantha-f - barley >gi 861199 (U26916)
NCBI Description
                  protoporphyrin IX Mg-chelatase subunit precursor [Hordeum
                  vulgare]
Seq. No.
                  401099
                  LIB3431-040-P1-K2-C4
Seq. ID
Method
                  BLASTN
                  q5295936
NCBI GI
BLAST score
                  36
                  3.0e-11
E value
Match length
                  48
% identity
                  94
                  Oryza sativa genomic DNA, chromosome 6, clone:P0681F10,
NCBI Description
                  complete sequence
Seq. No.
                  401100
                  LIB3431-040-P1-K2-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3559814
BLAST score
                  658
E value
                  4.0e-69
Match length
                  146
% identity
                  (Y15781) transketolase 1 [Capsicum annuum]
NCBI Description
                  401101
Seq. No.
Seq. ID
                  LIB3431-040-P1-K2-C6
                  BLASTX
Method
NCBI GI
                  g2501356
BLAST score
                  523
E value
                  3.0e-53
Match length
                  139
% identity
                  74
                  TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK)
NCBI Description
                  >gi_1658322_emb_CAA90427_ (Z50099) transketolase precursor
                  [Solanum tuberosum]
Seq. No.
                  401102
                  LIB3431-040-P1-K2-C7
Seq. ID
Method
                  BLASTX
                  g4995921
NCBI GI
```

230

BLAST score

```
4.0e-19
E value
Match length
                   56
                   79
% identity
                   (AJ006708) HMG1 protein [Zea mays]
NCBI Description
Seq. No.
                   401103
Seq. ID
                  LIB3431-040-P1-K2-C8
Method
                  BLASTX
NCBI GI
                   g1747294
BLAST score
                   613
E value
                   8.0e-64
Match length
                   141
% identity
                   86
NCBI Description
                   (D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
                   401104
Seq. No.
Seq. ID
                   LIB3431-040-P1-K2-D1
Method
                   BLASTN
NCBI GI
                   q5042437
BLAST score
                   199
E value
                   1.0e-108
Match length
                   199
% identity
                   100
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.
                   401105
Seq. ID
                   LIB3431-040-P1-K2-D11
Method
                   BLASTX
NCBI GI
                   g2570511
BLAST score
                   648
E value
                   6.0e-68
Match length
                   127
% identity
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   401106
Seq. ID
                  LIB3431-040-P1-K2-D12
Method
                   BLASTX
NCBI GI
                   a2570511
BLAST score
                   472
                   2.0e-47
E value
Match length
                   96
                   95
% identity
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                   401107
Seq. No.
Seq. ID
                  LIB3431-040-P1-K2-D2
Method
                  BLASTX
NCBI GI
                   q3914587
BLAST score
                  144
                   3.0e-09
E value
Match length
                   30
% identity
                  100
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_1076711_pir__S49992
                   ribulose-1,5-bisphosphate carboxylase/oxygenase - Aegilops
```

squarrosa >gi_599620_emb_CAA58150_ (X83095) rbcS gene

Method

BLASTX

Seq. No. 401108 Seq. ID LIB3431-040-P1-K2-D4 Method BLASTX NCBI GI g132105 BLAST score 559 E value 1.0e-57 Match length 122 % identity 86 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa] Seq. No. 401109 Seq. ID LIB3431-040-P1-K2-D8 Method BLASTX NCBI GI q3345477 BLAST score 218 E value 6.0e-18 Match length 58 69 % identity NCBI Description (AB016283) carbonic anhydrase [Oryza sativa] Seq. No. 401110 Seq. ID LIB3431-040-P1-K2-E1 Method BLASTX NCBI GI q115787 BLAST score 405 E value 1.0e-39 Match length 90 % identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCI TYPE I CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] Seq. No. 401111 Seq. ID LIB3431-040-P1-K2-E10 Method BLASTX NCBI GI q4490317 BLAST score 364 1.0e-34 E value Match length 133 % identity (AL035678) putative protein [Arabidopsis thaliana] NCBI Description Seq. No. 401112 Seq. ID LIB3431-040-P1-K2-E11

[Aegilops squarrosa]

```
q4490317
NCBI GI
BLAST score
                   319
E value
                   3.0e-29
Match length
                   158
% identity
                   42
                   (AL035678) putative protein [Arabidopsis thaliana]
NCBI Description
                   401113
Seq. No.
Seq. ID
                   LIB3431-040-P1-K2-E12
Method
                   BLASTX
NCBI GI
                   q729668
BLAST score
                   228
                   1.0e-18
E value
Match length
                   66
% identity
                   HISTONE H1 >gi_2147479_pir__S65059 histone H1,
NCBI Description
                   drought-inducible - Lycopersicon pennellii >gi_436823
                   (U01890) Solanum pennellii histone H1 [Solanum pennellii]
Seq. No.
                   401114
                   LIB3431-040-P1-K2-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q120661
BLAST score
                   198
E value
                   1.0e-16
Match length
                   90
% identity
                   60
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
NCBI Description
                   PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
                   dehydrogenase A-subunit precursor [Nicotiana tabacum]
Seq. No.
                   401115
                   LIB3431-040-P1-K2-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   503
E value
                   3.0e-51
Match length
                   104
                   88
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   401116
Seq. ID
                   LIB3431-040-P1-K2-E4
Method
                   BLASTX
NCBI GI
                   g2407281
BLAST score
                   254
E value
                   3.0e-22
Match length
                   68
                   75
% identity
```

```
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
                  401117
Seq. No.
Seq. ID
                  LIB3431-040-P1-K2-E5
Method
                  BLASTN
NCBI GI
                  g3819221
BLAST score
                  84
                  3.0e-39
E value
Match length
                  282
                  83
% identity
                  Hordeum vulgare partial mRNA; clone cMWG0721
NCBI Description
Seq. No.
                  401118
                  LIB3431-040-P1-K2-E8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2407281
BLAST score
                  455
E value
                  2.0e-45
Match length
                  119
                  77
% identity
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  401119
                  LIB3431-040-P1-K2-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1174745
BLAST score
                  359
E value
                  3.0e - 34
Match length
                  80
                  89
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                  >gi_1363523_pir__S53761 triose-phosphate isomerase (EC
                  5.3.1.1) precursor, chloroplast - rye
                  >qi 609262 emb CAA83533 (Z32521) triosephosphate isomerase
                   [Secale cereale] >gi 1095494 prf 2109226B triosephosphate
                  isomerase [Secale cereale]
Seq. No.
                  401120
Seq. ID
                  LIB3431-040-P1-K2-F10
Method
                  BLASTX
NCBI GI
                  g3885894
BLAST score
                  507
E value
                  2.0e-51
Match length
                  132
% identity
                  77
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
                  401121
Seq. No.
Seq. ID
                  LIB3431-040-P1-K2-F11
Method
                  BLASTX
NCBI GI
                  q2104959
BLAST score
                  324
E value
                  2.0e-30
                  77
Match length
% identity
                  74
```

```
NCBI Description (U96925) immunophilin [Vicia faba]
Seq. No.
                    401122
Seq. ID
                    LIB3431-040-P1-K2-F4
Method
                    BLASTX
NCBI GI
                    g120657
BLAST score
                    293
E value
                    2.0e-27
Match length
                    89
% identity
                    79
                    GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                    CHLOROPLAST >gi_66024_pir__DEZMG3 glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                    (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                    maize >gi_168479 (M18976) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_ (X15408)
                    glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.
                    401123
Seq. ID
                    LIB3431-040-P1-K2-F5
Method
                    BLASTX
NCBI GI
                    q4455158
BLAST score
                    249
E value
                    4.0e-21
Match length
                    71
% identity
                    63
NCBI Description (AL021687) kinase-like protein [Arabidopsis thaliana]
                    401124
Seq. No.
Seq. ID
                    LIB3431-040-P1-K2-F8
Method
                    BLASTX
NCBI GI
                    q3850581
BLAST score
                    252
                    1.0e-21
E value
Match length
                    84
% identity
NCBI Description
                    (AC005278) EST gb N96383 comes from this gene. [Arabidopsis
                    thaliana]
                    401125
Seq. No.
Seq. ID
                    LIB3431-040-P1-K2-G1
Method
                    BLASTN
                    g596077
NCBI GI
BLAST score
                    62
                    1.0e-26
E value
Match length
                    78
% identity
                    95
NCBI Description
                    Zea mays thiamine biosynthetic enzyme (thi1-1) mRNA,
                    complete cds
                    401126
Seq. No.
Seq. ID
                    LIB3431-040-P1-K2-G12
Method
                    BLASTX
NCBI GI
                    q2570515
BLAST score
                    456
```

7.0e-49

133

E value Match length

```
% identity
                  (AF022740) glycolate oxidase [Oryza sativa]
NCBI Description
Seq. No.
                  401127
                  LIB3431-040-P1-K2-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914603
BLAST score
                  707
E value
                  7.0e-75
Match length
                  146
% identity
                  95
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
                  401128
Seq. No.
                  LIB3431-040-P1-K2-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  214
                  1.0e-117
E value
Match length
                  309
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  401129
Seq. No.
                  LIB3431-040-P1-K2-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                  q461498
BLAST score
                  248
                  2.0e-21
E value
                  84
Match length
                  55
% identity
                  ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC
NCBI Description
                  TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2)
                  (ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC
                  2.6.1.2) - proso millet >gi 296204_emb_CAA49199_ (X69421)
                  alanine aminotransferase [Panicum miliaceum]
                  401130
Seq. No.
Seq. ID
                  LIB3431-040-P1-K2-G5
                  BLASTX
Method
                  g4138290
NCBI GI
BLAST score
                  360
E value
                  7.0e-35
Match length
                  95
                  75
% identity
NCBI Description
                  (AJ005841) thioredoxin M [Oryza sativa]
Seq. No.
                  401131
                  LIB3431-040-P1-K2-G7
Seq. ID
Method
                  BLASTX
                  g3080420
NCBI GI
                  392
BLAST score
```

6.0e-38

E value

```
Match length
                  142
% identity
                  56
                  (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                  401132
Seq. No.
Seq. ID
                  LIB3431-040-P1-K2-G8
Method
                  BLASTX
                  g3080420
NCBI GI
                  389
BLAST score
                  1.0e-37
E value
                  120
Match length
                  62
% identity
                  (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                  thaliana]
                  401133
Seq. No.
Seq. ID
                  LIB3431-040-P1-K2-H10
Method
                  BLASTN
NCBI GI
                  g6103440
BLAST score
                  93
E value
                  5.0e-45
Match length
                  149
% identity
                  91
NCBI Description
                  Oryza sativa metallothionein-like protein (ML2) mRNA,
                  complete cds
Seq. No.
                  401134
Seq. ID
                  LIB3431-040-P1-K2-H12
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  146
E value
                  3.0e-76
Match length
                  186
% identity
                  95
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                  401135
Seq. No.
                  LIB3431-040-P1-K2-H2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3135542
BLAST score
                  39
E value
                  8.0e-13
Match length
                  67
                  90
% identity
NCBI Description Oryza sativa aquaporin (PIP2a) mRNA, complete cds
Seq. No.
                  401136
                  LIB3431-040-P1-K2-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4584342
BLAST score
                  221
E value
                  6.0e-18
Match length
                  120
                  42
% identity
NCBI Description (AC007127) putative ubiquitin protein [Arabidopsis
```

thaliana] 401137 Seq. No. Seq. ID LIB3431-040-P1-K2-H6 Method BLASTX NCBI GI g4079798 BLAST score 540 E value 2.0e-55 Match length 107 % identity 99 (AF052203) 23 kDa polypeptide of photosystem II [Oryza NCBI Description sativa] Seq. No. 401138 LIB3431-040-P1-K2-H8 Seq. ID Method BLASTX NCBI GI g2407281 BLAST score 616 E value 3.0e-64 Match length 118 97 % identity NCBI Description (AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] Seq. No. 401139 Seq. ID LIB3431-040-P1-K2-H9 Method BLASTX NCBI GI q2072555 BLAST score 348 E value 7.0e-33 Match length 62 % identity NCBI Description (AF001396) metallothionein-like protein [Oryza sativa] >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like protein [Oryza sativa] Seq. No. 401140 Seq. ID LIB3431-040-P1-N1-A10 Method BLASTN NCBI GI q2072554 BLAST score 301 E value 1.0e-169 Match length 333 % identity NCBI Description Oryza sativa metallothionein-like protein mRNA, complete Seq. No. 401141 Seq. ID LIB3431-040-P1-N1-B12 Method BLASTX NCBI GI q2754849 BLAST score 169 E value 7.0e-12 Match length 42 79 % identity NCBI Description (AF039000) putative serine-glyoxylate aminotransferase

[Fritillaria agrestis]

```
Seq. No.
                   401142
Seq. ID
                   LIB3431-040-P1-N1-B6
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   712
E value
                   2.0e-75
Match length
                   130
% identity
                   100
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   401143
                   LIB3431-040-P1-N1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q871931
BLAST score
                   263
                   9.0e-23
E value
Match length
                   80
% identity
                   70
                   (D30763) ferredoxin [Oryza sativa]
NCBI Description
                   401144
Seq. No.
Seq. ID
                   LIB3431-040-P1-N1-C11
Method
                   BLASTX
NCBI GI
                   g517500
                   333
BLAST score
                   3.0e-31
E value
Match length
                   81
% identity
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                   protein [Zea mays] >gi_444338_prf__1906386A photosystem II
                   OE17 protein [Pisum sativum]
Seq. No.
                   401145
                   LIB3431-040-P1-N1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3126854
BLAST score
                   324
E value
                   4.0e-30
Match length
                   67
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   401146
Seq. No.
Seq. ID
                   LIB3431-040-P1-N1-C2
Method
                   BLASTX
                   g4995921
NCBI GI
BLAST score
                   218
```

1.0e-17

E value

```
56
Match length
                  75
% identity
NCBI Description
                  (AJ006708) HMG1 protein [Zea mays]
Seq. No.
                  401147
                  LIB3431-040-P1-N1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1747294
BLAST score
                  290
E value
                   6.0e-26
Match length
                  55
% identity
                  100
                  (D45383) vacuolar H+-pyrophosphatase [Oryza sativa]
NCBI Description
Seq. No.
                   401148
                  LIB3431-040-P1-N1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5295936
BLAST score
                  56
E value
                  1.0e-22
Match length
                  124
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone:P0681F10,
NCBI Description
                  complete sequence
Seq. No.
                  401149
                  LIB3431-040-P1-N1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2529342
BLAST score
                  157
E value
                  2.0e-10
                  37
Match length
% identity
                  84
                  (L76554) transketolase [Spinacia oleracea]
NCBI Description
Seq. No.
                  401150
Seq. ID
                  LIB3431-040-P1-N1-C8
Method
                  BLASTN
NCBI GI
                  q218207
BLAST score
                  170
                  1.0e-90
E value
Match length
                  262
% identity
                  91
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS1139
Seq. No.
                  401151
Seq. ID
                  LIB3431-040-P1-N1-D12
Method
                  BLASTX
NCBI GI
                  g115794
                  446
BLAST score
E value
                   3.0e-44
                  96
Match length
% identity
                  89
                  CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
NCBI Description
                  III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding
```

```
>gi 19277 emb CAA42818 (X60275) LHCII type III
                  [Lycopersicon esculentum]
                  401152
Seq. No.
Seq. ID
                  LIB3431-040-P1-N1-D3
Method
                  BLASTX
NCBI GI
                  q606817
BLAST score
                  312
E value
                  2.0e-28
                  59
Match length
                  98
% identity
                  (U08404) carbonic anhydrase [Oryza sativa]
NCBI Description
                  >gi 5917783 gb AAD56038.1 AF182806 1 (AF182806) carbonic
                  anhydrase 3 [Oryza sativa]
Seq. No.
                  401153
Seq. ID
                  LIB3431-040-P1-N1-D5
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  609
E value
                  2.0e-63
Match length
                  112
% identity
                  99
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401154
Seq. ID
                  LIB3431-040-P1-N1-D9
Method
                  BLASTX
NCBI GI
                  q551047
BLAST score
                  275
                  3.0e-29
E value
Match length
                  71
% identity
NCBI Description
                  (X79277) type II LHCI [Lolium temulentum]
Seq. No.
                  401155
                  LIB3431-040-P1-N1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  546
E value
                  6.0e-56
Match length
                  99
% identity
                  100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
```

protein type III precursor (cab-13) - tomato

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

```
Seq. No.
                  401156
                  LIB3431-040-P1-N1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  512
E value
                  9.0e-63
Match length
                  120
                  97
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401157
Seq. ID
                  LIB3431-040-P1-N1-E7
Method
                  BLASTN
NCBI GI
                  q20181
BLAST score
                  127
E value
                  5.0e-65
Match length
                  163
% identity
                  94
NCBI Description Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
                  401158
Seq. No.
Seq. ID
                  LIB3431-040-P1-N1-E8
Method
                  BLASTN
NCBI GI
                  q22239
BLAST score
                  44
E value
                  2.0e-15
Match length
                  68
% identity
NCBI Description Maize cytosolic mRNA for subunit A of chloroplast GAPDH
                  (GapA) glyceraldehyde-3-phosphate dehydrogenase
                  401159
Seq. No.
Seq. ID
                  LIB3431-040-P1-N1-E9
Method
                  BLASTX
NCBI GI
                  q347451
BLAST score
                  149
E value
                  2.0e-09
Match length
                  32
% identity
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
```

401160

Seq. No.

Seq. ID

```
LIB3431-040-P1-N1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1174745
BLAST score
                  355
                  1.0e-33
E value
                  85
Match length
                  84
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM)
NCBI Description
                  >gi 1363523 pir S53761 triose-phosphate isomerase (EC
                  5.3.1.1) precursor, chloroplast - rye
                  >gi 609262 emb CAA83533 (Z32521) triosephosphate isomerase
                  [Secale cereale] >gi 1095494 prf 2109226B triosephosphate
                  isomerase [Secale cereale]
Seq. No.
                  401161
                  LIB3431-040-P1-N1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885894
BLAST score
                  233
E value
                  2.0e-19
Match length
                  61
% identity
                  79
NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
Seq. No.
                  401162
Seq. ID
                  LIB3431-040-P1-N1-F4
Method
                  BLASTN
NCBI GI
                  q3345476
BLAST score
                  267
E value
                  1.0e-148
Match length
                  315
% identity
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds
Seq. No.
                  401163
Seq. ID
                  LIB3431-040-P1-N1-G3
Method
                  BLASTX
NCBI GI
                  q167097
BLAST score
                  179
E value
                  1.0e-25
Match length
                  76
% identity
                  (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                  [Hordeum vulgare]
                  401164
Seq. No.
Seq. ID
                  LIB3431-040-P1-N1-G4
Method
                  BLASTX
NCBI GI
                  q3785996
BLAST score
                  238
E value
                  5.0e-20
Match length
                  97
% identity
                  51
NCBI Description
                  (AC005499) putative annexin [Arabidopsis thaliana]
Seq. No.
```

LIB3431-040-P1-N1-G6

E value

2.0e-32

```
Method
                   BLASTN
NCBI GI
                   g4138289
BLAST score
                   354
                   0.0e+00
E value
                   354
Match length
                   100
% identity
NCBI Description Oryza sativa mRNA for thioredoxin M
Seq. No.
                   401166
Seq. ID
                  LIB3431-040-P1-N1-G8
Method
                  BLASTX
                   g3080420
NCBI GI
BLAST score
                   175
E value
                   2.0e-12
                   43
Match length
                   74
% identity
                   (AL022604) putative sugar transporter protein [Arabidopsis
NCBI Description
                   thaliana]
                   401167
Seq. No.
                  LIB3431-040-P1-N1-H1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2072554
BLAST score
                   370
E value
                   0.0e + 00
Match length
                   378
% identity
                   99
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
Seq. No.
                   401168
Seq. ID
                   LIB3431-040-P1-N1-H12
Method
                  BLASTX
NCBI GI
                   q4079798
BLAST score
                   392
E value
                   6.0e-38
Match length
                   79
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
Seq. No.
                   401169
Seq. ID
                   LIB3431-040-P1-N1-H3
Method
                  BLASTX
NCBI GI
                   q2662310
BLAST score
                   158
E value
                   8.0e-21
Match length
                   56
% identity
NCBI Description
                   (AB009307) bpwl [Hordeum vulgare]
                   401170
Seq. No.
Seq. ID
                   LIB3431-040-P1-N1-H4
Method
                  BLASTX
NCBI GI
                   g3126854
BLAST score
                   343
```

NCBI GI

```
Match length
                   67
                   97
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   401171
Seq. No.
Seq. ID
                   LIB3431-040-P1-N1-H7
Method
                   BLASTX
NCBI GI
                   q347451
BLAST score
                   376
E value
                   4.0e-36
                   69
Match length
                   99
% identity
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                   satival
                   401172
Seq. No.
                   LIB3431-040-P1-N1-H9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g218209
BLAST score
                   149
E value
                   5.0e-78
Match length
                   329
% identity
                   96.
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS2106
                   401173
Seq. No.
Seq. ID
                   LIB3431-041-P1-N1-A10
Method
                   BLASTN
NCBI GI
                   g3126853
BLAST score
                   230
E value
                   1.0e-126
Match length
                   249
                   99
% identity
NCBI Description
                   Oryza sativa chlorophyll a/b binding protein (RCABP89)
                   mRNA, nuclear gene encoding chloroplast protein, complete
                   cds
Seq. No.
                   401174
Seq. ID
                   LIB3431-041-P1-N1-A2
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   432
E value
                   1.0e-42
Match length
                   82
% identity
                   100
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   401175
Seq. No.
Seq. ID
                   LIB3431-041-P1-N1-A3
Method
                   BLASTX
```

q4079798

NCBI GI

g2072554

```
BLAST score
                   277
                   2.0e-24
E value
Match length
                   52
                   100
% identity
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   401176
Seq. No.
Seq. ID
                   LIB3431-041-P1-N1-A4
                   BLASTX
Method
                   q2982301
NCBI GI
BLAST score
                   255
E value
                   8.0e-22
                   91
Match length
% identity
                   (AF051235) YGL010w-like protein [Picea mariana]
NCBI Description
                   401177
Seq. No.
                   LIB3431-041-P1-N1-A6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q6093827
BLAST score
                   169
                   1.0e-11
E value
                   97
Match length
% identity
                   41
                   PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
NCBI Description
                   [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
                   PROTEIN PSBY-2] >gi_2956690 emb_CAA11248_ (AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928 (AF079800) PsbY
                   precursor [Arabidopsis thaliana]
Seq. No.
                   401178
Seq. ID
                   LIB3431-041-P1-N1-A7
Method
                   BLASTX
NCBI GI
                   g120661
BLAST score
                   225
E value
                   2.0e-18
Match length
                   43
                   95
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
NCBI Description
                   PRECURSOR >gi 170237 (M14417) glyceraldehyde-3-phosphate
                   dehydrogenase A-subunit precursor [Nicotiana tabacum]
Seq. No.
                   401179
                   LIB3431-041-P1-N1-A9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g11640
BLAST score
                   45
E value
                   4.0e-16
Match length
                   137
% identity
                   42
NCBI Description Liverwort Marchantia polymorpha chloroplast genome DNA
Seq. No.
                   401180
                   LIB3431-041-P1-N1-B1
Seq. ID
Method
                   BLASTN
```

BLAST score

274

```
BLAST score
                   395
E value
                   0.0e + 00
Match length
                   403
                   100
% identity
                   Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
Seq. No.
                   401181
                   LIB3431-041-P1-N1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1835731
                   300
BLAST score
                    3.0e-27
E value
                   77
Match length
                   75
% identity
                    (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                    401182
Seq. ID
                   LIB3431-041-P1-N1-B12
Method
                   BLASTX
NCBI GI
                   g6094430
BLAST score
                   191
                   7.0e-19
E value
Match length
                    55
% identity
                    95
                   TUBULIN ALPHA-2 CHAIN (ALPHA-TUBULIN 2) >gi 2511533
NCBI Description
                    (AF008121) alpha-tubulin 2 [Eleusine indica]
Seq. No.
                    401183
Seq. ID
                   LIB3431-041-P1-N1-B5
Method
                   BLASTX
NCBI GI
                   g2970051
BLAST score
                   249
E value
                    3.0e-21
Match length
                    60
% identity
                    77
NCBI Description
                    (AB012110) ARG10 [Vigna radiata]
Seq. No.
                    401184
                   LIB3431-041-P1-N1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115793
BLAST score
                   309
E value
                    3.0e-28
Match length
                    63
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR
                   (CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_
                    (X63197) type III LHCII CAB precursor protein [Hordeum
                   vulgare]
Seq. No.
                    401185
                   LIB3431-041-P1-N1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g417260
```

Method

BLASTX

```
4.0e-24
E value
                    79
Match length
                    71
% identity
                    LIGHT REGULATED PROTEIN PRECURSOR >gi_422003 pir S33632
NCBI Description
                    lir1 protein - rice >gi 20263 emb CAA\overline{4}8706 (X68807)
                    light-regulated gene [Oryza sativa]
Seq. No.
                    401186
                    LIB3431-041-P1-N1-B8
Seq. ID
Method
                    BLASTX
                    g2997591
NCBI GI
                    238
BLAST score
E value
                    6.0e-20
Match length
                    61
% identity
                    79
                    (AF020814) glucose-6-phosphate/phosphate-translocator
NCBI Description
                    precursor [Pisum sativum]
Seq. No.
                    401187
                    LIB3431-041-P1-N1-C1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q131225
BLAST score
                    216
E value
                    2.0e-17
Match length
                    56
% identity
                    PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                    V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I
                    hydrophobic protein [Hordeum vulgare]
                    401188
Seq. No.
Seq. ID
                    LIB3431-041-P1-N1-C10
Method
                    BLASTX
NCBI GI
                    q131225
BLAST score
                    327
E value
                    3.0e - 30
Match length
                    92
% identity
                    PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                    V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I
                    hydrophobic protein [Hordeum vulgare]
                    401189
Seq. No.
                    LIB3431-041-P1-N1-C11
Seq. ID
Method
                    BLASTN
NCBI GI
                    g20262
BLAST score
                    265
                    1.0e-147
E value
                    272
Match length
                    99
% identity
NCBI Description O.sativa light-induced mRNA
                    401190
Seq. No.
                    LIB3431-041-P1-N1-C12
Seq. ID
```

NCBI GI

q218154

```
g2570511
NCBI GI
BLAST score
                    163
E value
                    2.0e-26
Match length
                    74
                    80
% identity
NCBI Description
                     (AF022738) chlorophyll a-b binding protein [Oryza sativa]
Seq. No.
                    401191
Seq. ID
                    LIB3431-041-P1-N1-C5
                    BLASTX
Method
NCBI GI
                    q6015059
BLAST score
                    422
E value
                    2.0e-41
Match length
                    83
                    100
% identity
                    ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096
NCBI Description
                     (AF030517) translation elongation factor-1 alpha; EF-1
                    alpha [Oryza sativa]
Seq. No.
                     401192
                    LIB3431-041-P1-N1-C8
Seq. ID
Method
                    BLASTX
NCBI GI
                    q730510
BLAST score
                    150
E value
                     1.0e-09
Match length
                     45
                     67
% identity
                    RAS-RELATED PROTEIN RIC1 >gi_542150_pir_S38740 GTP-binding protein - rice >gi_432607_gb_AAB28535_ (S66160) ras-related GTP binding protein possessing GTPase activity=ric1 [Oryza
NCBI Description
                    sativa=rice, var. Yamahoushi, callus, Peptide, 202 aa]
                     [Oryza sativa]
Seq. No.
                     401193
Seq. ID
                    LIB3431-041-P1-N1-D2
                    BLASTN
Method
NCBI GI
                    q6006355
BLAST score
                    88
E value
                    1.0e-41
Match length
                    130
% identity
                     46
                    Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
NCBI Description
Seq. No.
                     401194
                    LIB3431-041-P1-N1-D3
Seq. ID
Method
                    BLASTX
NCBI GI
                    q4877984
BLAST score
                    262
                    1.0e-22
E value
Match length
                    53
% identity
NCBI Description
                     (AF145755) THA4 [Zea mays]
Seq. No.
                    401195
Seq. ID
                    LIB3431-041-P1-N1-D7
Method
                    BLASTN
```

```
BLAST score
                   46
                   1.0e-16
E value
Match length
                   46
% identity
                   100
                  Oryza sativa gene for cytoplasmic aldolase, complete cds,
NCBI Description
                   clone:Aldp
                   401196
Seq. No.
Seq. ID
                  LIB3431-041-P1-N1-E10
Method
                  BLASTX
NCBI GI
                   q3582335
BLAST score
                   493
                   1.0e-49
E value
Match length
                   105
% identity
                   84
NCBI Description
                   (AC005496) unknown protein [Arabidopsis thaliana]
                   401197
Seq. No.
                  LIB3431-041-P1-N1-E11
Seq. ID
Method
                  BLASTX
                   g3738261
NCBI GI
BLAST score
                   171
E value
                   3.0e-12
Match length
                   58
% identity
                   67
NCBI Description
                   (AB018412) chloroplast phosphoglycerate kinase [Populus
                  nigra]
                   401198
Seq. No.
                  LIB3431-041-P1-N1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                   g416266
BLAST score
                   44
E value
                   2.0e-15
Match length
                  126
                   83
% identity
NCBI Description
                  Rice mRNA for oxygen-evolving protein, partial sequence
                   401199
Seq. No.
                  LIB3431-041-P1-N1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3075487
BLAST score
                   308
                   1.0e-173
E value
Match length
                   315
% identity
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
                  mRNA, complete cds
Seq. No.
                   401200
                  LIB3431-041-P1-N1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3885887
BLAST score
                   465
                  0.0e+00
E value
Match length
                   465
```

100

% identity

```
NCBI Description Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
                  401201
Seq. No.
Seq. ID
                  LIB3431-041-P1-N1-E8
Method
                  BLASTX
NCBI GI
                  g3386621
BLAST score
                  157
                  2.0e-10
E value
Match length
                  36
                  81
% identity
                  (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  401202
                  LIB3431-041-P1-N1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3980406
BLAST score
                  360
E value
                  4.0e-34
                  105
Match length
% identity
NCBI Description
                   (AC004561) putative tropinone reductase [Arabidopsis
                  thaliana]
Seq. No.
                  401203
                  LIB3431-041-P1-N1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3377797
BLAST score
                  225
E value
                  2.0e-18
Match length
                  68
% identity
                   (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
Seq. No.
                  401204
                  LIB3431-041-P1-N1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1835730
                                                           BLAST score
                  123
E value
                  7.0e-63
Match length
                  147
% identity
                  96
NCBI Description
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
                  complete cds
Seq. No.
                  401205
Seq. ID
                  LIB3431-041-P1-N1-F2
Method
                  BLASTX
NCBI GI
                  q131225
BLAST score
                  364
E value
                  1.0e-34
Match length
                  99
% identity
                  72
```

```
PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                   precursor - barley >qi 167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
Seq. No.
                   401206
                   LIB3431-041-P1-N1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131225
BLAST score
                   143
E value
                   6.0e-09
Match length
                   53
                   49
% identity
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
                   401207
Seq. No.
Seq. ID
                   LIB3431-041-P1-N1-F5
Method
                   BLASTN
NCBI GI
                   q2293567
BLAST score
                   79
E value
                   2.0e-36
                   181
Match length
% identity
NCBI Description Oryza sativa HvB12D homolog mRNA, complete cds
                   401208
Seq. No.
                   LIB3431-041-P1-N1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2980805
                   322
BLAST score
                   1.0e-29
E value
                   80
Match length
% identity
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]
                   401209
Seq. No.
                   LIB3431-041-P1-N1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1084455
                   362
BLAST score
                   2.0e-34
E value
                   69
Match length
% identity
                   100
NCBI Description
                   peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                   >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
Seq. No.
                   401210
                   LIB3431-041-P1-N1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   a82080
BLAST score
                   145
                   1.0e-09
E value
                   33
Match length
```

82

% identity

```
chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                   401211
Seq. No.
Seq. ID
                  LIB3431-041-P1-N1-G3
Method
                  BLASTX
NCBI GI
                  q517500
BLAST score
                  251
                   1.0e-21
E value
                  73
Match length
                   70
% identity
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
                   401212
Seq. No.
                  LIB3431-041-P1-N1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2696804
BLAST score
                  152
E value
                   5.0e-10
Match length
                  28
% identity
                   100
                   (AB009665) water channel protein [Oryza sativa]
NCBI Description
Seq. No.
                   401213
Seq. ID
                  LIB3431-041-P1-N1-H3
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                   351
E value
                   4.0e-33
Match length
                   69
% identity
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa]
Seq. No.
                   401214
Seq. ID
                  LIB3431-041-P1-N1-H6
Method
                  BLASTN
NCBI GI
                  g2570512
BLAST score
                   48
E value
                  2.0e-18
Match length
                   48
                  100
% identity
NCBI Description
                  Oryza sativa chlorophyll a-b binding protein mRNA, complete
Seq. No.
                  401215
Seq. ID
                  LIB3431-041-P1-N1-H7
Method
                  BLASTX
NCBI GI
                  q5410350
BLAST score
                  216
E value
                  3.0e-17
Match length
                  45
% identity
NCBI Description (AF124045) unknown [Sorghum bicolor]
```

```
401216
Seq. No.
Seq. ID
                   LIB3431-041-P1-N1-H8
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   235
                    1.0e-19
E value
Match length
                   55
% identity
                    (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                    401217
Seq. No.
                   LIB3431-041-P2-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                    380
E value
                    3.0e-59
Match length
                    135
% identity
                   87
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
Seq. No.
                    401218
Seq. ID
                   LIB3431-041-P2-K1-A3
Method
                   BLASTX
NCBI GI
                   q4079798
BLAST score
                   218
E value
                    3.0e-18
Match length
                    50
% identity
NCBI Description
                    (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                    sativa]
Seq. No.
                    401219
Seq. ID
                   LIB3431-041-P2-K1-A7
Method
                   BLASTX
                   g120657
NCBI GI
BLAST score
                   575
E value
                   2.0e-59
Match length
                   136
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                   CHLOROPLAST >gi_66024_pir__DEZMG3
                   glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                   maize >gi_168479 (M18976) glyceraldehyde-3-phosphate
                   dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_ (X15408)
                   qlyceraldehyde-3-phosphate dehydrogenase [Zea mays]
Seq. No.
                    401220
Seq. ID
                   LIB3431-041-P2-K1-B1
Method
                   BLASTN
NCBI GI
                   q6103440
BLAST score
                    313
```

```
E value
                  1.0e-176
Match length
                  332
                  99
% identity
                  Oryza sativa metallothionein-like protein (ML2) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  401221
Seq. ID
                  LIB3431-041-P2-K1-B10
Method
                  BLASTX
NCBI GI
                  q1835731
                  297
BLAST score
                  4.0e-31
E value
Match length
                  90
                  80
% identity
NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                  401222
Seq. No.
                  LIB3431-041-P2-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4958922
BLAST score
                  219
E value
                  1.0e-17
                  88
Match length
                  53
% identity
NCBI Description (AB027757) NADPH oxidoreductase homolog [Cicer arietinum]
Seq. No.
                  401223
Seq. ID
                  LIB3431-041-P2-K1-B12
Method
                  BLASTX
NCBI GI
                  q6094430
                  200
BLAST score
                  6.0e-16
E value
Match length
                  70
% identity
NCBI Description
                  TUBULIN ALPHA-2 CHAIN (ALPHA-TUBULIN 2) >gi 2511533
                   (AF008121) alpha-tubulin 2 [Eleusine indica]
Seq. No.
                  401224
Seq. ID
                  LIB3431-041-P2-K1-B6
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                  494
E value
                  5.0e-50
Match length
                  95
% identity
NCBI Description
                  (AF022738) chlorophyll a-b binding protein [Oryza sativa]
Seq. No.
                  401225
Seq. ID
                  LIB3431-041-P2-K1-B7
Method
                  BLASTN
NCBI GI
                  g20262
BLAST score
                  296
E value
                  1.0e-166
Match length
                  328
% identity
                  98
```

NCBI Description O.sativa light-induced mRNA

Method

BLASTX

```
Seq. No.
                   401226
Seq. ID
                  LIB3431-041-P2-K1-B9
Method
                   BLASTX
NCBI GI
                   g1652217
BLAST score
                   269
E value
                   1.0e-23
Match length
                   107
                   54
% identity
NCBI Description
                   (D90903) hypothetical protein [Synechocystis sp.]
Seq. No.
                   401227
Seq. ID
                  LIB3431-041-P2-K1-C11
Method
                   BLASTX
NCBI GI
                   q417260
BLAST score
                   322
                   1.0e-29
E value
                   80
Match length
% identity
                   75
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                   lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
                   401228
Seq. No.
Seq. ID
                  LIB3431-041-P2-K1-C12
Method
                   BLASTX
NCBI GI
                   g4689380
BLAST score
                   402
E value
                   2.0e-39
Match length
                   78
% identity
                   95
                   (AF139465) LHCII type III chlorophyll a/b binding protein
NCBI Description
                   [Vigna radiata]
                   401229
Seq. No.
Seq. ID
                  LIB3431-041-P2-K1-C2
Method
                  BLASTX
NCBI GI
                   g4582455
BLAST score
                   185
E value
                   9.0e-14
Match length
                   99
                   36
% identity
NCBI Description
                   (AC007071) putative receptor protein kinase [Arabidopsis
                   thaliana]
                   401230
Seq. No.
                  LIB3431-041-P2-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2662343
BLAST score
                   711
E value
                  2.0e-75
Match length
                  140
% identity
                   99
                   (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
                   401231
Seq. No.
                  LIB3431-041-P2-K1-C7
Seq. ID
```

Seq. ID

```
NCBI GI
                  g3551954
BLAST score
                   349
E value
                   9.0e-33
Match length
                  137
% identity
                   (AF082030) senescence-associated protein 5 [Hemerocallis
NCBI Description
                  hybrid cultivar]
Seq. No.
                  401232
Seq. ID
                  LIB3431-041-P2-K1-C8
Method
                  BLASTN
NCBI GI
                  q432606
BLAST score
                  75
                   4.0e-34
E value
Match length
                  154
                  99
% identity
                  ricl=ras-related GTP binding protein possessing GTPase
NCBI Description
                  activity [Oryza sativa=rice, Yamahoushi, callus, mRNA, 955
                  401233
Seq. No.
                  LIB3431-041-P2-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1707998
BLAST score
                  612
E value
                  1.0e-63
Match length
                  150
% identity
                  SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                   (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)
                   (SHMT) >gi 481944 pir__S40218 glycine
                  hydroxymethyltransferase (EC 2.1.2.1) - potato
                  >gi_438247_emb_CAA81082_ (Z25863) glycine
                  hydroxymethyltransferase [Solanum tuberosum]
Seq. No.
                  401234
Seq. ID
                  LIB3431-041-P2-K1-D2
Method
                  BLASTN
                  a6006355
NCBI GI
BLAST score
                  132
                  6.0e-68
E value
Match length
                  197
% identity
                  46
                  Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
NCBI Description
                  401235
Seq. No.
Seq. ID
                  LIB3431-041-P2-K1-D3
Method
                  BLASTX
NCBI GI
                  q4877984
BLAST score
                  369
E value
                  3.0e-35
Match length
                  143
                  57
% identity
NCBI Description
                  (AF145755) THA4 [Zea mays]
                  401236
Seq. No.
```

LIB3431-041-P2-K1-D6

Seq. No.

401241

```
Method
                  BLASTX
NCBI GI
                  g5903095
                  159
BLAST score
E value
                  2.0e-10
Match length
                  49
% identity
                  61
NCBI Description (AC008017) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  401237
                  LIB3431-041-P2-K1-D7
Seq. ID
                  BLASTN .
Method
NCBI GI
                  q218154
BLAST score
                  46
E value
                  1.0e-16
Match length
                  46
                  100
% identity
                  Oryza sativa gene for cytoplasmic aldolase, complete cds,
NCBI Description
                  clone:Aldp
Seq. No.
                  401238
Seq. ID
                  LIB3431-041-P2-K1-E10
Method
                  BLASTX
NCBI GI
                  q3582335
BLAST score
                  745
E value
                  3.0e-88
Match length
                  165
% identity
NCBI Description
                  (AC005496) unknown protein [Arabidopsis thaliana]
                  401239
Seq. No.
Seq. ID
                  LIB3431-041-P2-K1-E11
Method
                  BLASTX
NCBI GI
                  g129915
BLAST score
                  493
E value
                  9.0e-50
Match length
                  131
% identity
                  78
                  PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 66912 pir _TVWTGC phosphoglycerate kinase (EC 2.7.2.3)
                  precursor, chloroplast - wheat >gi_21833_emb_CAA33303_
                  (X15233) phosphoglycerate kinase (AA 1 - 480) [Triticum
                  aestivum] >gi_3293043_emb_CAA51931_ (X73528)
                  phosphoglycerate kinase [Triticum aestivum]
Seq. No.
                  401240
Seq. ID
                  LIB3431-041-P2-K1-E12
Method
                  BLASTX
NCBI GI
                  q3128167
BLAST score
                  202
E value
                  2.0e-15
Match length
                  155
% identity
NCBI Description
                  (AC004521) hypothetical protein [Arabidopsis thaliana]
                  >gi 3212874 (AC004005) hypothetical protein [Arabidopsis
                  thaliana]
```

Seq. No.

401246

```
Seq. ID
                   LIB3431-041-P2-K1-E2
                   BLASTN
Method
NCBI GI
                   g6015437
BLAST score
                   36
E value
                   3.0e-11
Match length
                   36
                   100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                   401242
Seq. No.
                   LIB3431-041-P2-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3986695
BLAST score
                   519
E value
                   7.0e-53
Match length
                   122
% identity
                   86
NCBI Description
                   (AF101423) ribosomal protein L12 [Cichorium intybus]
Seq. No.
                   401243
Seq. ID
                   LIB3431-041-P2-K1-E5
Method
                   BLASTX
NCBI GI
                   q131388
BLAST score
                   188
E value
                   4.0e-14
Match length
                   87
                   56
% identity
                   OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                   THYLAKOID MEMBRANE PROTEIN) >gi 100831_pir__S16260
                   photosystem II oxygen-evolving complex protein 1 - common
                   wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408) 33kDa oxygen evolving protein of photosystem II [Triticum
                   aestivum]
Seq. No.
                   401244
Seq. ID
                   LIB3431-041-P2-K1-E6
Method
                   BLASTX
NCBI GI
                   q3075488
BLAST score
                   426
E value
                   2.0e-51
Match length
                   126
% identity
NCBI Description
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                   401245
Seq. ID
                   LIB3431-041-P2-K1-E7
Method
                   BLASTN
NCBI GI
                   q3885887
BLAST score
                   355
E value
                   0.0e + 00
Match length
                   363
% identity
                   100
                   Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                   complete cds
```

Seq. ID

```
LIB3431-041-P2-K1-E8
Seq. ID
Method
                  BLASTX
                  g3386621
NCBI GI
BLAST score
                  511
                  7.0e-52
E value
                  117
Match length
                  85
% identity
                  (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  401247
                  LIB3431-041-P2-K1-E9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3980400
BLAST score
                  487
                  5.0e-49
E value
                  166
Match length
% identity
                  58
                   (AC004561) putative tropinone reductase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  401248
Seq. ID
                  LIB3431-041-P2-K1-F1
Method
                  BLASTX
NCBI GI
                  q3377797
BLAST score
                  295
E value
                  1.0e-26
Match length
                  116
                  53
% identity
                  (AF075597) Similar to 60S ribosome protein L19; coded for
NCBI Description
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
                  401249
Seq. No.
Seq. ID
                  LIB3431-041-P2-K1-F11
Method
                  BLASTN
NCBI GI
                  q2072554
BLAST score
                  307
                  1.0e-172
E value
Match length
                  319
% identity
                  99
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  401250
Seq. No.
Seq. ID
                  LIB3431-041-P2-K1-F12
Method
                  BLASTX
NCBI GI
                  q1835731
                  537
BLAST score
                  7.0e-55
E value
                  114
Match length
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                  401251
```

LIB3431-041-P2-K1-F2

```
Method
                   BLASTX
NCBI GI
                   q131225
BLAST score
                   386
E value
                   1.0e-37
Match length
                   83
                   90
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
Seq. No.
                   401252
                   LIB3431-041-P2-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2660677
BLAST score
                   418
E value
                   4.0e-41
Match length
                   124
                   62
% identity
NCBI Description
                   (AC002342) unknown protein [Arabidopsis thaliana]
                   401253
Seq. No.
                   LIB3431-041-P2-K1-F5
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2293567
BLAST score
                   165
E value
                   6.0e-88
                   197
Match length
                   96
% identity
                   Oryza sativa HvB12D homolog mRNA, complete cds
NCBI Description
                   401254
Seq. No.
Seq. ID
                   LIB3431-041-P2-K1-F6
                   BLASTN
Method
                   g3821780
NCBI GI
BLAST score
                   36
E value
                   8.0e-11
Match length
                   36
                   100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
                   401255
Seq. No.
                   LIB3431-041-P2-K1-F7
Seq. ID
Method
                   BLASTX
                   g2980805
NCBI GI
BLAST score
                   596
                   8.0e-62
E value
Match length
                   145
                   77
% identity
                   (AL022197) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   401256
                   LIB3431-041-P2-K1-F8
Seq. ID
                   BLASTX
Method
                   g4007792
NCBI GI
BLAST score
                   316
```

6.0e-29

E value

E value

3.0e-18

```
148
 Match length
                    43
 % identity
 NCBI Description
                    (AL034463) Xenopus 14s cohesin smc1 subunit homolog
                    [Schizosaccharomyces pombe]
                    401257
 Seq. No.
 Seq. ID
                    LIB3431-041-P2-K1-F9
 Method
                    BLASTX
 NCBI GI
                    g1084455
 BLAST score
                    565
                    3.0e-58
 E value
                    125
 Match length
 % identity
                    86
 NCBI Description
                    peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice
                    >gi 600767 (L29469) cyclophilin 2 [Oryza sativa]
 Seq. No.
                    401258
 Seq. ID
                    LIB3431-041-P2-K1-G11
 Method
                    BLASTX
 NCBI GI
                    g1168537
 BLAST score
                    532
 E value
                    2.0e-54
 Match length
                    125
 % identity
                    75
 NCBI Description
                    ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732
                    aspartic proteinase (EC 3.4.23.-) - rice
                    >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase
                    [Oryza sativa]
                    401259
Seq. No.
 Seq. ID
                    LIB3431-041-P2-K1-G12
 Method
                    BLASTX
 NCBI GI
                    q82080
 BLAST score
                    154
 E value
                    3.0e-10
 Match length
                    57
 % identity
                    56
 NCBI Description
                    chlorophyll a/b-binding protein type III precursor - tomato
                    >gi 226872 prf 1609235A chlorophyll a/b binding protein
                    [Lycopersicon esculentum]
 Seq. No. .
                    401260
 Seq. ID
                    LIB3431-041-P2-K1-G7
 Method
                    BLASTX
 NCBI GI
                    q2293480
 BLAST score
                    228
 E value
                    4.0e-19
 Match length
                    51
 % identity
 NCBI Description
                    (AF011331) glycine-rich protein [Oryza sativa]
 Seq. No.
                    401261
 Seq. ID
                    LIB3431-041-P2-K1-G8
 Method
                    BLASTN
 NCBI GI
                    q3819215
 BLAST score
                    49
```

```
69
Match length
                  93
% identity
NCBI Description
                  Hordeum vulgare partial mRNA; clone cMWG0706
                  401262
Seq. No.
                  LIB3431-041-P2-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q119958
BLAST score
                  428
E value
                  4.0e-42
                  123
Match length
                  70
% identity
                  FERREDOXIN III PRECURSOR (FD III) >gi 168473 (M73831)
NCBI Description
                  ferredoxin [Zea mays] >gi 1864001 dbj BAA19251 (AB001387)
                  Fd III [Zea mays] >gi_444686_prf__1907324C
                  ferredoxin: ISOTYPE=III [Zea mays]
                  401263
Seq. No.
Seq. ID
                  LIB3431-041-P2-K1-H1
Method
                  BLASTN
NCBI GI
                  g2570510
BLAST score
                  102
E value
                  2.0e-50
Match length
                  149
                  92
% identity
NCBI Description
                  Oryza sativa chlorophyll a-b binding protein mRNA, complete
                  401264
Seq. No.
Seq. ID
                  LIB3431-041-P2-K1-H10
Method
                  BLASTX
NCBI GI
                  q542200
BLAST score
                  143
                  7.0e-09
E value
Match length
                  55
% identity
NCBI Description
                  hypothetical protein - garden asparagus
                  >gi 452714 emb CAA54526 (X77320) unknown [Asparagus
                  officinalis]
                  401265
Seq. No.
Seq. ID
                  LIB3431-041-P2-K1-H3
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  682
                  6.0e-72
E value
Match length
                  148
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
```

carboxylase S [Oryza sativa]

```
Seq. No.
                   401266
Seq. ID
                  LIB3431-041-P2-K1-H7
Method
                  BLASTN
NCBI GI
                   g5410347
                  90
BLAST score
E value
                   6.0e-43
Match length
                  258
% identity
                  84
                  Sorghum bicolor BAC clone 110K5, partial sequence
NCBI Description
Seq. No.
                   401267
Seq. ID
                  LIB3431-041-P2-K1-H8
Method
                  BLASTX
NCBI GI
                   q3126854
BLAST score
                   634
E value
                   2.0e-66
Match length
                   122
% identity
                   98
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   401268
Seq. No.
Seq. ID
                  LIB3431-042-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q2407281
BLAST score
                   662
E value
                   1.0e-69
Match length
                  129
                   95
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq. No.
                   401269
Seq. ID
                  LIB3431-042-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q4733937
BLAST score
                   343
E value
                   3.0e-32
Match length
                   142
% identity
NCBI Description
                  (AF080245) sesquiterpene synthase [Elaeis oleifera]
                   401270
Seq. No.
                  LIB3431-042-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3183079
BLAST score
                   620
E value
                   1.0e-64
Match length
                  141
% identity
                  84
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
NCBI Description
                  >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate
                  dehydrogenase [Oryza sativa]
Seq. No.
                   401271
                  LIB3431-042-P1-K1-A4
Seq. ID
Method
                  BLASTX
```

% identity

100

```
NCBI GI
                   q1261917
BLAST score
                   318
E value
                   3.0e-29
                   98
Match length
% identity
                   (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
NCBI Description
Seq. No.
                   401272
                   LIB3431-042-P1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2129608
BLAST score
                   594
E value
                   1.0e-61
Match length
                   138
% identity
                   81
                   GTP-binding protein, 68K - Arabidopsis thaliana >gi 807577
NCBI Description
                   (L38614) GTP-binding protein [Arabidopsis thaliana]
Seq. No.
                   401273
                   LIB3431-042-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g6056199
BLAST score
                   281
E value
                   6.0e-25
Match length
                   116
% identity
NCBI Description
                   (AC009400) unknown protein [Arabidopsis thaliana]
                   401274
Seq. No.
Seq. ID
                   LIB3431-042-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g347451
BLAST score
                   255
E value
                   6.0e-22
Match length
                   99
% identity
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                   sativa]
                   401275
Seq. No.
Seq. ID
                   LIB3431-042-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g4972067
BLAST score
                   247
E value
                   6.0e-21
Match length
                   106
% identity
NCBI Description
                   (AL078467) putative protei [Arabidopsis thaliana]
                   401276
Seq. No.
Seq. ID
                   LIB3431-042-P1-K1-B11
Method
                   BLASTN
NCBI GI
                   q4959460
BLAST score
                   36
E value
                   1.0e-10
Match length
                   36
```

```
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
Seq. No.
                   401277
Seq. ID
                   LIB3431-042-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   g729135
BLAST score
                   584
E value
                   2.0e-60
Match length
                   144
                   76
% identity
NCBI Description
                   CAFFEIC ACID 3-O-METHYLTRANSFERASE
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                   3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612 catechol O-methyltransferase (EC \overline{2.1.1.6}) - maize
                   >qi 168532 (M73235) O-methyltransferase [Zea mays]
                   401278
Seq. No.
                   LIB3431-042-P1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5733882
                   299
BLAST score
E value
                   5.0e-27
Match length
                   136
                   52
% identity
                   (AC007932) Similar to gb_Y12465 serine/threonine,kinase
NCBI Description
                   from Sorghum bicolor and contains a PF 00069 Eukaryotic
                   protein kinase domain. [Arabidopsis thaliana]
                   401279
Seq. No.
                   LIB3431-042-P1-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2065017
BLAST score
                   290
E value
                   5.0e-26
Match length
                   115
% identity
NCBI Description
                  (Y09822) hypothetical protein [Arabidopsis thaliana]
                   401280
Seq. No.
                   LIB3431-042-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q871931
BLAST score
                   416
E value
                   9.0e-41
                   111
Match length
% identity
NCBI Description (D30763) ferredoxin [Oryza sativa]
                   401281
Seq. No.
                   LIB3431-042-P1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q133936
BLAST score
                   221
E value
                   6.0e-18
Match length
                   70
                   67
% identity
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70867_pir__R3RZ3
```

Seq. ID

```
ribosomal protein S3 - rice chloroplast
>gi_12025_emb_CAA33934_ (X15901) ribosomal protein S3
                   [Oryza sativa] >gi 226646 prf 1603356BW ribosomal protein
                   S3 [Oryza sativa]
                   401282
Seq. No.
Seq. ID
                   LIB3431-042-P1-K1-B9
Method
                   BLASTN
NCBI GI
                   q2286152
BLAST score
                   53
E value
                   8.0e-21
Match length
                   73
                   93
% identity
                   Zea mays cytoplasmic malate dehydrogenase mRNA, complete
NCBI Description
                   401283
Seq. No.
                   LIB3431-042-P1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2754849
BLAST score
                   574
E value
                   3.0e-59
Match length
                   124
% identity
                   89
NCBI Description
                   (AF039000) putative serine-glyoxylate aminotransferase
                   [Fritillaria agrestis]
                   401284
Seq. No.
Seq. ID
                   LIB3431-042-P1-K1-C11
                   BLASTX
Method
NCBI GI
                   q132105
BLAST score
                   525
E value
                   1.0e-53
Match length
                   115
                   86
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   401285
                   LIB3431-042-P1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4567284
BLAST score
                   162
E value
                   5.0e-11
Match length
                   51
% identity
                   63
NCBI Description
                   (AC006841) unknown protein [Arabidopsis thaliana]
                   401286
Seq. No.
```

LIB3431-042-P1-K1-C4

Method BLASTX NCBI GI q1483563 BLAST score 676 E value 3.0e-71 Match length 139

91

NCBI Description (X99825) leucine aminopeptidase [Petroselinum crispum]

Seq. No. Seq. ID

% identity

401287 LIB3431-042-P1-K1-C5

Method BLASTX NCBI GI q132105 BLAST score 546 5.0e-56 E value Match length 129 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribúlose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 401288

Seq. ID LIB3431-042-P1-K1-C6

Method BLASTX NCBI GI q3915131 BLAST score 613 E value 7.0e-64 Match length 119 100 % identity

THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1) NCBI Description

>gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin h [Oryza sativa] >gi 1930072 (U92541) thioredoxin h [Oryza

sativa]

401289 Seq. No.

LIB3431-042-P1-K1-C7 Seq. ID

Method BLASTX NCBI GI g417260 412 BLAST score E value 2.0e-40 126 Match length % identity

LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 NCBI Description

lir1 protein - rice >gi 20263 emb CAA48706_ (X68807)

light-regulated gene [Oryza sativa]

401290 Seq. No.

Seq. ID LIB3431-042-P1-K1-C8

Method BLASTX g4079798 NCBI GI 335 BLAST score

```
3.0e - 31
E value
Match length
                   111
% identity
                   62
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
Seq. No.
                   401291
Seq. ID
                   LIB3431-042-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   g2911068
BLAST score
                   199
E value
                   2.0e-15
Match length
                   43
% identity
                   79
                   (AL021960) G10-like protein [Arabidopsis thaliana]
NCBI Description
                   401292
Seq. No.
Seq. ID
                   LIB3431-042-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   q322867
BLAST score
                   520
                   5.0e-53
E value
Match length
                   135
% identity
                   75
                   translation initiation factor eIF-4F isozyme form subunit
NCBI Description
                  p82 - wheat
Seq. No.
                   401293
                   LIB3431-042-P1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3914603
BLAST score
                   287
                   1.0e-25
E value
Match length
                   134
% identity
                   51
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                   CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                   activase [Oryza sativa]
                   401294
Seq. No.
Seq. ID
                   LIB3431-042-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g733454
                   503
BLAST score
E value
                   6.0e-51
Match length
                   118
% identity
NCBI Description
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
Seq. No.
                   401295
Seq. ID
                  LIB3431-042-P1-K1-D6
Method
                  BLASTX
                  g3913018
NCBI GI
                   740
BLAST score
```

9.0e-79

E value

```
143
Match length
                   99
% identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                    (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                   aldolase [Oryza sativa]
                   401296
Seq. No.
Seq. ID
                   LIB3431-042-P1-K1-D7
                   BLASTX
Method
NCBI GI
                   q320618
                   565
BLAST score
                   3.0e-58
E value
                   124
Match length
% identity
                   86
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
Seq. No.
                   401297
Seq. ID
                   LIB3431-042-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   652
E value
                   2.0e-68
Match length
                   122
                   99
% identity
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
Seq. No.
                   401298
Seq. ID
                   LIB3431-042-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   536
E value
                   7.0e-55
Match length
                   118
% identity
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
Seq. No.
                   401299
Seq. ID
                   LIB3431-042-P1-K1-E1
Method
                   BLASTN
NCBI GI
                   a6016845
BLAST score
                   89
                   3.0e-42
E value
Match length
                   146
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
```

```
Seq. No.
                   401300
                   LIB3431-042-P1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g100796
BLAST score
                   712
E value
                   2.0e-75
Match length
                   143
% identity
                   93
                   phosphoribulokinase (EC 2.7.1.19) - wheat
NCBI Description
Seq. No.
                   401301
                   LIB3431-042-P1-K1-E3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g902200
BLAST score
                   296
E value
                   1.0e-166
Match length
                   388
% identity
                   49
NCBI Description
                   Z.mays complete chloroplast genome
Seq. No.
Seq. ID
                   LIB3431-042-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   472
E value
                   2.0e-47
Match length
                   105
                   85
% identity
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   401303
Seq. ID
                   LIB3431-042-P1-K1-E6
Method
                   BLASTX
                   g3582335
NCBI GI
BLAST score
                   728
E value
                   2.0e-77
Match length
                   141
% identity
                   (AC005496) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   401304
Seq. ID
                   LIB3431-042-P1-K1-E7
Method
                   BLASTN
NCBI GI
                   a2072724
BLAST score
                   384
                   0.0e + 00
E value
Match length
                   403
% identity
                   99
NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog1
Seq. No.
                   401305
                   LIB3431-042-P1-K1-E8
Seq. ID
```

```
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  657
                  5.0e-69
E value
                  140
Match length
% identity
                  89
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401306
                  LIB3431-042-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2570515
BLAST score
                  640
                  5.0e-67
E value
Match length
                  134
% identity
                  (AF022740) glycolate oxidase [Oryza sativa]
NCBI Description
                  401307
Seq. No.
                  LIB3431-042-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  677
                  2.0e-71
E value
Match length
                  132
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401308
                  LIB3431-042-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  432
E value
                  1.0e-42
Match length
                  122
% identity
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
```

401309

Seq. No.

Method

BLASTX

```
Seq. ID
                  LIB3431-042-P1-K1-F11
Method
                  BLASTN
NCBI GI
                  g2407280
BLAST score
                  44
                  4.0e-16
E value
Match length
                  56
% identity
                  95
                  Oryza sativa ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit mRNA, complete cds
                  401310
Seq. No.
Seq. ID
                  LIB3431-042-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  q6015437
BLAST score
                  36
                  1.0e-10
E value
                  36
Match length
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  401311
Seq. No.
                  LIB3431-042-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3868756
BLAST score
                  699
                  5.0e-74
E value
Match length
                  136
% identity
                  93
NCBI Description (D86611) catalase [Oryza sativa]
                  401312
Seq. No.
Seq. ID
                  LIB3431-042-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g548603
BLAST score
                  372
E value
                  1.0e-35
Match length
                  113
% identity
                  69
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                  barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                  401313
Seq. ID
                  LIB3431-042-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g1353352
BLAST score
                  197
E value
                  4.0e-15
Match length
                  54
% identity
NCBI Description
                  (U31975) alanine aminotransferase [Chlamydomonas
                  reinhardtii]
Seq. No.
                  401314
Seq. ID
                  LIB3431-042-P1-K1-G10
```

Method

BLASTX

```
NCBI GI
                  q3789954
BLAST score
                  667
                  3.0e-70
E value
Match length
                  124
                  100
% identity
NCBI Description
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                  sativa]
Seq. No.
                  401315
Seq. ID
                  LIB3431-042-P1-K1-G11
                  BLASTN
Method
NCBI GI
                  g5803242
BLAST score
                  86
E value
                  2.0e-40
                  157
Match length
                  20
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
NCBI Description
Seq. No.
                  401316
Seq. ID
                  LIB3431-042-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q1173347
BLAST score
                  711
E value
                  2.0e-75
Match length
                  141
% identity
                  94
NCBI Description
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7) P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi 14265 emb CAA46507
                  (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  401317
Seq. ID
                  LIB3431-042-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q1708424
BLAST score
                  408
E value
                  8.0e-40
Match length
                  112
% identity
                  65
NCBI Description
                  ISOFLAVONE REDUCTASE HOMOLOG >gi 1230614 (U48590)
                  isoflavone reductase-like protein [Lupinus albus]
Seq. No.
                  401318
Seq. ID
                  LIB3431-042-P1-K1-G3
Method
                  BLASTN
NCBI GI
                  q1658312
BLAST score
                  104
E value
                  3.0e-51
Match length
                  104
                  50
% identity
NCBI Description
                  O.sativa osr40q2 gene
                  401319
Seq. No.
Seq. ID
                  LIB3431-042-P1-K1-G4
```

```
NCBI GI
                  q132105
BLAST score
                  632
E value
                  4.0e-66
                  135
Match length
                  88
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_ RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401320
Seq. ID
                  LIB3431-042-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g3426051
BLAST score
                  577
E value
                  1.0e-59
Match length
                  135
% identity
                  84
NCBI Description
                  (AC005168) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  401321
Seq. ID
                  LIB3431-042-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g3915096
BLAST score
                  507
E value
                  6.0e-58
Match length
                  137
% identity
NCBI Description
                  TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID
                  4-HYDROXYLASE) (CA4H) (C4H) (P450C4H) (CYTOCHROME P450 73)
                  >gi 1574976 (U47293) trans-cinnamate 4-hydroxylase [Populus
                  tremuloides]
Seq. No.
                  401322
Seq. ID
                  LIB3431-042-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  304
E value
                  1.0e-27
Match length
                  76
% identity
NCBI Description (272488) CP12 [Nicotiana tabacum]
Seq. No.
                  401323
Seq. ID
                  LIB3431-042-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q2190992
BLAST score
                  301
E value
                  3.0e-27
Match length
                  117
% identity
```

NCBI Description (AF004358) glutathione S-transferase TSI-1 [Aegilops

tauschii]

```
Seq. No.
                   401324
Seq. ID
                   LIB3431-042-P1-K1-H1
Method
                   BLASTX
NCBI GI
                   g128191
BLAST score
                   480
E value
                   3.0e-48
Match length
                   134
                   77
% identity
                   NITRATE REDUCTASE [NAD(P)H] >gi_66210 pir RDBHNP nitrate
NCBI Description
                   reductase (NAD(P)H) (EC 1.6.6.2) - barley
                   >gi_19065_emb_CAA42739_ (X60173) nitrate reductase
                   (NAD(P)H) [Hordeum vulgare]
Seq. No.
                   401325
                   LIB3431-042-P1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3789954
BLAST score
                   615
E value
                   4.0e-64
Match length
                   115
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   401326
Seq. No.
Seq. ID
                   LIB3431-042-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   q1173347
BLAST score
                   201
E value
                   1.0e-15
Match length
                   66
% identity
NCBI Description
                   SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7) P2ASE)
                   >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                   3.1.3.37) precursor - wheat >gi 14265 emb CAA46507
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                   aestivum]
Seq. No.
                   401327
Seq. ID
                   LIB3431-042-P1-K1-H2
Method
                   BLASTX.
NCBI GI
                   q6093778
BLAST score
                   370
E value
                   2.0e-35
Match length
                   103
% identity
NCBI Description
                   PROTEASOME COMPONENT C3 (MACROPAIN SUBUNIT C3)
                   (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C3)
                   >gi_2511574_emb_CAA73619.1_ (Y13176) multicatalytic
endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520)
                   20S proteasome subunit PAB1 [Arabidopsis thaliana]
                   >gi 4966368 gb AAD34699.1_AC006341_27 (AC006341) Identical
                   to gb Y13176 Arabidopsis thaliana mRNA for proteasome
                   subunit prc3. ESTs gb H36972, gb T22551 and gb_T13800 come
```

from this gene 401328 Seq. No. Seq. ID LIB3431-042-P1-K1-H3 Method BLASTX NCBI GI g3420052 BLAST score 485 E value 8.0e-51 Match length 137 77 % identity (AC004680) putative ubiqinone reductase [Arabidopsis NCBI Description thaliana] 401329 Seq. No. Seq. ID LIB3431-042-P1-K1-H4 Method BLASTX NCBI GI g3288821 BLAST score 666 E value 4.0e-70 Match length 138 % identity 90 NCBI Description (AF063901) alanine:qlyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana] Seq. No. 401330 Seq. ID LIB3431-042-P1-K1-H5 Method BLASTX NCBI GI g82080 BLAST score 455 E value 2.0e-45 Match length 131 % identity NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi_226872_prf__1609235A chlorophyll a/b binding protein [Lycopersicon esculentum] 401331 Seq. No. Seq. ID LIB3431-042-P1-K1-H6 Method BLASTX NCBI GI g115815 BLAST score 275 E value 1.0e-24 Match length 57 % identity NCBI Description CHLOROPHYLL A-B BINDING PROTEIN M9 PRECURSOR (LHCII TYPE I CAB-M9) (LHCP) >gi_100866_pir__S13098 chlorophyll a/b-binding protein precursor - maize >gi_22355_emb_CAA39376_ (X55892) light-harvesting

Seq. No. 401332

Seq. ID LIB3431-042-P1-K1-H7

Method BLASTX
NCBI GI g3914466
BLAST score 366

chlorophyll a/b binding protein [Zea mays]

Method

BLASTX

```
5.0e-35
E value
Match length
                  67
% identity
                  97
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi 2981214 (AF052429) photosystem I complex PsaN
                  subunit precursor [Zea mays]
Seq. No.
                  401333
Seq. ID
                  LIB3431-042-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  g3885887
BLAST score
                  371
E value
                  0.0e + 00
Match length
                  378
% identity
                  100
NCBI Description
                  Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
                  401334
Seq. No.
Seq. ID
                  LIB3431-042-P1-N1-A3
Method
                  BLASTX
NCBI GI
                  q3183079
BLAST score
                  210
E value
                  1.0e-16
                  58
Match length
                  74
% identity
                  MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
NCBI Description
                  >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate
                  dehydrogenase [Oryza sativa]
Seq. No.
                  401335
                  LIB3431-042-P1-N1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1071925
                  194
BLAST score
E value
                  9.0e-15
Match length
                  51
% identity
NCBI Description
                  Cw-19 peptide, non specific lipid transfer protein,
                  precursor - barley >gi_510528_emb_CAA48623_ (X68656) Cw-19
                  peptide, non specific lipid transfer protein [Hordeum
                  vulgare]
                  401336
Seq. No.
                  LIB3431-042-P1-N1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129825
BLAST score
                  391
E value
                  1.0e-37
                  93
Match length
                  83
% identity
                  dynamin-like protein phragmoplastin 12 - soybean
NCBI Description
                  >gi 1217994 (U25547) SDL [Glycine max]
                  401337
Seq. No.
                  LIB3431-042-P1-N1-A8
Seq. ID
```

```
NCBI GI
                   q6056199
BLAST score
                   149
                   2.0e-09
E value
                   80
Match length
                   39
% identity
                   (AC009400) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   401338
                   LIB3431-042-P1-N1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4972067
BLAST score
                   195
                   2.0e-15
E value
Match length
                   107
% identity
                   50
                   (AL078467) putative protei [Arabidopsis thaliana]
NCBI Description
                   401339
Seq. No.
Seq. ID
                   LIB3431-042-P1-N1-B12
Method
                   BLASTX
NCBI GI
                   q729135
BLAST score
                   315
E value
                   7.0e-29
Match length
                   74
                   78
% identity
NCBI Description
                  CAFFEIC ACID 3-O-METHYLTRANSFERASE
                   (S-ADENOSYSL-L-METHIONINE: CAFFEIC ACID
                   3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir___$28612
                   catechol O-methyltransferase (EC 2.1.1.6) - maize
                   >gi 168532 (M73235) O-methyltransferase [Zea mays]
Seq. No.
                   401340
Seq. ID
                   LIB3431-042-P1-N1-B3
Method
                   BLASTX
NCBI GI
                   q3158476
BLAST score
                   270
                   2.0e-23
E value
Match length
                   65
                   75
% identity
NCBI Description
                   (AF067185) aquaporin 2 [Samanea saman]
Seq. No.
                   401341
                   LIB3431-042-P1-N1-B4
Seq. ID
Method
                   BLASTX
                   g2065019
NCBI GI
BLAST score
                   258
E value
                   3.0e-22
Match length
                   95
% identity
                   25
                   (Y09823) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   401342
Seq. No.
Seq. ID
                   LIB3431-042-P1-N1-B5
Method
                   BLASTX
                   g871931
NCBI GI
BLAST score
                   161
```

8.0e-11

E value

E value

4.0e-38

```
Match length
                  44
                  75
% identity
NCBI Description
                   (D30763) ferredoxin [Oryza sativa]
                  401343
Seq. No.
Seq. ID
                  LIB3431-042-P1-N1-B6
Method
                  BLASTN
NCBI GI
                  q11957
BLAST score
                  368
                  0.0e + 00
E value
Match length
                  492
                  95
% identity
                  Rice complete chloroplast genome
NCBI Description
Seq. No.
                  401344
                  LIB3431-042-P1-N1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g517500
                  393
BLAST score
E value
                  4.0e-38
                  94
Match length
                  82
% identity
NCBI Description
                   (M87435) precursor of the oxygen evolving complex 17 kDa
                  protein [Zea mays] >gi_444338_prf__1906386A photosystem II
                  OE17 protein [Pisum sativum]
Seq. No.
                  401345
                  LIB3431-042-P1-N1-B9
Seq. ID
Method
                  BLASTX
                  g517500
NCBI GI
BLAST score
                  421
E value
                  2.0e-41
Match length
                  112
% identity
NCBI Description
                   (M87435) precursor of the oxygen evolving complex 17 kDa
                  protein [Zea mays] >gi_444338_prf__1906386A photosystem II
                  OE17 protein [Pisum sativum]
Seq. No.
                  401346
                  LIB3431-042-P1-N1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131225
BLAST score
                  311
E value
                  1.0e-28
Match length
                  76
                  76
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  401347
Seq. ID
                  LIB3431-042-P1-N1-C10
Method
                  BLASTX
NCBI GI
                  q2754849
BLAST score
                  394
```

Method

BLASTX

```
87
Match length
                   86
% identity
                    (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                   [Fritillaria agrestis]
Seq. No.
                   401348
                   LIB3431-042-P1-N1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   421
                   3.0e-41
E value
                   76
Match length
                   100
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   401349
Seq. ID
                   LIB3431-042-P1-N1-C4
Method
                   BLASTX
NCBI GI
                   q1483563
BLAST score
                   265
E value
                   6.0e-23
Match length
                   53
% identity
                   92
NCBI Description
                   (X99825) leucine aminopeptidase [Petroselinum crispum]
Seq. No.
                   401350
                   LIB3431-042-P1-N1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q671740
BLAST score
                   227
E value
                   1.0e-18
Match length
                   56
                   79
% identity
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
Seq. No.
                   401351
                   LIB3431-042-P1-N1-C6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q454881
BLAST score
                   207
E value
                   1.0e-113
                   234
Match length
                   97
% identity
NCBI Description Rice gene for thioredoxin h, complete cds
                   401352
Seq. No.
                   LIB3431-042-P1-N1-C7
Seq. ID
```

BLAST score

68

```
NCBI GI
                   q417260
BLAST score
                   406
E value
                   2.0e-39
Match length
                   128
% identity
                   65
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                   lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                   light-regulated gene [Oryza sativa]
Seq. No.
                   401353
Seq. ID
                   LIB3431-042-P1-N1-C9
Method
                   BLASTN
NCBI GI
                   q4079797
BLAST score
                   66
E value
                   1.0e-28
Match length
                   246
                   81
% identity
                  Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
NCBI Description
                   complete cds
                   401354
Seq. No.
                   LIB3431-042-P1-N1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   522
E value
                   4.0e-53
                   94
Match length
% identity
                   100
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   401355
                   LIB3431-042-P1-N1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q115787
                   402
BLAST score
E value
                   5.0e-39
                   77
Match length
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                   protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   401356
                   LIB3431-042-P1-N1-D12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g452439
```

BLAST score

220

```
1.0e-29
E value
Match length
                   201
                   87
% identity
                   Wheat (clone p80k-34) initiation factor isozyme 4F p82
NCBI Description
                   subunit mRNA, complete cds
Seq. No.
                   401357
                   LIB3431-042-P1-N1-D6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2407279
BLAST score
                   188
                    4.0e-14
E value
Match length
                   40
                   95
% identity
NCBI Description
                    (AF017362) aldolase [Oryza sativa]
                   401358
Seq. No.
Seq. ID
                   LIB3431-042-P1-N1-D7
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   417
                    6.0e-41 `
E value
Match length
                   79
% identity
                   100
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
Seq. No.
                    401359
                   LIB3431-042-P1-N1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3036951
BLAST score
                   341
E value
                    6.0e-32
Match length
                   66
% identity
NCBI Description
                    (AB012639) light harvesting chlorophyll a/b-binding protein
                    [Nicotiana sylvestris]
Seq. No.
                   401360
Seq. ID
                   LIB3431-042-P1-N1-D9
Method
                   BLASTX
NCBI GI
                   q3036951
BLAST score
                   334
E value
                   4.0e-31
Match length
                   66
% identity
                   97
NCBI Description
                    (AB012639) light harvesting chlorophyll a/b-binding protein
                    [Nicotiana sylvestris]
Seq. No.
                   401361
Seq. ID
                   LIB3431-042-P1-N1-E10
Method
                   BLASTX
NCBI GI
                   q6041819
```

NCBI GI

```
1.0e-17
E value
Match length
                    95
% identity
                    (AC009918) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    401362
Seq. ID
                    LIB3431-042-P1-N1-E2
Method
                    BLASTX
NCBI GI
                    g21839
BLAST score
                    361
                    3.0e - 34
E value
Match length
                    74
% identity
                    (X57952) phosphoribulokinase [Triticum aestivum]
NCBI Description
                    401363
Seq. No.
Seq. ID
                    LIB3431-042-P1-N1-E3
                    BLASTX
Method
NCBI GI
                    g1173275
BLAST score
                    653
                    2.0e-68
E value
                    147
Match length
                    91
% identity
NCBI Description
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
                    >gi_2119068_pir__S58630 ribosomal protein S7 - maize .
chloroplast >gi_902274_emb_CAA60339_ (X86563) ribosomal
                    protein S7 [Zea mays] >gi 902298 emb CAA60362 (X86563)
                    ribosomal protein S7 [Zea mays]
Seq. No.
                    401364
                    LIB3431-042-P1-N1-E5
Seq. ID
Method
                    BLASTX
NCBI GI
                    g115787
BLAST score
                    578
E value
                    1.0e-59
Match length
                    111
                    100
% identity
                    CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                    CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
                    401365
Seq. No.
Seq. ID
                    LIB3431-042-P1-N1-E6
Method
                    BLASTX
NCBI GI
                    g3582335
BLAST score
                    191
E value
                    2.0e-14
Match length
                    62
% identity
NCBI Description
                    (AC005496) unknown protein [Arabidopsis thaliana]
Seq. No.
                    401366
                    LIB3431-042-P1-N1-E7
Seq. ID
Method
                    BLASTN
```

q2072726

```
BLAST score
                  396
E value
                  0.0e + 00
Match length
                  455
                  97
% identity
NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2
Seq. No.
                  401367
Seq. ID
                  LIB3431-042-P1-N1-E8
Method
                  BLASTX
NCBI GI
                  a671740
BLAST score
                  320
E value
                  1.0e-29
Match length
                  61
% identity
                  98
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                  401368
                  LIB3431-042-P1-N1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  326
E value
                  3.0e-30
Match length
                  61
% identity
                  100
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overrightarrow{EC} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401369
Seq. ID
                  LIB3431-042-P1-N1-F1
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  233
E value
                  3.0e-19
Match length
                  47
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                   401370
                  LIB3431-042-P1-N1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115813
BLAST score
                  233
E value
                  2.0e-19
Match length
                  53
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
```

```
Seq. No.
                  401371
Seq. ID
                  LIB3431-042-P1-N1-F11
Method
                  BLASTN
NCBI GI
                  q2407280
BLAST score
                  44
                  4.0e-16
E value
Match length
                  56
% identity
                  95
NCBI Description
                  Oryza sativa ribulose 1,5-bisphosphate carboxylase small
                  subunit mRNA, complete cds
Seq. No.
                  401372
Seq. ID
                  LIB3431-042-P1-N1-F12
Method
                  BLASTX
NCBI GI
                  g733456
BLAST score
                  306
E value
                  6.0e-28
Match length
                  67
% identity
NCBI Description
                   (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
                  [Zea mays]
Seq. No.
                  401373
                  LIB3431-042-P1-N1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548603
BLAST score
                  204
                  2.0e-16
E value
Match length
                  42
% identity
                  93
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                  barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                  401374
                  LIB3431-042-P1-N1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3929924
                  298
BLAST score
E value
                  6.0e-27
Match length
                  56
% identity
                  100
NCBI Description (AB020502) catalase [Oryza sativa]
Seq. No.
                  401375
Seq. ID
                  LIB3431-042-P1-N1-F7
Method
                  BLASTX
NCBI GI
                  q548603
BLAST score
                  562
E value
                  7.0e-58
Match length
                  110
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi 478404 pir JQ2247 photosystem I chain D precursor -
```

```
Seq. No.
                  401376
                  LIB3431-042-P1-N1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1353352
BLAST score
                  197
E value
                   4.0e-15
Match length
                  54
                  72
% identity
NCBI Description
                   (U31975) alanine aminotransferase [Chlamydomonas
                  reinhardtii]
                  401377
Seq. No.
Seq. ID
                  LIB3431-042-P1-N1-G10
Method
                  BLASTX
                  q3789954
NCBI GI
                  174
BLAST score
                  2.0e-12
E value
Match length
                  31
% identity
                  100
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
Seq. No.
                   401378
Seq. ID
                  LIB3431-042-P1-N1-G11
Method
                  BLASTN
                  q4680189
NCBI GI
BLAST score
                  84
E value
                  3.0e-39
Match length
                  148
% identity
                  23
NCBI Description
                  Oryza sativa subsp. indica putative dnaJ-like protein,
                  putative myb-related protein, putative farnesyl
                  pyrophosphate synthase, and hypothetical protein genes,
                  complete cds
Seq. No.
                  401379
Seq. ID
                  LIB3431-042-P1-N1-G2
Method
                  BLASTX
                  q1708424
NCBI GI
BLAST score
                  274
E value
                  4.0e-24
Match length
                  92
% identity
                  57
                  ISOFLAVONE REDUCTASE HOMOLOG >gi_1230614 (U48590)
NCBI Description
                  isoflavone reductase-like protein [Lupinus albus]
                  401380
Seq. No.
Seq. ID
                  LIB3431-042-P1-N1-G3
Method
                  BLASTN
NCBI GI
                  q1658312
BLAST score
                  100
E value
                  9.0e-49
                  103
Match length
                  50
% identity
NCBI Description O.sativa osr40g2 gene
```

barley >qi 167085 (M98254) PSI-D subunit [Hordeum vulgare]

BLAST score

343

```
401381
Seq. No.
                   LIB3431-042-P1-N1-G4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g132105
BLAST score
                   295
E value
                   1.0e-26
                   57
Match length
% identity
                   98
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   401382
Seq. ID
                   LIB3431-042-P1-N1-G6
Method
                   BLASTX
NCBI GI
                   q3915088
BLAST score
                   254
E value
                   9.0e-22
                   75
Match length
% identity
                   63
                   TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID
NCBI Description
                   4-HYDROXYLASE) (CA4H) (C4H) (P450C4H) (CYTOCHROME P450 73)
                   >gi_903872 (L38898) trans-cinnamate 4-monooxygenase
                   [Petroselinum crispum]
                   401383
Seq. No.
                   LIB3431-042-P1-N1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1617197
BLAST score
                   276
E value
                   3.0e-24
Match length
                   71
% identity
NCBI Description
                   (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                   401384
                   LIB3431-042-P1-N1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1617197
BLAST score
                   189
E value
                   3.0e-14
Match length
                   39
% identity
NCBI Description
                   (Z72488) CP12 [Nicotiana tabacum]
                   401385
Seq. No.
                   LIB3431-042-P1-N1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g128191
```

NCBI GI

```
E value
                   4.0e-32
Match length
                  73
                  88
% identity
                  NITRATE REDUCTASE [NAD(P)H] >gi_66210_pir__RDBHNP nitrate
NCBI Description
                  reductase (NAD(P)H) (EC 1.6.6.2) - barley
                  >gi_19065_emb_CAA42739_ (X60173) nitrate reductase
                   (NAD(P)H) [Hordeum vulgare]
Seq. No.
                  401386
                  LIB3431-042-P1-N1-H10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3789953
BLAST score
                  68
E value
                  3.0e-30
                  100
Match length
                   92
% identity
                  Oryza sativa chlorophyll a/b-binding protein precursor
NCBI Description
                   (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
Seq. No.
                   401387
Seq. ID
                  LIB3431-042-P1-N1-H12
Method
                  BLASTN
NCBI GI
                  q5852077
BLAST score
                  179
E value
                  3.0e-96
Match length
                  218
% identity
NCBI Description
                  Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                  clone: b6015
Seq. No.
                   401388
Seq. ID
                  LIB3431-042-P1-N1-H2
Method
                  BLASTN
NCBI GI
                  q169820
BLAST score
                  90
E value
                   7.0e-43
Match length
                  373
                  82
% identity
NCBI Description
                  Oryza sativa triosephosphate isomerase (Rictpi) mRNA,
                  complete cds
Seq. No.
                  401389
Seq. ID
                  LIB3431-042-P1-N1-H3
Method
                  BLASTX
NCBI GI
                  q5734585
BLAST score
                  307
E value
                  5.0e-28
Match length
                  82
% identity
                   (AJ245861) putative internal rotenone-insensitive NADH
NCBI Description
                  dehydrogenase [Solanum tuberosum]
                  401390
Seq. No.
Seq. ID
                  LIB3431-042-P1-N1-H7
Method
                  BLASTX
```

q3914466

```
BLAST score
                  366
E value
                  5.0e-35
Match length
                  67
                  97
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                  (PSI-N) >gi 2981214 (AF052429) photosystem I complex PsaN
                  subunit precursor [Zea mays]
Seq. No.
                  401391
                  LIB3431-043-P1-K1-A1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q132105
BLAST score
                  735
E value
                  4.0e-78
                  156
Match length
                  90
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401392
Seq. ID
                  LIB3431-043-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  628
E value
                  1.0e-65
Match length
                  119
% identity
NCBI Description
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  401393
Seq. ID
                  LIB3431-043-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  q3885887
BLAST score
                  112
E value
                  2.0e-56
Match length
                  143
% identity
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  401394
Seq. ID
                  LIB3431-043-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q3150410
BLAST score
                  277
E value
                  2.0e-24
Match length
                  96
% identity
                  60
```

NCBI Description (AC004165) unknown protein [Arabidopsis thaliana]

```
Seq. No.
                    401395
 Seq. ID
                   LIB3431-043-P1-K1-A3
 Method
                   BLASTX
 NCBI GI
                    g3004555
 BLAST score
                    220
                    1.0e-17
 E value
Match length
                    164
 % identity
 NCBI Description
                    (AC003673) similar to salt inducible protein [Arabidopsis
                    thalianal
                    401396
 Seq. No.
                    LIB3431-043-P1-K1-A5
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    q4959460
 BLAST score
                    36
 E value
                    1.0e-10
Match length
                    36
                    100
 % identity
NCBI Description
                   Zea mays RACB small GTP binding protein mRNA, complete cds
                    401397
 Seq. No.
                   LIB3431-043-P1-K1-A7
 Seq. ID
Method
                   BLASTX
 NCBI GI
                    g125606
                              .i `
BLAST score
                    184
                    2.0e-13
 E value
                    59
Match length
                    61
 % identity
                   PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248
NCBI Description
                   pyruvate kinase (EC 2.7.1.40) - potato
                   >gi 22576 emb CAA37727 (X53688) pyruvate kinase [Solanum
                    tuberosum]
 Seq. No.
                    401398
                   LIB3431-043-P1-K1-A8
 Seq. ID
Method
                   BLASTX
NCBI GI
                    g3551954
 BLAST score
                    468
                    8.0e-47
E value
Match length
                    145
 % identity
NCBI Description
                    (AF082030) senescence-associated protein 5 [Hemerocallis
                   hybrid cultivar]
 Seq. No.
                    401399
                   LIB3431-043-P1-K1-A9
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g2570499
BLAST score
                   191
                    1.0e-14
E value
Match length
                    38
 % identity
                    100
NCBI Description
                    (AF022732) 23kDa polypeptide of photosystem II [Oryza
                    sativa]
```

401400

Seq. No.

```
LIB3431-043-P1-K1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g132105
BLAST score
                   690
E value
                   8.0e-73
                   147
Match length
% identity
                   89
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   401401
Seq. ID
                   LIB3431-043-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g2499417
BLAST score
                   499
E value
                   2.0e-50
Match length
                   120
                   78
% identity
NCBI Description
                   GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
                   >gi 1085826 pir S49248 H-protein - Flaveria anomala
                   >gi 547558 emb CAA85761 (Z37524) H-protein [Flaveria
                   anomala]
Seq. No.
                   401402
Seq. ID
                   LIB3431-043-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   q4079798
BLAST score
                   537
E value
                   7.0e-55
Match length
                   104
% identity
NCBI Description
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                   satival
Seq. No.
                   401403
Seq. ID
                   LIB3431-043-P1-K1-B3
Method -
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   584
E value
                   2.0e-60
Match length
                   110
% identity
                   97
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
```

sativa] >gi 226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

```
Seq. No.
                  401404
Seq. ID
                  LIB3431-043-P1-K1-B4
                  BLASTX
Method
NCBI GI
                  g3258238
BLAST score
                  157
E value
                  2.0e-10
                  108
Match length
% identity
                  30
                   (AP000007) 224aa long hypothetical protein [Pyrococcus
NCBI Description
                  horikoshii]
Seq. No.
                  401405
Seq. ID
                  LIB3431-043-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g2982453
BLAST score
                  224
E value
                  3.0e-22
Match length
                  72
% identity
NCBI Description
                   (AL022223) fructose-bisphosphate aldolase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                  401406
                  LIB3431-043-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  839
E value
                  3.0e-90
Match length
                  175
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401407
Seq. ID
                  LIB3431-043-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  q732174
BLAST score
                  531
E value
                  3.0e-54
Match length
                  144
% identity
                  PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA
NCBI Description
                  HELICASE KO3H1.2 >gi_3878176_emb_CAA82662.1_ (Z29560)
                  similar to DEAH subfamily RNA helicases, especially yeast
                  pre-mRNA splicing factors 22 and 16; cDNA EST EMBL:D27770
                  comes from this gene; cDNA EST EMBL: D27769 comes from this
                  gene; cDNA EST EMBL:D36247 comes from thi...
                  >gi_4249768_gb_AAD13795_ (AF120269) sex determination
```

protein MOG-1 [Caenorhabditis elegans]

```
Seq. No.
                   401408
                   LIB3431-043-P1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   521
E value
                    4.0e-53
Match length
                   115
% identity
                   86
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
                    401409
Seq. No.
Seq. ID
                   LIB3431-043-P1-K1-C10
Method
                   BLASTN
NCBI GI
                    q21832
BLAST score
                    39
                    1.0e-12
E value
Match length
                    43
% identity
                    98
                   Wheat mRNA for chloroplast phosphoglycerate kinase (EC
NCBI Description
                    2.7.2.3)
                    401410
Seq. No.
                    LIB3431-043-P1-K1-C12
Seq. ID
Method
                    BLASTX
NCBI GI
                    g5360230
BLAST score
                    1053
                    1.0e-115
E value
Match length
                    204
                    96
% identity
NCBI Description
                    (AB015287) Ran [Oryza sativa]
Seq. No.
                    401411
                    LIB3431-043-P1-K1-C2
Seq. ID
Method
                    BLASTX
NCBI GI
                    q115787
BLAST score
                    489
E value
                    2.0e-49
Match length
                    117
                    85
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                    CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                    protein 2R precursor - rice >gi_20182_emb_CAA32109
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
                    401412
Seq. No.
Seq. ID
                    LIB3431-043-P1-K1-C4
Method
                    BLASTX
                    g2072555
NCBI GI
BLAST score
                    175
```

2.0e-12

E value

```
32
Match length
% identity
                  100
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  401413
Seq. No.
Seq. ID
                  LIB3431-043-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q676884
BLAST score
                  289
                  9.0e-26
E value
                  77
Match length
% identity
                  71
                  (D29681) The expression is induced by Pi starvation.
NCBI Description
                  [Nicotiana tabacum] >gi 1094819 prf _2106387C Al-induced
                  protein [Nicotiana tabacum]
Seq. No.
                  401414
Seq. ID
                  LIB3431-043-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  q1661159
BLAST score
                  81
E value
                  5.0e-38
Match length
                  85
% identity
                  99
                  Oryza sativa chlorophyll a/b binding protein (kcdl895)
NCBI Description
                  mRNA, complete cds
                  401415
Seq. No.
Seq. ID
                  LIB3431-043-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q1835731
BLAST score
                  507
E value
                  2.0e-51
Match length
                  123
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                  401416
Seq. ID
                  LIB3431-043-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q4587556
BLAST score
                  433
E value
                  1.0e-42
Match length
                  140
% identity
NCBI Description
                  (AC006577) Similar to gi_1653162 (p)ppGpp
                  3-pyrophosphohydrolase from Synechocystis sp genome
                  gb_D90911. EST gb_W43807 comes from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  401417
                  LIB3431-043-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2618686
```

402

BLAST score

Seq. ID

```
E value
                  5.0e-39
Match length
                  163
% identity
                  48
NCBI Description
                  (AC002510) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3431-043-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  q3618309
BLAST score
                  157
E value
                  3.0e-83
Match length
                  173
                  97
% identity
                  Oryza sativa mRNA for zinc finger protein, complete cds,
NCBI Description
                  clone:E10707
                  401419
Seq. No.
                  LIB3431-043-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1718097
BLAST score
                  448
E value
                  2.0e-44
Match length
                  125
                  62
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
NCBI Description
                  (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016
                  lysosomal membrane protein DVA41 - slime mold
                  (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar
                  ATPase subunit DVA41 [Dictyostelium discoideum]
Seq. No.
                  401420
Seq. ID
                  LIB3431-043-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  486
                  6.0e-49
E value
Match length
                  88
% identity
                  100
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  401421
Seq. No.
Seq. ID
                  LIB3431-043-P1-K1-D3
Method
                  BLASTX
                  g115787
NCBI GI
BLAST score
                  515
                  2.0e-52
E value
Match length
                  121
% identity
                  86
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                 401422
Seq. No.
```

LIB3431-043-P1-K1-D5

```
Method
                   BLASTX
NCBI GI
                   g417260
BLAST score
                   407
E value
                   1.0e-39
Match length
                   128
                   65
% identity
NCBI Description
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
                   lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                   light-regulated gene [Oryza sativa]
                   401423
Seq. No.
Seq. ID
                   LIB3431-043-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   530
E value
                   4.0e-54
                   121
Match length
% identity
                   83
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   401424
Seq. ID
                   LIB3431-043-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   q4583548
BLAST score
                   723
E value
                   1.0e-76
Match length
                   183
% identity
                   (AJ010820) chloroplast FtsY homolog [Arabidopsis thaliana]
NCBI Description
                   401425
Seq. No.
Seq. ID
                   LIB3431-043-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   q1749676
BLAST score
                   147
E value
                   3.0e-09
Match length
                   82
% identity
                   (D89234) similar to Saccharomyces cerevisiae ORF YGR205W,
NCBI Description
                   EMBL Accession Number Z72990 [Schizosaccharomyces pombe]
Seq. No.
                   401426
Seq. ID
                   LIB3431-043-P1-K1-E1
Method
                   BLASTN
NCBI GI
                   q2773153
BLAST score
                   489
                   0.0e + 00
E value
Match length
                   496
% identity
                   100
                   Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                   (Asr1) mRNA, complete cds
```

401427

Seq. No.

```
LIB3431-043-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  378
                  3.0e-36
E value
Match length
                  112
% identity
                  66
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >qi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                  401428
Seq. ID
                  LIB3431-043-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  741
E value
                  1.0e-78
Match length
                  169
                  88
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                  401429
                  LIB3431-043-P1-K1-E3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q6006355
BLAST score
                  221
E value
                  1.0e-121
                  297
Match length
                  100
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
NCBI Description
Seq. No.
                  401430
Seq. ID
                  LIB3431-043-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  a3256035
BLAST score
                  238
E value
                  9.0e-20
Match length
                  135
% identity
                   (Y14274) putative serine/threonine protein kinase [Sorghum
NCBI Description
                  bicolor]
Seq. No.
                  401431
Seq. ID
                  LIB3431-043-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  q3789954
BLAST score
                  465
E value
                  2.0e-46
Match length
                  87
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
```

sativa]

% identity

```
Seq. No.
                   401432
Seq. ID
                   LIB3431-043-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   q729478
BLAST score
                   413
                   2.0e-40
E value
Match length
                   158
% identity
                   53
                   FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                   >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1
                   (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
                   a region of the predicted gene.; similar to
                   ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
                   401433
Seq. No.
                   LIB3431-043-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4585882
BLAST score
                   721
                   2.0e-76
E value
Match length
                   159
                   81
% identity
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   401434
                   LIB3431-043-P1-K1-F2
Seq. ID
Method
                   BLASTX
                   q2407281
NCBI GI
BLAST score
                   688
                   2.0e-72
E value
Match length
                   133
% identity
                   97
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq. No.
                   401435
                   LIB3431-043-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2443402
BLAST score
                   824
E value
                   2.0e-88
Match length
                   162
% identity
                   100
NCBI Description
                   (D87745) orthophosphate dikinase [Oryza sativa]
                   >qi 2443405 dbj BAA22420 (D87952) orthophosphate dikinase
                   [Oryza sativa]
Seq. No.
                   401436
Seq. ID
                   LIB3431-043-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g2739375
BLAST score
                   150
E value
                   2.0e-09
Match length
                   95
```

E value

4.0e-23

```
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
Seq. No.
                   401437
Seq. ID
                   LIB3431-043-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   q417488
BLAST score
                   580
                   3.0e-72
E value
                   155
Match length
                   85
% identity
                   ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
NCBI Description
                   H) >qi 100452 pir A40995 starch phosphorylase (EC 2.4.1.1)
                   H - potato >gi 169473 (M69038) alpha-glucan phosphorylase
                   type H isozyme [Solanum tuberosum]
                   401438
Seq. No.
Seq. ID
                   LIB3431-043-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   581
E value
                   3.0e-60
Match length
                   109
% identity
                   100
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   401439
Seq. No.
                   LIB3431-043-P1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131388
BLAST score
                   469
                   7.0e-47
E value
                   145
Match length
                   69
% identity
NCBI Description
                   OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                   THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260
                   photosystem II oxygen-evolving complex protein 1 - common
                   wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
33kDa oxygen evolving protein of photosystem II [Triticum
                   aestivum]
                   401440
Seq. No.
Seq. ID
                   LIB3431-043-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g3126854
BLAST score
                   671
E value
                   2.0e-76
Match length
                   144
% identity
                   99
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   401441
                   LIB3431-043-P1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5596468
BLAST score
                   266
```

BLAST score

```
Match length
                   82
% identity
                   59
                   (AL096882) putative protein [Arabidopsis thaliana]
NCBI Description
                   401442
Seq. No.
                   LIB3431-043-P1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4454459
BLAST score
                   564
E value
                   5.0e-58
Match length
                   133
                   82
% identity
                   (AC006234) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   401443
                   LIB3431-043-P1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5091616
BLAST score
                   643
E value
                   3.0e-67
                   202
Match length
% identity
NCBI Description
                   (ACO07454) F23M19.3 [Arabidopsis thaliana]
                   401444
Seq. No.
Seq. ID
                   LIB3431-043-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   586
E value
                   1.0e-60
Match length
                   133
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                   protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   401445
Seq. ID
                   LIB3431-043-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   q115787
BLAST score
                   554
                   5.0e-57
E value
Match length
                   126
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   401446
Seq. ID
                   LIB3431-043-P1-K1-H1
Method
                   BLASTX
NCBI GI
                   g5926718
```

```
E value
                   1.0e-55
Match length
                   154
                    69
% identity
NCBI Description
                   (AB007911) PRA2 [Pisum sativum]
                   401447
Seq. No.
Seq. ID
                   LIB3431-043-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g3914603
BLAST score
                   728
                   3.0e-77
E value
                   144
Match length
% identity
                   97
                   RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                   CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                    (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                   activase [Oryza sativa]
Seq. No.
                   401448
Seq. ID
                   LIB3431-043-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   g2146745
BLAST score
                   493
E value
                   9.0e-53
Match length
                   168
% identity
                    67
                   protein kinase (EC 2.7.1.-) - Arabidopsis thaliana
NCBI Description
                   >gi_642132_dbj_BAA08215_ (D45354) protein kinase
                    [Arabidopsis thaliana]
Seq. No.
                    401449
                   LIB3431-043-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115802
BLAST score
                   195
E value
                   8.0e-15
Match length
                   36
% identity
                   100
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
                   CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco
                   >gi 19827 emb CAA41188 (X58230) chlorophyll a/b binding
                   protein [Nicotiana tabacum]
Seq. No.
                   401450
Seq. ID
                   LIB3431-043-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q132096
BLAST score
                   922
E value
                   1.0e-100
Match length
                   175
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR
                   (RUBISCO SMALL SUBUNIT A) >gi_68095_pir__RKRZS6 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS2106) - rice >gi 218210 dbj BAA00539_
                    (D00644) small subunit of ribulose-1,5-bisphosphate
```

Seq. No.

Seq. ID Method

NCBI GI

401456

BLASTX

g4079798

LIB3431-043-P1-N1-A9

carboxylase (RuBPC) [Oryza sativa] 401451 Seq. No. Seq. ID LIB3431-043-P1-K1-H6 Method BLASTX NCBI GI g3986110 BLAST score 431 E value 2.0e-42 121 Match length % identity 69 (AB012716) heat shock protein 70 cognate [Salix gilgiana] NCBI Description 401452 Seq. No. LIB3431-043-P1-K1-H8 Seq. ID Method BLASTX NCBI GI q5669656 BLAST score 273 6.0e-24 E value Match length 98 56 % identity NCBI Description (AF096263) ER33 protein [Lycopersicon esculentum] Seq. No. 401453 Seq. ID LIB3431-043-P1-N1-A11 Method BLASTX NCBI GI q3126854 BLAST score 300 E value 3.0e-27 Match length 57 100 % identity NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa] 401454 Seq. No. Seq. ID LIB3431-043-P1-N1-A12 Method BLASTN NCBI GI q3885887 BLAST score 389 E value 0.0e + 00Match length 397 99 % identity Oryza sativa high mobility group protein (HMG) mRNA, NCBI Description complete cds 401455 Seq. No. LIB3431-043-P1-N1-A4 Seq. ID Method BLASTN NCBI GI q11957 BLAST score 98 E value 1.0e-47 340 Match length 41 % identity Rice complete chloroplast genome NCBI Description

E value

Match length

% identity

4.0e-21

48

```
BLAST score
                   339
                   9.0e-32
E value
Match length
                   66
                   98
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
Seq. No.
                   401457
                   LIB3431-043-P1-N1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   508
E value
                   1.0e-51
Match length
                   91
                   100
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   401458
Seq. ID
                   LIB3431-043-P1-N1-B11
Method
                   BLASTX
NCBI GI
                   g2499417
BLAST score
                   309
E value
                   3.0e-28
Match length
                   71
% identity
NCBI Description
                   GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
                   >gi_1085826_pir__S49248 H-protein - Flaveria anomala
                   >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria
                   anomala]
Seq. No.
                   401459
Seq. ID
                   LIB3431-043-P1-N1-B2
Method
                   BLASTX
NCBI GI
                   g4079798
BLAST score
                   183
E value
                   2.0e-13
Match length
                   34
% identity
NCBI Description
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                   sativa]
                   401460
Seq. No.
Seq. ID
                   LIB3431-043-P1-N1-B3
Method
                   BLASTX
NCBI GI
                   q347451
BLAST score
                   248
```

```
NCBI Description (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                    sativa]
                    401461
Seq. No.
                    LIB3431-043-P1-N1-B4
Seq. ID
                    BLASTN
Method
NCBI GI
                    g20262
BLAST score
                    191
                    1.0e-103
E value
                    379
Match length
                    88
% identity
NCBI Description O.sativa light-induced mRNA
Seq. No.
                    401462
                    LIB3431-043-P1-N1-B6
Seq. ID
Method
                    BLASTX
NCBI GI
                    g132105
BLAST score
                    165
E value
                    2.0e-11
                    32
Match length
                    97
% identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
Seq. No.
                    401463
                    LIB3431-043-P1-N1-C1
Seq. ID
Method
                    BLASTX
NCBI GI
                    q115787
BLAST score
                    409
E value
                    6.0e-40
                    77
- Match length
% identity
                    100
                    CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                    CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
Seq. No.
                    401464
 Seq. ID
                    LIB3431-043-P1-N1-C12
Method
                    BLASTN
NCBI GI
                    q5360229
BLAST score
                    397
E value
                    0.0e + 00
Match length
                    401
 % identity
                    100
NCBI Description Oryza sativa mRNA for Ran, complete cds
Seq. No.
                    401465
Seq. ID
                  · LIB3431-043-P1-N1-C2
```

```
Method
                   BLASTX
NCBI GI
                   g226263
BLAST score :
                   213
E value
                   5.0e-17
Match length
                   47
% identity
                  chlorophyll a/b binding protein [Glycine max]
NCBI Description
Seq. No.
                   401466
                   LIB3431-043-P1-N1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1835731
BLAST score
                   314
                   8.0e-29
E value
Match length
                  80
% identity
                   79
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                   401467
Seq. No.
Seq. ID
                   LIB3431-043-P1-N1-D1
Method
                  BLASTX
NCBI GI
                   g1661160
BLAST score
                   185
                   7.0e-14
E value
Match length
                  54
% identity
                   69
NCBI Description
                  (U74295) chlorophyll a/b binding protein [Oryza sativa]
                   401468
Seq. No.
                  LIB3431-043-P1-N1-D10
Seq. ID
Method
                  BLASTX
                  g3618310
NCBI GI
BLAST score
                   367
                   4.0e-35
E value
Match length
                  70
                  100
% identity
NCBI Description
                   (AB001883) zinc finger protein [Oryza sativa]
                   401469
Seq. No.
                  LIB3431-043-P1-N1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                   383
                   5.0e-37
E value
                  71
Match length
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  401470
Seq. No.
                  LIB3431-043-P1-N1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512125
BLAST score
                  243
                  1.0e-20
E value
Match length
                  45
```

100

% identity

Match length

```
(AF133340) putative chlorophyll a/b-binding protein
NCBI Description
                   [Phalaenopsis sp. 'KCbutterfly']
                   401471
Seq. No.
                   LIB3431-043-P1-N1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q417260
BLAST score
                   300
E value
                   3.0e-27
                   76
Match length
                   75
% identity
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                   lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                   light-regulated gene [Oryza sativa]
                   401472
Seq. No.
Seq. ID
                   LIB3431-043-P1-N1-D7
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   428
E value
                   3.0e-42
Match length
                   81
% identity
                   100
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   401473
Seq. ID
                   LIB3431-043-P1-N1-D8
Method
                   BLASTX
NCBI GI
                   q4583548
BLAST score
                   346
E. value
                   1.0e-32
Match length
                   79
% identity
NCBI Description
                   (AJ010820) chloroplast FtsY homolog [Arabidopsis thaliana]
Seq. No.
                   401474
Seq. ID
                   LIB3431-043-P1-N1-D9
Method
                   BLASTX
NCBI GI
                   q1749676
BLAST score
                   143
E value
                   9.0e-09
Match length
                   76
% identity
                   45
NCBI Description
                   (D89234) similar to Saccharomyces cerevisiae ORF YGR205W,
                   EMBL Accession Number Z72990 [Schizosaccharomyces pombe]
Seq. No.
                   401475
Seq. ID
                   LIB3431-043-P1-N1-E10
Method
                   BLASTX
NCBI GI
                   q115813
BLAST score
                   253
E value
                   1.0e-21
```

BLAST score

```
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                   CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
Seq. ID
                   LIB3431-043-P1-N1-E12
Method
                   BLASTX
NCBI GI
                   q3036946
BLAST score
                   271
E value
                   8.0e-24
Match length
                   52
                   98
% identity
NCBI Description
                   (AB012637) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
                   401477
Seq. No.
                   LIB3431-043-P1-N1-E3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q6006355
BLAST score
                   43
E value
                   7.0e-15
Match length
                   123
% identity
                   Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
NCBI Description
                   401478
Seq. No.
                   LIB3431-043-P1-N1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3256035
BLAST score
                   195
E value
                   7.0e-15
Match length
                   67
                   55
% identity
                   (Y14274) putative serine/threonine protein kinase [Sorghum
NCBI Description
                   bicolor]
                   401479
Seq. No.
                   LIB3431-043-P1-N1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q128690
BLAST score
                   535
E value
                   1.0e-54
Match length
                   118
% identity
                   89
                   NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST
NCBI Description
                   >gi_66161_pir__DERZN3 NADH dehydrogenase (ubiquinone) (EC
1.6.5.3) chain 3 - rice chloroplast >gi_11989_emb_CAA34001_
                   (X15901) ndhC; NADH dehydrogenase ND3 [Oryza sativa]
                   >gi 226610 prf 1603356AG NADH dehydrogenase ND3 [Oryza
                   sativa]
Seq. No.
                   401480
                   LIB3431-043-P1-N1-E8
Seq. ID
Method
                   BLASTN
                   q3819688
NCBI GI
```

```
E value
                  1.0e-13
Match length
                   49
                  96
% identity
NCBI Description
                  Hordeum vulgare genomic DNA fragment; clone MWG2318.uni
                  401481
Seq. No.
                  LIB3431-043-P1-N1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q693920
BLAST score
                  325
E value
                   3.0e-30
Match length
                   64
% identity
                   (U21113) chlorophyll a/b binding protein [Solanum
NCBI Description
                  tuberosum]
                  401482
Seq. No.
                  LIB3431-043-P1-N1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g517500
BLAST score
                  299
                  3.0e-27
E value
                  76
Match length
                  80
% identity
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi_444338_prf__1906386A photosystem II
                  OE17 protein [Pisum sativum]
                  401483
Seq. No.
Seq. ID
                  LIB3431-043-P1-N1-F2
Method
                  BLASTX
NCBI GI
                  g347451
                  181
BLAST score
                  3.0e-13
E value
Match length
                  35
% identity
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
                  401484
Seq. No.
                  LIB3431-043-P1-N1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2443402
BLAST score
                  174
                  2.0e-12
E value
                  32
Match length
                  100
% identity
                   (D87745) orthophosphate dikinase [Oryza sativa]
NCBI Description
                  >gi_2443405_dbj_BAA22420_ (D87952) orthophosphate dikinase
                   [Oryza sativa]
Seq. No.
                  401485
                  LIB3431-043-P1-N1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2754849
                  288
BLAST score
```

8.0e-26

E value

```
63
Match length
                  89
% identity
NCBI Description
                   (AF039000) putative serine-glyoxylate aminotransferase
                   [Fritillaria agrestis]
Seq. No.
                  401486
                  LIB3431-043-P1-N1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417488
BLAST score
                  152
E value
                  4.0e-16
Match length
                  51
% identity
NCBI Description
                  ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE
                  H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1)
                  H - potato >gi_169473 (M69038) alpha-glucan phosphorylase
                  type H isozyme [Solanum tuberosum]
                  401487
Seq. No.
Seq. ID
                  LIB3431-043-P1-N1-G10
Method
                  BLASTX
NCBI GI
                  q4006895
BLAST score
                  158
E value
                  3.0e-10
                  51
Match length
% identity
                  49
                  (Z99708) putative protein [Arabidopsis thaliana]
NCBI Description
                  401488
Seq. No.
                  LIB3431-043-P1-N1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  277
                  2.0e-24
E value
                  52
Match length
% identity
                  100
NCBI Description
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  401489
Seq. No.
                  LIB3431-043-P1-N1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3126854
                  200
BLAST score
                  2.0e-19
E value
                  53
Match length
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  401490
                  LIB3431-043-P1-N1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5596468
BLAST score
                  145
E value
                  5.0e-09
Match length
                  43
% identity
                  65
                  (AL096882) putative protein [Arabidopsis thaliana]
NCBI Description
```

```
401491
Seq. No.
Seq. ID
                  LIB3431-043-P1-N1-G8
Method
                  BLASTX
NCBI GI
                  g3036942
BLAST score
                  247
E value
                  5.0e-21
Match length
                  46
% identity
                  100
NCBI Description
                   (AB012636) light harvesting chlorophyll a/b-binding protein
                  [Nicotiana sylvestris]
Seq. No.
                  401492
Seq. ID
                  LIB3431-043-P1-N1-G9
Method
                  BLASTN
NCBI GI
                  g20181
BLAST score
                  52
E value
                  3.0e-20
Match length
                  72
                  93
% identity
NCBI Description Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
                  401493
Seq. No.
                 LIB3431-043-P1-N1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g303736
BLAST score
                  152
                  7.0e-10
E value
Match length
                  80
% identity
                  49
                  (D12541) GTP-binding protein [Pisum sativum]
NCBI Description
                  >gi 738934 prf 2001457B GTP-binding protein [Pisum
                  sativum]
                  401494
Seq. No.
                  LIB3431-043-P1-N1-H10
Seq. ID
                  BLASTX
Method
                  g167097
NCBI GI
BLAST score
                  151
                  5.0e-17
E value
Match length
                  52
% identity
NCBI Description
                  (M55449) ribulose 1,5-bisphosphate carboxylase activase
                  [Hordeum vulgare]
                  401495
Seq. No.
                  LIB3431-043-P1-N1-H11
Seq. ID
Method
                  BLASTN
                  g3377792
NCBI GI
BLAST score
                  131
                  2.0e-67
E value
                  284
Match length
% identity
NCBI Description
                  Oryza sativa ribulose-1,5-bisphosphate
                  carboxylase/oxygenase activase (rca) mRNA, complete cds
```



```
401496
Seq. No.
Seq. ID
                  LIB3431-043-P1-N1-H3
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  163
                  4.0e-11
E value
Match length
                  31
% identity
                  100
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  401497
Seq. No.
Seq. ID
                  LIB3431-043-P1-N1-H4
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  301
E value
                  3.0e-27
                  57
Match length
% identity
                  100
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                  401498
Seq. ID
                  LIB3431-043-P1-N1-H5
Method
                  BLASTN
NCBI GI
                  q3218542
BLAST score
                  36
E value
                  1.0e-10
Match length
                  119
% identity
NCBI Description Oryza sativa AOX1b and AOX1a genes, complete cds
                  401499
Seq. No.
Seq. ID
                  LIB3431-043-P1-N1-H6
Method
                  BLASTN
NCBI GI
                  q473216
BLAST score
                  36
E value
                  1.0e-10
Match length
                  44
% identity
NCBI Description P.sativum (little marvel) HSC71.0 mRNA
                  401500
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q320618
BLAST score
                  457
E value
                  1.0e-45
Match length
                  106
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
```

Seq. No. 401501

[Oryza satīva]



```
LIB3431-044-P1-K1-A10
Seq. ID
Method
                   BLASTX
                   g3647283
NCBI GI
                   278
BLAST score
E value
                   1.0e-45
                   147
Match length
% identity
                   63
NCBI Description
                   (AJ011418) ubiquitin activating enzyme [Lycopersicon
                   esculentum]
                   401502
Seq. No.
                   LIB3431-044-P1-K1-A11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   8.0e-20
Match length
                   44
% identity
                   100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi 6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   401503
Seq. ID
                   LIB3431-044-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   q2662343
BLAST score
                   815
E value
                   2.0e-87
Match length
                   159
% identity
NCBI Description
                   (D63581) EF-1 alpha [Oryza sativa]
                   401504
Seq. No.
Seq. ID
                   LIB3431-044-P1-K1-A4
Method
                   BLASTX
NCBI GI
                   q1173275
BLAST score
                   653
E value
                   3.0e-74
Match length
                   150
% identity
NCBI Description
                   CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
                   >gi_2119068_pir__S58630 ribosomal protein S7 - maize
                   chloroplast >gi_902274_emb_CAA60339 (X86563) ribosomal protein S7 [Zea mays] >gi_902298_emb_CAA60362 (X86563)
                   ribosomal protein S7 [Zea mays]
Seq. No.
                   401505
Seq. ID
                   LIB3431-044-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   g3126854
BLAST score
                   656
                   5.0e-69
E value
Match length
                   123
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
```

401506

Seq. No.

```
LIB3431-044-P1-K1-A6
Seq. ID
Method
                  BLASTX
                  g1835731
NCBI GI
BLAST score
                  594
E value
                  2.0e-61
                  126
Match length
                  91
% identity
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                  401507
                  LIB3431-044-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q729477
BLAST score
                  603
E value
                  1.0e-62
Match lèngth
                  126
                  87
% identity
NCBI Description
                  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR)
                  >gi_320548_pir__A44974 ferredoxin--NADP+ reductase (EC
                  1.18.1.2) precursor - common ice plant >gi_167256 (M25528)
                  ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
                  [Mesembryanthemum crystallinum] >gi_226768_prf__1604475A
                  ferredoxin NADP reductase [Mesembryanthemum crystallinum]
Seq. No.
                  401508
Seq. ID
                  LIB3431-044-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  a3402711
BLAST score
                  349
E value
                  5.0e-33
Match length
                  120
% identity
NCBI Description
                  (AC004261) putative RNA-binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  401509
Seq. ID
                  LIB3431-044-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  a3789954
BLAST score
                  240
E value
                  2.0e-20
Match length
                  60
                  77
% identity
NCBI Description
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                  sativa] ·
Seq. No.
                  401510
Seq. ID
                  LIB3431-044-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
                  6.0e-20
E value
Match length
                  44
% identity
                  100
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
```

```
Seq. No.
                  401511
Seq. ID
                  LIB3431-044-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g1731181
BLAST score
                  195
E value
                  7.0e-15
                  136
Match length
% identity
                  38
                  HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II
NCBI Description
                  >gi_3874230_emb_CAA90107.1_ (Z49909) weak similarity with a
                  B. Flavum translocation protein (Swiss Prot accession
                  number P38376); cDNA EST yk220e10.5 comes from this gene;
                  cDNA EST yk549e12.3 comes from this gene; cDNA EST
                  yk618d6.3 comes from this gene
Seq. No.
                  401512
Seq. ID
                  LIB3431-044-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  717
E value
                  5.0e-76
Match length
                  137
% identity
NCBI Description
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
                  401513
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  513
E value
                  4.0e-52
Match length
                  131
                  80
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir__A48527 photosystem I protein psaK precursor
                  - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
Seq. No.
                  401514
Seq. ID
                  LIB3431-044-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g4972093
BLAST score
                  227
E value
                  1.0e-18
Match length
                  131
% identity
                  (AL078468) putative protein [Arabidopsis thaliana]
NCBI Description
                  401515
Seq. No.
                  LIB3431-044-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3063524
BLAST score
                  183
E value
                  2.0e-13
```

37

Match length

```
% identity
NCBI Description
                   (AF052305) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  401516
Seq. ID
                  LIB3431-044-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  35
E value
                  6.0e-10
Match length
                  35
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                   401517
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-B7
Method
                 · BLASTX
NCBI GI
                  g2827150
BLAST score
                  559
E value
                  2.0e-57
Match length
                  148
% identity
NCBI Description
                   (AF029895) acetyl-coenzyme A carboxylase [Triticum
                  aestivum]
                  401518
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q2344892
BLAST score
                  213
E value
                  7.0e-17
Match length
                  68
% identity
NCBI Description
                   (AC002388) unknown protein [Arabidopsis thaliana]
Seq. No.
                  401519
Seq. ID
                  LIB3431-044-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q1495768
BLAST score
                  152
E value
                  8.0e-10
Match length
                  144
% identity
                  45
                   (Z68506) chloroplast inner envelope protein, 110 kD
NCBI Description
                   (IEP110) [Pisum sativum]
Seq. No.
                  401520
Seq. ID
                  LIB3431-044-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q2130082
BLAST score
                  442
E value
                  1.0e-43
Match length
                  169
% identity
                  51
                  protein kinase Xa21 (EC 2.7.1.-) - rice >gi 1122443
NCBI Description
                  (U37133) receptor kinase-like protein [Oryza sativa]
                  >gi_2586085 (U72723) receptor kinase-like protein [Oryza
```

E value

2.0e-16

```
kinase-like protein [Oryza sativa]
                   401521
Seq. No.
Seq. ID
                   LIB3431-044-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g2688824
BLAST score
                   181
                   3.0e-13
E value
Match length
                   111
                   41
% identity
                   .(U93273) putative auxin-repressed protein [Prunus
NCBI Description
                   armeniaca]
                   401522
Seq. No.
                   LIB3431-044-P1-K1-C3
Seq. ID
                   BLASTX
Method
NCBI GI
                   g548603
                   295
BLAST score
                   1.0e-26
E value
                   56
Match length
% identity
                   98
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                   >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                   barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
Seq. ID
                   LIB3431-044-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   g3789952
BLAST score
                   651
E value
                   2.0e-68
Match length
                   128
% identity
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                   sativa]
Seq. No.
                   401524
Seq. ID
                   LIB3431-044-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g399213
BLAST score
                   877
E value
                   1.0e-94
Match length
                   181
% identity
NCBI Description
                   ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
                   CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato >gi_170435 (M32604) ATP-dependent protease (CD4B)
                   [Lycopersicon esculentum]
                   401525
Seq. No.
Seq. ID
                   LIB3431-044-P1-K1-D12
Method
                   BLASTN
NCBI GI
                   q5295936
BLAST score
                   46
```

longistaminata] >gi 1586408 prf 2203451A receptor

```
Match length
                  93
                  85
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0681F10,
                  complete sequence
                  401526
Seq. No.
                  LIB3431-044-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2492515
BLAST score
                  662
E value
                  2.0e-69
Match length
                  155
                  86
% identity
                  CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
NCBI Description
                  >gi 2129924 pir S58298 ATPase - pepper (fragment)
                  >gi 929013 emb CAA62084 (X90472) ATPase [Capsicum annuum]
                  401527
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-D6
                  BLASTX .
Method
NCBI GI
                  g1652164
BLAST score
                  490
E value
                  3.0e-49
Match length
                  167
% identity
                  61
                   (D90903) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                  401528
                  LIB3431-044-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3618310
BLAST score
                  439
E value
                  3.0e-43
Match length
                  132
% identity
                  69
NCBI Description
                  (AB001883) zinc finger protein [Oryza sativa]
Seq. No.
                  401529
                  LIB3431-044-P1-K1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3126854
BLAST score
                  784
E value
                  8.0e-84
Match length
                  151
% identity
                  97
NCBI Description
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  401530
                  LIB3431-044-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  670
E value
                  2.0e-70
Match length
                  151
% identity
                  88
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
```

V) (PSI-L) >gi 100605_pir__A39759 photosystem I 18K protein

NCBI GI

```
hydrophobic protein [Hordeum vulgare]
                  401531
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  762
                  3.0e-81
E value
Match length
                  149
                  99
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  401532
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g5042409
BLAST score
                  442
E value
                  1.0e-43
Match length
                  136
% identity
                  (AC006193) Putative membrane related protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  401533
Seq. ID
                  LIB3431-044-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g5702231
                  190
BLAST score
E value
                  3.0e-14
Match length
                  108
% identity
                  (AF145386) hypersensitive reaction associated Ca2+-binding
NCBI Description
                  protein [Phaseolus vulgaris]
Seq. No.
                  401534
Seq. ID
                  LIB3431-044-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g548605
BLAST score
                  590
E value
                  5.0e-61
Match length
                  130
% identity
                  90
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                  barley >qi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
Seq. No.
                  401535
                  LIB3431-044-P1-K1-E9
Seq. ID
Method
                  BLASTN
```

precursor - barley >gi 167087 (M61146) photosystem I

g3821780

```
BLAST score
                   36
                   1.0e-10
E value
Match length
                   47
                   66
% identity
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   401536
Seq. ID
                   LIB3431-044-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g2827665
BLAST score
                   605
E value
                   6.0e-63
Match length
                   141
                   73
% identity
                   (AL021637) vacuolar sorting receptor-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   401537
Seq. No.
                   LIB3431-044-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q6091733
BLAST score
                   219
E value
                   2.0e-17
Match length
                   65
% identity
                   62
NCBI Description
                   (AC010797) unknown protein [Arabidopsis thaliana]
                   401538
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   q2982453
BLAST score
                   636
                   2.0e-66
E value
                   157
Match length
% identity
                   82
NCBI Description
                   (AL022223) fructose-bisphosphate aldolase-like protein
                   [Arabidopsis thaliana]
                   401539
Seq. No.
                   LIB3431-044-P1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q115787
                   720
BLAST score
E value
                   3.0e-76
                   157
Match length
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   401540
                  LIB3431-044-P1-K1-F5
Seq. ID
Method
                   BLASTX
                   q2147484
NCBI GI
```

766

BLAST score

```
1.0e-81
E value
Match length
                  170
% identity
                  85
                  homeotic protein - Phalaenopsis sp >gi_1173622 (U34743)
NCBI Description
                  homeobox protein [Phalaenopsis sp. 'hybrid SM9108']
Seq. No.
                  401541
Seq. ID
                  LIB3431-044-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1644427
BLAST score
                  452
                  7.0e-45
E value
                  130
Match length
% identity
                   66
                   (U74610) glyoxalase II [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   401542
                  LIB3431-044-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1617197
BLAST score
                  301
E value
                   3.0e-27
Match length
                  76
% identity
NCBI Description
                   (Z72488) CP12 [Nicotiana tabacum]
                   401543
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  218
E value
                  2.0e-17
Match length
                   44
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                   401544
                  LIB3431-044-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1352461
BLAST score
                  388
E value
                  2.0e-37
Match length
                  90
% identity
                  83
NCBI Description
                  IN2-2 PROTEIN
Seq. No.
                  401545
Seq. ID
                  LIB3431-044-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q4972067
BLAST score
                  287
E value
                  2.0e-27
Match length
                  166
% identity
NCBI Description
                   (AL078467) putative protei [Arabidopsis thaliana]
```

```
401546
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-G10
                  BLASTX
Method
NCBI GI
                   g3132476
BLAST score
                   579
                   9.0e-60
E value
Match length
                   167
% identity
                   66
                   (AC003096) unknown protein [Arabidopsis thaliana]
NCBI Description
                   401547
Seq. No.
                   LIB3431-044-P1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   616
E value
                   4.0e-64
Match length
                   134
% identity
                   87
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   401548
Seq. ID
                   LIB3431-044-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   g4490728
BLAST score
                   290
E value
                   6.0e-26
Match length
                   65
                   75
% identity
NCBI Description
                   (AL035709) putative protein [Arabidopsis thaliana]
Seq. No.
                   401549
Seq. ID
                   LIB3431-044-P1-K1-G3
Method
                   BLASTN
NCBI GI
                   q19094
BLAST score
                   48
E value
                   4.0e-18
Match length
                   64
% identity
                   94
                  H.vulgare mRNA PsaN for photosystem I subunit N
NCBI Description
                   401550
Seq. No.
Seq. ID
                   LIB3431-044-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g1684851
BLAST score
                   212
                   6.0e-17
E value
Match length
                   62
% identity
                   (U77935) DnaJ-like protein [Phaseolus vulgaris]
NCBI Description
Seq. No.
                   401551
Seq. ID.
                   LIB3431-044-P1-K1-G6
```

Method

BLASTN

```
Method
                  BLASTX
NCBI GI
                  q1052960
BLAST score
                  848
                  3.0e-91
E value
Match length
                  172
% identity
                  91
NCBI Description
                  (U37437) PNIL34 [Ipomoea nil]
Seq. No.
                  401552
Seq. ID
                  LIB3431-044-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  237
E value
                  1.0e-19
Match length
                  44
% identity
                  100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  401553
Seq. No.
                  LIB3431-044-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129675
BLAST score
                  218
E value
                  1.0e-17
Match length
                  84
% identity
                  probable chlorophyll synthetase G4 - Arabidopsis thaliana
NCBI Description
                  >gi 972938 (U19382) putative chlorophyll synthetase
                   [Arabidopsis thaliana] >gi 3068709 (AF049236) putative
                  chlorophyll synthetase [Arabidopsis thaliana]
                  401554
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q4531444
BLAST score
                  320
E value
                  1.0e-44
Match length
                  151
% identity
                   (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  401555
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q3202024
BLAST score
                  743
E value
                  6.0e-79
Match length
                  159
                  86
% identity
NCBI Description
                   (AF069315) thylakoid-bound L-ascorbate peroxidase precursor
                   [Mesembryanthemum crystallinum]
                  401556
Seq. No.
                  LIB3431-044-P1-K1-H2
Seq. ID
```

```
BLAST score
                  542
E value
                  0.0e+00
Match length
                  557
                  99
% identity
                  O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2
NCBI Description
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g2554675
BLAST score
                  745
E value
                   3.0e-79
Match length
                   166
% identity
                   90
                  Three-Dimensional Structure Of Glycolate Oxidase With Bound
NCBI Description
                  Active-Site Inhibitors >gi 2624594_pdb_1AL7
                  Three-Dimensional Structures Of Glycolate Oxidase With
                  Bound Active-Site Inhibitors
                  401558
Seq. No.
Seq. ID
                  LIB3431-044-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  731
E value
                  1.0e-77
Match length
                  155
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                   401559
Seq. ID
                  LIB3431-044-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  756
E value
                  1.0e-80
Match length
                  144
% identity
NCBI Description
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   401560
                  LIB3431-044-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  776
E value
                  7.0e-83
Match length
                  168
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
```

g2072726

NCBI GI

```
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
```

```
Seq. No.
                  401561
Seq. ID
                  LIB3431-044-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  830
E value
                  4.0e-89
Match length
                  173
                  91
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401562
                  LIB3431-044-P1-N1-A1
Seq. ID
                  BLASTN
Method
NCBI GI
                  g218171
BLAST score
                  58
                  2.0e-24
E value
                  84
Match length
                  93
% identity
NCBI Description
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
                  a/b binding protein of photosystem II (LHCPII), complete
                  401563
Seq. No.
Seq. ID
                  LIB3431-044-P1-N1-A10
Method
                  BLASTX
NCBI GI
                  q2982309
BLAST score
                  194
E value
                  8.0e-15
Match length
                  46
% identity
NCBI Description
                  (AF051239) probable ubiquitin activating enzyme 2 [Picea
```

Seq. No. 401564

Seq. ID LIB3431-044-P1-N1-A11

mariana]

Method BLASTN
NCBI GI g2072554
BLAST score 240
E value 1.0e-132
Match length 248

% identity

```
% identity
NCBI Description
                    Oryza sativa metallothionein-like protein mRNA, complete
                    cds
                     401565
Seq. No.
Seq. ID
                    LIB3431-044-P1-N1-A12
Method
                    BLASTN
NCBI GI
                    g2662340
BLAST score
                    59
E value
                     8.0e-25
                    91
Match length
                     91
% identity
                    Oryza sativa mRNA for EF-1 alpha, complete cds
NCBI Description
Seq. No.
                     401566
                    LIB3431-044-P1-N1-A4
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1173275
BLAST score
                     640
E value
                    7.0e-67
Match length
                    149
% identity
                    89
NCBI Description
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
                    >gi_2119068_pir__ S58630 ribosomal protein S7 - maize
chloroplast >gi_902274_emb_CAA60339_ (X86563) ribosomal
protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563)
                    ribosomal protein S7 [Zea mays]
Seq. No.
                    401567
Seq. ID
                    LIB3431-044-P1-N1-A5
Method
                    BLASTN
NCBI GI
                    g2570512
BLAST score
                    88
E value
                    8.0e-42
Match length
                     195
% identity
NCBI Description
                    Oryza sativa chlorophyll a-b binding protein mRNA, complete
                     401568
Seq. No.
Seq. ID
                    LIB3431-044-P1-N1-A6
Method
                    BLASTX
NCBI GI
                    q1835731
BLAST score
                    436
E value
                     4.0e-43
Match length
                    94
% identity
NCBI Description
                    (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                    401569
Seq. No.
                    LIB3431-044-P1-N1-A7
Seq. ID
Method
                    BLASTN
NCBI GI
                    a1835730
BLAST score
                    51
E value
                    3.0e-20
Match length
                    59
```

```
NCBI Description Oryza sativa photosystem II 10 kDa polypeptide mRNA,
                  complete cds
Seq. No.
                  401570
Seq. ID
                  LIB3431-044-P1-N1-A9
Method
                  BLASTN
NCBI GI
                  g3789953
BLAST score
                  267
E value
                  1.0e-148
Match length
                  275
% identity
                  99
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein precursor
                   (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  401571
Seq. No.
                  LIB3431-044-P1-N1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  113
E value
                  5.0e-57
Match length
                  164
                  93
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
Seq. No.
                  401572
Seq. ID
                  LIB3431-044-P1-N1-B11
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  410
E value
                  4.0e-40
Match length
                  78
                  99
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  401573
                                                                  Sec. 5
Seq. ID
                  LIB3431-044-P1-N1-B12
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  187
                  2.0e-14
E value
Match length
                  38
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi_539055_pir__A48527 photosystem I protein psaK precursor
                  - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
Seq. No.
                  401574
                  LIB3431-044-P1-N1-B2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g19086
BLAST score
                  56
                  1.0e-22
E value
                  100
Match length
```

Seq. ID

```
% identity
                   91
NCBI Description
                  Hordeum vulgare pot. psaE mRNA
                   401575
Seq. No.
                   LIB3431-044-P1-N1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2344892
BLAST score
                   182
E value
                   2.0e-13
Match length
                   41
% identity
                   (AC002388) unknown protein [Arabidopsis thaliana]
NCBI Description
                   401576
Seq. No.
                   LIB3431-044-P1-N1-C11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1777706
BLAST score
                   59
E value
                   1.0e-24
Match length
                   71
% identity
                   96
NCBI Description
                   Zea mays 18S ribosomal RNA gene, partial sequence
Seq. No.
                   401577
Seq. ID
                   LIB3431-044-P1-N1-C4
Method
                   BLASTX
NCBI GI
                   q2829916
BLAST score
                   297
E value
                   7.0e-27
Match length
                   72
% identity
NCBI Description
                   (AC002291) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   401578
Seq. ID
                   LIB3431-044-P1-N1-C9
Method
                   BLASTN
NCBI GI
                   g3789951
BLAST score
                   157
E value
                   6.0e-83
Match length
                   300
                   93
% identity
NCBI Description
                   Oryza sativa chlorophyll a/b-binding protein presursor
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
                   401579
Seq. No.
Seq. ID
                   LIB3431-044-P1-N1-D6
Method
                   BLASTX
NCBI GI
                   g1652164
BLAST score
                   145
                   6.0e-09
E value
Match length
                   59
% identity
                   (D90903) hypothetical protein [Synechocystis sp.]
NCBI Description
                   401580
Seq. No.
```

LIB3431-044-P1-N1-E10

```
BLASTX
Method
NCBI GI
                   g3618310
BLAST score
                   308
E value
                   4.0e-28
Match length
                   67
                   91
% identity
                   (AB001883) zinc finger protein [Oryza sativa]
NCBI Description
Seq. No.
                   401581
                   LIB3431-044-P1-N1-E11
Seq. ID
                   BLASTX
Method
NCBI GI
                   q115802
BLAST score
                   170
E value
                   3.0e-12
                   32
Match length
                   97
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco
                   >qi 19827 emb CAA41188 (X58230) chlorophyll a/b binding
                   protein [Nicotiana tabacum]
Seq. No.
                   401582
Seq. ID
                   LIB3431-044-P1-N1-E5
Method
                   BLASTN
NCBI GI
                   q20177
BLAST score
                   150
E value
                   5.0e-79
Match length
                   176
                   97
% identity
NCBI Description
                   Rice cab1R gene for light harvesting chlorophyll
                   a/b-binding protein
                   401583
Seq. No.
Seq. ID
                   LIB3431-044-P1-N1-E8
Method
                   BLASTX
NCBI GI
                   q548605
BLAST score
                   198
E value
                   1.0e-15
Match length
                   44
                   89
% identity
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi_539055_pir__A48527 photosystem I protein psaK precursor

    barley >gi_304220 (L12707) photosystem I PSI-K subunit

                   [Hordeum vulgare]
Seq. No.
                   401584
Seq. ID
                   LIB3431-044-P1-N1-F11
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   376
E value
                   4.0e-36
Match length
                   71
                   100
% identity
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

NCBI GI

g115787

```
Seq. No.
                   401585
Seq. ID
                   LIB3431-044-P1-N1-F3
                   BLASTN
Method
NCBI GI
                   g20181
BLAST score
                   76
                   1.0e-34
E value
Match length
                   118
% identity
                   94
                   Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                   a/b-binding protein
                   401586
Seq. No.
Seq. ID
                   LIB3431-044-P1-N1-F6
Method
                   BLASTX
NCBI GI
                   g1644427
BLAST score
                   343
                   3.0e-32
E value
Match length
                   79
% identity
                   80
                   (U74610) glyoxalase II [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   401587
Seq. ID
                   LIB3431-044-P1-N1-F7
Method
                   BLASTX
NCBI GI
                   q1617197
BLAST score
                   148
E value
                   2.0e-09
Match length
                   30
% identity
                   87
NCBI Description
                   (Z72488) CP12 [Nicotiana tabacum]
                   401588
Seq. No.
Seq. ID
                   LIB3431-044-P1-N1-F8
Method
                   BLASTN
NCBI GI
                   g2072554
BLAST score
                   209
E value
                   1.0e-114
Match length
                   265
% identity
                   97
NCBI Description
                   Oryza sativa metallothionein-like protein mRNA, complete
Seq. No.
                   401589
Seq. ID
                   LIB3431-044-P1-N1-F9
Method
                   BLASTX
NCBI GI
                   g2462750
BLAST score
                   204
E value
                   6.0e-16
Match length
                   58
% identity
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                   401590
Seq. No.
Seq. ID
                   LIB3431-044-P1-N1-G11
Method
                   BLASTX
```

NCBI GI

```
BLAST score
                  389
                  1.0e-37
E value
Match length
                  75
                  99
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  401591
Seq. No.
Seq. ID
                  LIB3431-044-P1-N1-G6
Method
                  BLASTX
NCBI GI
                  g1052960
BLAST score
                  224
                  3.0e-18
E value
Match length
                  54
% identity
                  81
NCBI Description
                  (U37437) PNIL34 [Ipomoea nil]
                  401592
Seq. No.
Seq. ID
                  LIB3431-044-P1-N1-G9
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  307
E value
                  5.0e-28
Match length
                  55
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  401593
Seq. ID
                  LIB3431-044-P1-N1-H12
Method
                  BLASTX
NCBI GI
                  g4996602
BLAST score
                  268
                  2.0e-23
E value
Match length
                  71
% identity
NCBI Description
                  (AB022273) thylakoid-bound ascorbate peroxidase [Nicotiana
                  tabacum]
Seq. No.
                  401594
Seq. ID
                  LIB3431-044-P1-N1-H2
Method
                  BLASTN
NCBI GI
                  g2072726
BLAST score
                  430
E value
                  0.0e + 00
Match length
                  468
% identity
                  98
NCBI Description
                  O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2
Seq. No.
                  401595
Seq. ID
                  LIB3431-044-P1-N1-H3
                  BLASTN
Method
```

q2570514

```
250
BLAST score
                   1.0e-138
E value
Match length
                   281
% identity
                   98
                   Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
NCBI Description
                   401596
Seq. No.
                   LIB3431-044-P1-N1-H4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g218207 .
BLAST score
                   255
                   1.0e-141
E value
Match length
                   278
% identity
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   p0SSS1139
Seq. No.
                   401597
Seq. ID
                   LIB3431-044-P1-N1-H5
Method
                   BLASTN
NCBI GI
                   g3126853
BLAST score
                   89
E value
                   1.0e-42
Match length
                   116
% identity
                   95
                   Oryza sativa chlorophyll a/b binding protein (RCABP89)
NCBI Description
                   mRNA, nuclear gene encoding chloroplast protein, complete
                   401598
Seq. No.
Seq. ID
                   LIB3431-044-P1-N1-H6
                   BLASTX
Method
NCBI GI
                   g132105
BLAST score
                   293
E value
                   2.0e-26
Match length
                   57
% identity
                   96
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   401599
Seq. ID
                   LIB3431-045-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g4680340
                   429
BLAST score
                   3.0e-42
E value
Match length
                   134
% identity
                   (AF128457) putative nucleolysin [Oryza sativa subsp.
NCBI Description
```

```
indica]
                  401600
Seq. No.
Seq. ID
                  LIB3431-045-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  g5441876
BLAST score
                  106
                  2.0e-52
E value
Match length
                  327
                  35
% identity
                  Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
NCBI Description
                  (contiq b)
                  401601
Seq. No.
Seq. ID
                  LIB3431-045-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g4689380
BLAST score
                  640
                  5.0e-67
E value
Match length
                  139
% identity
NCBI Description
                  (AF139465) LHCII type III chlorophyll a/b binding protein
                  [Vigna radiata]
Seq. No.
                  401602
Seq. ID
                  LIB3431-045-P1-K1-A3
Method .
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  752
E value
                  4.0e-80
Match length
                  160
                  90
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401603
Seq. ID
                  LIB3431-045-P1-K1-A4
```

```
      Seq. No.
      401603

      Seq. ID
      LIB3431-045-P1-K1-A4

      Method
      BLASTX

      NCBI GI
      g132105

      BLAST score
      794

      E value
      5.0e-85

      Match length
      168
```

- 90

NCBI Description

% identity

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

```
sativa] >gi_226375_prf__1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]
```

```
401604
Seq. No.
Seq. ID
                   LIB3431-045-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q4581146
BLAST score
                   587
                   7.0e-61
E value
Match length
                   142
                   82
% identity
NCBI Description
                   (AC006919) putative fructose-bisphosphate aldolase,
                   cytoplasmic [Arabidopsis thaliana]
Seq. No.
                   401605
Seq. ID
                   LIB3431-045-P1-K1-A6
Method
                   BLASTX
NCBI GI '
                   g2407281
BLAST score
                   814
E value
                   2.0e-87
Match length
                   154
                   99
% identity
                    (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
                   401606
Seq. No.
                   LIB3431-045-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g871931
BLAST score
                   517
E value
                   2.0e-52
Match length
                   131
% identity
                   80
NCBI Description
                   (D30763) ferredoxin [Oryza sativa]
Seq. No.
                   401607
Seq. ID
                   LIB3431-045-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   654
E value
                   1.0e-68
Match length
                   127
% identity
                   98
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   401608
Seq. ID
                   LIB3431-045-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   q3885886
BLAST score
                   502
                   8.0e-51
E value
```

80

Match length % identity

Match length

144

```
(AF093631) Rieske Fe-S precursor protein [Oryza sativa]
NCBI Description
Seq. No.
                   401609
                   LIB3431-045-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3549656
                   258
BLAST score
E value
                   3.0e-22
Match length
                   91
% identity
                   58
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
                   401610
Seq. No.
Seq. ID
                   LIB3431-045-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   q2662343
BLAST score
                   464
                   1.0e-58
E value
Match length
                   140
% identity
                   97
NCBI Description (D63581) EF-1 alpha [Oryza sativa]
Seq. No.
                   401611
Seq. ID
                   LIB3431-045-P1-K1-B3
Method .
                   BLASTX
NCBI GI
                   q4914330
BLAST score
                   488
E value
                   4.0e-49
Match length
                   121
% identity
                   67
NCBI Description (AC005489) F14N23.16 [Arabidopsis thaliana]
Seq. No.
                   401612
                   LIB3431-045-P1-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   302
E value
                   2.0e-27
Match length
                   58
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   401613
                   LIB3431-045-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q6056413
                   595
BLAST score
                   9.0e-62
E value
```

Method

BLASTX

```
% identity
NCBI Description
                    (AC009525) Unknown protein [Arabidopsis thaliana]
                    401614
Seq. No.
Seq. ID
                    LIB3431-045-P1-K1-B6
Method
                    BLASTX
NCBI GI
                    g2191152
                    222
BLAST score
                    8.0e-18
E value
Match length
                    117
% identity
                    (AF007269) A IG002N01.31 gene product [Arabidopsis
NCBI Description
                    thaliana] -
                    401615
Seq. No.
Seq. ID
                    LIB3431-045-P1-K1-B7
                    BLASTX
Method
NCBI GI
                    q1495768
BLAST score
                    329
E value
                    2.0e-30
Match length
                    149
% identity
                    46
                    (Z68506) chloroplast inner envelope protein, 110 kD
NCBI Description
                    (IEP110) [Pisum sativum]
Seq. No.
                    401616
Seq. ID
                    LIB3431-045-P1-K1-B8
Method
                    BLASTX
NCBI GI
                    g132105
BLAST score
                    690
E value
                    8.0e-73
Match length
                    147
                    89
% identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi_226375_prf _1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
Seq. No.
                    401617
Seq. ID
                    LIB3431-045-P1-K1-B9
Method
                    BLASTX
NCBI GI
                    q3169012
BLAST score
                    485
E value
                    1.0e-48
Match length
                    123
% identity
                    76
NCBI Description
                    (AJ002610) putative calmodulin binding transporter protein
                    [Hordeum vulgare]
Seq. No.
                    401618
                    LIB3431-045-P1-K1-C1
Seq. ID
```

Seq. ID

```
q320618
NCBI GI
BLAST score
                   356
                   8.0e-34
E value
Match length
                   84
% identity
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   401619
Seq. No.
Seq. ID
                   LIB3431-045-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   g3885894
                   551
BLAST score
                   1.0e-56
E value
Match length
                   136
% identity
                   80
NCBI Description (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
Seq. No.
                   401620
                   LIB3431-045-P1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q444790
                   255
BLAST score
E value
                   7.0e-22
Match length
                   124
                   52
% identity
NCBI Description
                   nucleotide translocator [Arabidopsis thaliana]
Seq. No.
                   401621
Seq. ID.
                   LIB3431-045-P1-K1-C9
Method
                   BLASTN
NCBI GI
                   g2306980
BLAST score
                   37
E value
                   7.0e-12
Match length
                   41
% identity
                   Oryza sativa photosystem I antenna protein (Lhca) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   401622
Seq. ID
                   LIB3431-045-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g2497903
BLAST score
                   220
                   9.0e-18
E value
                   59
Match length
% identity
                   68
                   METALLOTHIONEIN-LIKE PROTEIN TYPE 2
NCBI Description
                   >gi_1752831_dbj_BAA14038.1_ (D89931) metallothionein-like
protein [Oryza sativa] >gi_1815628 (U43530)
                   metallothionein-like type \overline{2} [Oryza sativa]
Seq. No.
                   401623
```

LIB3431-045-P1-K1-D12

```
Method
                  BLASTX
NCBI GI
                  q1174780
BLAST score
                  534
E value
                  1.0e-54
Match length
                  113
% identity
                  88
                  TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR (ORANGE PERICARP
NCBI Description
                  2) >gi_320135_pir__PQ0450 tryptophan synthase (EC 4.2.1.20)
                  beta-2 chain precursor - maize (fragment) >gi 168574
                  (M76685) tryptophan synthase beta-subunit [Zea mays]
Seq. No.
                  401624
Seq. ID
                  LIB3431-045-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q5051771
BLAST score
                  293
                  3.0e-26
E value
Match length
                  96
% identity
NCBI Description
                   (AL078637) putative protein [Arabidopsis thaliana]
                  401625
Seq. No.
Seq. ID
                  LIB3431-045-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  511
                  6.0e-52
E value
Match length
                  115
                  85
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401626
Seq. ID
                  LIB3431-045-P1-K1-D6
Method
                  BLASTX
                  g2072555
NCBI GI
BLAST score
                  175
                  2.0e-12
E value
Match length
                  32
                  100
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  401627
Seq. No.
Seq. ID
                  LIB3431-045-P1-K1-D8
Method
                  BLASTX
                  g115787
NCBI GI
BLAST score
                  717
                  4.0e-76
E value
```

Match length

120

```
145
Match length
                   96
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   401628
Seq. ID
                   LIB3431-045-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   q5803254
BLAST score
                   223
E value
                   4.0e-18
Match length
                   104
% identity
                   49
                   (AP000399) ESTs C97429(C60159), D22427(C11106),
NCBI Description
                   AU078031(E31854), D15683(C1084) correspond to a region of
                   the predicted gene; hypothetical protein [Oryza sativa]
Seq. No.
                   401629
Seq. ID
                   LIB3431-045-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g1651828
BLAST score
                   222
E value
                   5.0e-18
Match length
                   150
% identity
NCBI Description
                   (D90900) dihydrolipoamide dehydrogenase [Synechocystis sp.]
Seq. No.
                   401630
                   LIB3431-045-P1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2244749
BLAST score
                   724
E value
                   8.0e-77
Match length
                   161
% identity
NCBI Description
                   (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
Seq. No.
                   401631
                   LIB3431-045-P1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q21839
BLAST score
                   319
E value
                   2.0e-29
Match length
                   139
% identity
NCBI Description
                   (X57952) phosphoribulokinase [Triticum aestivum]
Seq. No.
                   401632
Seq. ID
                   LIB3431-045-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   q4741942
BLAST score
                   409
E value
                   8.0e-40
```

```
% identity
                  (AF134121) Lhca5 protein [Arabidopsis thaliana]
NCBI Description
                  401633
Seq. No.
Seq. ID
                  LIB3431-045-P1-K1-E4
Method
                  BLASTX
                  g3075488
NCBI GI
                  429
BLAST score
E value
                  2.0e-42
                  107
Màtch length
                  79
% identity
NCBI Description
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                  401634
Seq. No.
                  LIB3431-045-P1-K1-E6
Seq. ID
                  BLASTN
Method
                  g5042437
NCBI GI
BLAST score
                  58
E value
                  1.0e-23
                  97
Match length
% identity
                  90
                  Oryza sativa BAC T49B20 genomic sequence, complete sequence
NCBI Description
                  401635
Seq. No.
                  LIB3431-045-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  609
E value
                  3.0e-63
Match length
                  148
                  79
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  401636
                  LIB3431-045-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3212852
BLAST score
                  523
E value
                  4.0e-53
                  174
Match length
                  60
% identity
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  401637
                  LIB3431-045-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5733866
BLAST score
                  514
                  3.0e-52
E value
                  153
Match length
                  63
% identity
                  (AC007932) Contains similarity to gb_M73488
NCBI Description
                  1-aminocyclopropane-1-carboxylate deaminase from
                  Pseudomonas sp. ESTs gb_Z18033 and gb_Z34214 come from
```

this gene. [Arabidopsis thaliana] Seq. No. 401638 Seq. ID LIB3431-045-P1-K1-F12 Method BLASTN NCBI GI g2073379 BLAST score 165 E value 9.0e-88 Match length 203 95 % identity NCBI Description Rice CP26 mRNA, partial sequence 401639 Seq. No. Seq. ID LIB3431-045-P1-K1-F3 Method BLASTX NCBI GI g3126854 BLAST score 751 E value 8.0e-82 Match length 156 % identity NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa] Seq. No. 401640 Seq. ID LIB3431-045-P1-K1-F4 Method BLASTX NCBI GI. q3126854 BLAST score 613 E value 7.0e-64 117 Match length % identity (AF061577) chlorophyll a/b binding protein [Oryza sativa] NCBI Description Seq. No. 401641 LIB3431-045-P1-K1-F6 Seq. ID Method BLASTN NCBI GI g3618309 BLAST score 45 E value 3.0e-16 Match length 65 % identity Oryza sativa mRNA for zinc finger protein, complete cds, NCBI Description clone:E10707 Seq. No. 401642 LIB3431-045-P1-K1-F8 Seq. ID Method BLASTX NCBI GI g4587556 BLAST score 168 E value 8.0e-12 Match length 44 % identity 75 (ACO06577) Similar to gi_1653162 (p)ppGpp NCBI Description 3-pyrophosphohydrolase from Synechocystis sp genome

[Arabidopsis thaliana]

401643

Seq. No.

gb D90911. EST gb W43807 comes from this gene.

```
LIB3431-045-P1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q5734636
                  385
BLAST score
E value
                  5.0e-37
Match length
                  138
                  51
% identity
NCBI Description
                   (AP000391) Similar to putative lipase (AC006232) [Oryza
                  sativa]
                  401644
Seq. No.
                  LIB3431-045-P1-K1-G1
Seq. ID
                  BLASTX
Method
                  g2129538
NCBI GI
BLAST score
                  618
                  2.0e-64
E value
                  132
Match length
                  89
% identity
NCBI Description
                  AT103 protein - Arabidopsis thaliana >gi 1033195 (U38232)
                  AT103 [Arabidopsis thaliana]
Seq. No.
                  401645
Seq. ID
                  LIB3431-045-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q3914603
BLAST score
                  836
E value
                  6.0e-90
Match length
                  161
% identity
                  98
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
Seq. No.
                  401646
Seq. ID
                  LIB3431-045-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q3914603
BLAST score
                  881
E value
                  4.0e-95
Match length
                  169
% identity
                  99
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
Seq. No.
                  401647
Seq. ID
                  LIB3431-045-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q3928083 .
BLAST score
                  522
E value
                  4.0e-53
Match length
                  138
                  70
% identity
NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]
```

NCBI GI

```
Seq. No.
                   401648
Seq. ID
                  LIB3431-045-P1-K1-G5
Method
                  BLASTX
NCBI GI
                   g4006881
BLAST score
                   312
E value
                   7.0e-37
Match length
                  120
% identity
                   (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   401649
                  LIB3431-045-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3914005
BLAST score
                   470
E value
                   5.0e-47
Match length
                   105
                   90
% identity
NCBI Description
                  MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 1816586
                   (U85494) LON1 protease [Zea mays]
                   401650
Seq. No.
Seq. ID
                  LIB3431-045-P1-K1-G8
Method
                  BLASTX
NCBI GI
                   q2570515
BLAST score
                   244
                   2.0e-21
E value
Match length
                   92
% identity
                   (AF022740) glycolate oxidase [Oryza sativa]
NCBI Description
                   401651
Seq. No.
Seq. ID
                  LIB3431-045-P1-K1-H10
Method
                  BLASTX
NCBI GI
                   q3789952
BLAST score
                   207
E value
                   2.0e-16
Match length
                   41
% identity
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                   sativa]
Seq. No.
                   401652
Seq. ID
                  LIB3431-045-P1-K1-H11
Method
                  BLASTN
NCBI GI
                  q2331130
BLAST score
                  222
E value
                   1.0e-121
Match length
                  226
                  100
% identity
NCBI Description
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                   401653
Seq. No.
Seq. ID
                  LIB3431-045-P1-K1-H12
Method
                  BLASTX
```

g3510256

```
282
BLAST score
                   5.0e-25
E value
Match length
                   96
% identity
                   58
                   (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
                   401654
Seq. No.
                   LIB3431-045-P1-K1-H2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4097337
BLAST score
                   335
                   0.0e + 00
E value
                   406
Match length
                   100
% identity
NCBI Description
                   Oryza sativa metallothionein-like protein mRNA, complete
                   401655
Seq. No.
                   LIB3431-045-P1-K1-H3
-Seq. ID
Method
                   BLASTX
                   g5912299
NCBI GI
BLAST score
                   354
E value
                   2.0e-33
Match length
                   83
% identity
                   84
                   (AJ133787) gigantea homologue [Oryza sativa]
NCBI Description
                   401656
Seq. No.
                   LIB3431-045-P1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1172977
BLAST score
                   311
E value
                   6.0e-56
Match length
                   145
                   80
% identity
                   60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
NCBI Description
                   ribosomal protein L18 [Arabidopsis thaliana]
                   401657
Seq. No.
                   LIB3431-045-P1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1170871
                   854
BLAST score
E value
                   5.0e-92
Match length
                   166
% identity
NCBI Description
                   MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME)
                   (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME)
                   >gi_1076749_pir__S46499 NADP-dependent malic enzyme - rice
                   >gi_415315_dbj_BAA03949_ (D16499) NADP-dependent malic
                   enzyme [Oryza sativa]
Seq. No.
                   401658
                   LIB3431-045-P1-K1-H6
Seq. ID
Method
                   BLASTX
                   q3036949
NCBI GI
```

BLAST score

```
2.0e-27
E value
Match length
                   58
                   100
% identity
                   (AB012638) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                   401659
Seq. No.
Seq. ID
                  LIB3431-045-P1-N1-A10
Method
                   BLASTN
NCBI GI
                   q5441876
                   390
BLAST score
                   0.0e + 00
E value
                   454
Match length
% identity
                   96
                  Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
NCBI Description
                   (contig b)
                   401660
Seq. No.
Seq. ID
                   LIB3431-045-P1-N1-A2
Method
                   BLASTX
NCBI GI
                   g1070408
BLAST score
                   174
E value
                   2.0e-12
Match length
                   47
% identity
                   77
NCBI Description
                  ferredoxin [2Fe-2S] I - rice
                   401661
Seq. No.
Seq. ID
                  LIB3431-045-P1-N1-A3
Method
                   BLASTX
NCBI GI
                   g347451
BLAST score
                   326
E value
                   3.0e-30
Match length
                   61
% identity
                   100
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                   sativa]
Seq. No.
                   401662
                  LIB3431-045-P1-N1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g671740
                   301
BLAST score
E value
                   2.0e-27
Match length
                   57
% identity
                   100
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
Seq. No.
                   401663
Seq. ID
                   LIB3431-045-P1-N1-A5
Method
                   BLASTX
NCBI GI
                   q5419990
BLAST score
                   204
E value
                   5.0e-16
Match length
                   66
% identity
                   62
```

```
NCBI Description (AJ243524) putative fructose-bisphosphate aldolase [Phleum
                  pratense]
                  401664
Seq. No.
                  LIB3431-045-P1-N1-A6
Seq. ID
                  BLASTX
Method
                  g347451
NCBI GI
                  207
BLAST score
                  3.0e-16
E value
                  39
Match length
                  100
% identity
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
                  401665
Seq. No.
                  LIB3431-045-P1-N1-A7
Seq. ID
                  BLASTN
Method
                  g5670155
NCBI GI
                  113
BLAST score
                  1.0e-56
E value
                  353
Match length
                  88
% identity
                  Oryza sativa subsp. japonica BAC clone 34K24, complete
NCBI Description
                  sequence
                   401666
Seq. No.
Seq. ID
                  LIB3431-045-P1-N1-A8
Method
                  BLASTX
                  g115791
NCBI GI
                   194
BLAST score
                   8.0e-15
E value
Match length
                   44
                   82
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_81770_pir__S01961 chlorophyll a/b-binding
                  protein 2 precursor - soybean >gi_18548_emb_CAA31418_
                   (X12980) chlorophyll a/b binding preprotein (AA -33 to 223)
                   [Glycine max]
                   401667
Seq. No.
                   LIB3431-045-P1-N1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3885886
BLAST score
                   163
                   4.0e-11
E value
Match length
                   32
                   84
% identity
                   (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
NCBI Description
Seq. No.
                   401668
                   LIB3431-045-P1-N1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3549656
BLAST score
                   177
                   9.0e-13
E value
Match length
                   75
% identity
                   45
```

BLAST score

50

```
NCBI Description (AL031394) putative protein [Arabidopsis thaliana]
Seq. No.
                   401669
                   LIB3431-045-P1-N1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3892058
BLAST score
                   267
E value
                   3.0e-23
Match length
                   82
                   56
% identity
                   (AC002330) putative glutamate-/aspartate-binding peptide
NCBI Description
                   [Arabidopsis thaliana]
                   401670
Seq. No.
Seq. ID
                   LIB3431-045-P1-N1-B2
Method
                   BLASTN
NCBI GI
                   q2662342
BLAST score
                   58
                   7.0e-24
E value
Match length
                   89
                   95
% identity
                  Oryza sativa mRNA for EF-1 alpha, complete cds
NCBI Description
Seq. No.
                   401671
                   LIB3431-045-P1-N1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q132105
                   302
BLAST score
                   2.0e-27
E value
                   58
Match length
% identity
                   98
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   401672
                   LIB3431-045-P1-N1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q671740
BLAST score
                   277
E value
                   2.0e-24
Match length
                   53
% identity
                   100
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
Seq. No.
                   401673
Seq. ID
                   LIB3431-045-P1-N1-C1
Method
                   BLASTN
NCBI GI
                   q2306980
```

```
3.0e-19
E value
Match length
                  70
% identity
                  93
                  Oryza sativa photosystem I antenna protein (Lhca) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  401674
Seq. ID
                  LIB3431-045-P1-N1-C10
Method
                  BLASTX
NCBI GI
                  g3885894
BLAST score
                  213
                  5.0e-17
E value
Match length
                   66
% identity
                   65
                   (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
                  401675
Seq. No.
Seq. ID
                  LIB3431-045-P1-N1-C12
Method
                  BLASTN
NCBI GI
                  q20181
BLAST score
                  79
                  3.0e-36
E value
Match length
                  107
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
                  401676
Seq. No.
                  LIB3431-045-P1-N1-C9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2306980
BLAST score
                  87
                  4.0e-41
E value
Match length
                  175
%.identity
NCBI Description
                  Oryza sativa photosystem I antenna protein (Lhca) mRNA,
                  complete cds
Seq. No.
                  401677
Seq. ID
                  LIB3431-045-P1-N1-D10
Method
                  BLASTX
NCBI GI
                  q1835731
BLAST score
                  359
                  4.0e-34
E value
Match length
                  80
% identity
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                  401678
                  LIB3431-045-P1-N1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1815627
BLAST score
                  137
E value
                  7.0e-71
Match length
                  137
% identity
NCBI Description Oryza sativa metallothionein-like type 2 (OsMT-2) mRNA,
```

complete cds

```
Seq. No.
                     401679
 Seq. ID
                     LIB3431-045-P1-N1-D3
 Method
                     BLASTN
 NCBI GI
                     g3789953
 BLAST score
                     228
 E value
                     1.0e-125
 Match length
                     268
 % identity
                     96
                    Oryza sativa chlorophyll a/b-binding protein precursor
 NCBI Description
                     (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                     complete cds
 Seq. No.
                     401680
 Seq. ID
                    LIB3431-045-P1-N1-D5
 Method
                    BLASTX
 NCBI GI
                    g671740
 BLAST score
                    326
 E value
                    3.0e-30
 Match length
                    61
 % identity
                    100
 NCBI Description
                    (X84730) ribulose-bisphosphate carboxylase [synthetic
                    construct]
 Seq. No.
                    401681
 Seq. ID
                    LIB3431-045-P1-N1-D6
 Method
                    BLASTN
 NCBI GI
                    g2072554
 BLAST score
                    392
E value
                    0.0e + 00
Match length
                    407
 % identity
                    99
                    Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
Seq. No.
                    401682
Seq. ID
                    LIB3431-045-P1-N1-D8
Method
                    BLASTX
NCBI GI
                    g115787
BLAST score
                    403
E value
                    3.0e-39
Match length
                   76
% identity
                   100
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   401683
Seq. ID
                   LIB3431-045-P1-N1-E11
Method
                   BLASTX
NCBI GI
                   g2274988
BLAST score
                   291
E value
                   4.0e-26
Match length
                   74
```

% identity

82

```
% identity
NCBI Description
                   (AJ000226) partial sequence, homology to serine
                  hydroxymethyltransferases [Hordeum vulgare]
                   401684
Seq. No.
                  LIB3431-045-P1-N1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4741942
BLAST score
                   439
E value
                   2.0e-43
Match length
                  111
% identity
                   76
                   (AF134121) Lhca5 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   401685
                  LIB3431-045-P1-N1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3075487
BLAST score
                  314
E value
                   1.0e-176
Match length
                   314
                   100
% identity
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                  mRNA, complete cds
Seq. No.
                   401686
                  LIB3431-045-P1-N1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q461812
BLAST score
                   298
E value
                   6.0e-27
Match length
                  88
                   56
% identity
                  CYTOCHROME P450 72A1 (CYPLXXII) (PROBABLE
NCBI Description
                  GERANIOL-10-HYDROXYLASE) (GE10H) >gi 167484 (L10081)
                  Cytochrome P-450 protein [Catharanthus roseus]
                  >gi 445604 prf 1909351A cytochrome P450 [Catharanthus
                  roseus]
                   401687
Seq. No.
Seq. ID
                  LIB3431-045-P1-N1-E6
Method
                  BLASTN
NCBI GI
                  q5042437
BLAST score
                  135
                  1.0e-69
E value
                  196
Match length
% identity
                  92
NCBI Description
                  Oryza sativa BAC T49B20 genomic sequence, complete sequence
                  401688
Seq. No.
                  LIB3431-045-P1-N1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115813
BLAST score
                  257
E value
                  4.0e-22
Match length
                  61
```

E value

4.0e-99

```
CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                  401689
                  LIB3431-045-P1-N1-E8
Seq. ID
Method
                  BLASTX
                  g3789954
NCBI GI
BLAST score
                  357
E value
                  7.0e-34
Match length
                  66
% identity
                  100
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  401690
Seq. No.
                  LIB3431-045-P1-N1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  256
E value
                  4.0e-22
                  56
Match length
                  82
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  401691
Seq. ID
                  LIB3431-045-P1-N1-F1
Method
                  BLASTX
NCBI GI
                  g3212852
                  309
BLAST score
                  3.0e-28
E value
                  80
Match length
% identity
                  66
                  (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
                  401692
Seq. No.
                  LIB3431-045-P1-N1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5733866
BLAST score
                  343
                  3.0e-32
E value
                  86
Match length
                  69
% identity
                  (AC007932) Contains similarity to gb_M73488
NCBI Description
                  1-aminocyclopropane-1-carboxylate deaminase from
                  Pseudomonas sp. ESTs gb_Z18033 and gb_Z34214 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  401693
                  LIB3431-045-P1-N1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2073379
BLAST score
                  184
```

```
203
Match length
                   98
% identity
                  Rice CP26 mRNA, partial sequence
NCBI Description
Seq. No.
                   401694
                   LIB3431-045-P1-N1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   294
E value
                   2.0e-26
Match length
                   57
% identity
                   98
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   401695
Seq. No.
                   LIB3431-045-P1-N1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   192
E value
                   5.0e-19
Match length
                   61
                   89
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   401696
                   LIB3431-045-P1-N1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5734636
BLAST score
                   180
                   4.0e-13
E value
Match length
                   48
% identity
                   65
                   (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                   sativa]
Seq. No.
                   401697
Seq. ID
                   LIB3431-045-P1-N1-G1
Method
                   BLASTX
NCBI GI
                   g1052960
BLAST score
                   348
E value
                   8.0e-33
Match length
                   79
% identity
                   86
NCBI Description
                   (U37437) PNIL34 [Ipomoea nil]
                   401698
Seq. No.
                   LIB3431-045-P1-N1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g167097
BLAST score
                   151
                   6.0e-17
E value
Match length
                   52
                   88
% identity
                   (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                   [Hordeum vulgare]
```

Seq. No.

NCBI GI

```
Seq. ID
                   LIB3431-045-P1-N1-G2
Method
                  BLASTX
NCBI GI
                   q167097
BLAST score
                   151
E value
                   7.0e-15
Match length
                   47
% identity
NCBI Description
                   (M55449) ribulose 1,5-bisphosphate carboxylase activase
                   [Hordeum vulgare]
Seq. No.
                   401700
Seq. ID
                   LIB3431-045-P1-N1-G6
Method
                  BLASTX
NCBI GI
                   q3914005
BLAST score
                   328
                   2.0e-30
E value
                   73
Match length
                   89
% identity
                  MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 1816586
NCBI Description
                   (U85494) LON1 protease [Zea mays]
                   401701
Seq. No.
Seq. ID
                  LIB3431-045-P1-N1-G8
Method
                  BLASTN
                   g2570514
NCBI GI
BLAST score
                   206
                   1.0e-112
E value
Match length
                   326
                   91
% identity
                  Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
NCBI Description
Seq. No.
                   401702
                  LIB3431-045-P1-N1-H10
Seq. ID
Method
                  BLASTN
                   g3789951
NCBI GI
BLAST score
                   77
E value
                   2.0e-35
Match length
                  105
                   93
% identity
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
Seq. No.
                   401703
                  LIB3431-045-P1-N1-H2
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4105602
BLAST score
                   343
E value
                   0.0e + 00
Match length
                   371
                   98
% identity
                  Oryza sativa metallothionein (MTe) gene, complete cds
NCBI Description
Seq. No.
                   401704
                  LIB3431-045-P1-N1-H3
Seq. ID
Method
                  BLASTN
```

g5912298

BLAST score 45 5.0e-16 E value Match length 59 95 % identity Oryza sativa mRNA for gigantea homologue, partial NCBI Description Seq. No. 401705 Seq. ID LIB3431-045-P1-N1-H4 Method BLASTX NCBI GI g1172977 BLAST score 327 E value 2.0e-30 Match length 69 87 % identity NCBI Description 60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana] 401706 Seq. No. Seq. ID LIB3431-045-P1-N1-H6 Method BLASTX NCBI GI q3036951 BLAST score 301 E value 2.0e-27 Match length 58 100 % identity NCBI Description (AB012639) light harvesting chlorophyll a/b-binding protein [Nicotiana sylvestris] 401707 Seq. No. LIB3431-046-P1-K1-A1 Seq. ID Method BLASTX NCBI GI q1353352 BLAST score 483 1.0e-48 E value Match length 149 % identity NCBI Description (U31975) alanine aminotransferase [Chlamydomonas reinhardtii] 401708 Seq. No. LIB3431-046-P1-K1-A10 Seq. ID Method BLASTX NCBI GI q6006363 BLAST score 288 7.0e-26 E value 58 Match length % identity NCBI Description (AP000559) ESTs AU078183(C62904), C73912(E21020) correspond to a region of the predicted gene.; Similar to water stress inducible protein (U74296) [Oryza sativa]

401709 Seq. No. Seq. ID LIB3431-046-P1-K1-A11

Method BLASTX NCBI GI q4105561

BLAST score 684 E value 3.0e-72

```
Match length
                   139
% identity
NCBI Description
                   (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
                   401710
Seq. No.
Seq. ID
                   LIB3431-046-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   q115787
BLAST score
                   438
                   3.0e-43
E value
Match length
                   106
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   401711
Seq. ID
                   LIB3431-046-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   465
E value
                   1.0e-46
Match length
                   108
                   83
% identity
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   401712
Seq. No.
Seq. ID
                   LIB3431-046-P1-K1-A4
Method
                   BLASTX
NCBI GI
                   q2288969
BLAST score
                   422
E value
                   2.0e-41
Match length
                   122
% identity
                   (Y12862) glutathione transferase [Zea mays]
NCBI Description
Seq. No.
                   401713
                   LIB3431-046-P1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   712
E value
                   2.0e-75
                   159
Match length
% identity
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice .
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
```

Seq. No. 401714

[Oryza sativa]

chlorophyll a/b-binding protein [Oryza sativa]

>gi 227611 prf 1707316A chlorophyll a/b binding protein 1

Seq. No.

401719

```
LIB3431-046-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3075488
BLAST score
                   545
                   5.0e-56
E value
Match length
                   107
% identity
                   98
NCBI Description
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                   LIB3431-046-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q100454
BLAST score
                   627
E value
                   2.0e-65
Match length
                   154
                   77
% identity
                  photosystem II oxygen-evolving complex protein 1 - potato
NCBI Description
                   >gi_809113_emb_CAA35601_ (X17578) 33kDa precursor protein
                   of oxygen-evolving complex [Solanum tuberosum]
                   401716
Seq. No.
Seq. ID
                   LIB3431-046-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   a6093830
BLAST score
                   155
E value
                   2.0e-10
                   37
Match length
                   81
% identity
                   PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
NCBI Description
                   [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
                   PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor;
                  putative photosytem II peptide [Spinacia oleracea]
                   401717
Seq. No.
Seq. ID
                   LIB3431-046-P1-K1-B11
Method
                   BLASTX
                   a82080
NCBI GI
                   433
BLAST score
                   9.0e-43
E value
                   124
Match length
% identity
                   chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                   401718
Seq. ID
                   LIB3431-046-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q3395439
BLAST score
                   266
                   4.0e-23
E value
Match length
                   81
% identity
                   (AC004683) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

NCBI GI

g671740

```
Seq. ID
                  LIB3431-046-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g4959460
BLAST score
                  37
E value
                  2.0e-11
Match length
                  37
                  100
% identity
NCBI Description
                  Zea mays RACB small GTP binding protein mRNA, complete cds
Seq. No.
Seq. ID
                  LIB3431-046-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q4138290
BLAST score
                  582
E value
                  3.0e-60
Match length
                  128
% identity
NCBI Description
                   (AJ005841) thioredoxin M [Oryza sativa]
Seq. No.
                  401721
Seq. ID
                  LIB3431-046-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q629864
BLAST score
                  410
E value
                  6.0e-40
Match length
                  86
                  97
% identity
                  histone H2B - garden asparagus >gi 563329 emb CAA57778
NCBI Description
                   (X82362) histone 2B [Asparagus officinalis]
Seq. No.
                  401722
Seq. ID
                  LIB3431-046-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  q4680212
BLAST score
                  163
E value
                  3.0e-11
Match length
                  52
% identity
                  (AF114171) hypothetical protein [Sorghum bicolor]
NCBI Description
Seq. No.
                  401723
Seq. ID
                LIB3431-046-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  565
                  3.0e-58
E value
Match length
                  119
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  401724
                  LIB3431-046-P1-K1-C2
Seq. ID
Method
                  BLASTX
```

NCBI Description

```
BLAST score
                   583
E value
                   2.0e-60
                   109
Match length
                   98
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
Seq. No.
                   401725
Seq. ID
                   LIB3431-046-P1-K1-C4
Method
                   BLASTX
                   q2072555
NCBI GI
BLAST score
                   237
                   9.0e-20
E value
Match length
                   44
% identity
                   100
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   401726
Seq. ID
                   LIB3431-046-P1-K1-C6
Method
                   BLASTN
NCBI GI
                   q3377792
BLAST score
                   76
E value
                   4.0e-35
Match length
                   95
                   96
% identity
                   Oryza sativa ribulose-1,5-bisphosphate
NCBI Description
                   carboxylase/oxygenase activase (rca) mRNA, complete cds
Seq. No.
                   401727
Seq. ID
                   LIB3431-046-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   632
E value
                   4.0e-66
Match length
                   137
                   88
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   401728
Seq. ID
                   LIB3431-046-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   q1617197
BLAST score
                   293
E value
                   2.0e-26
Match length
                   76
% identity
```

(Z72488) CP12 [Nicotiana tabacum]

```
401729
Seq. No.
                  LIB3431-046-P1-K1-C9
Seq. ID
Method
                  BLASTN
                  g11957
NCBI GI
BLAST score
                  83
                  3.0e-39
E value
                  127
Match length
                  46
% identity
NCBI Description
                  Rice complete chloroplast genome
                  401730
Seq. No.
                  LIB3431-046-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115794
BLAST score
                  826
                  9.0e-89
E value
                  161
Match length
                  95
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
NCBI Description
                  III CAB-13) >gi 72748 pir CDTO33 chlorophyll a/b-binding
                  protein type III precursor (cab-13) - tomato
                  >gi_19277_emb_CAA42818_ (X60275) LHCII type III
                  [Lycopersicon esculentum]
Seq. No.
                 401731
Seq. ID
                  LIB3431-046-P1-K1-D12
Method
                  BLASTX
                  g3377841
NCBI GI
BLAST score
                  453
                  3.0e-45
E value
                  107
Match length
% identity
                  82
                   (AF075598) contains similarity to phosphofructokinases
NCBI Description
                   (Pfam; PFK.hmm, score; 36.60) [Arabidopsis thaliana]
                  401732
Seq. No.
Seq. ID
                  LIB3431-046-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g4099148
                  551
BLAST score
                  1.0e-56
E value
                  140
Match length
% identity
                  (U84268) YLP [Hordeum vulgare]
NCBI Description
                  401733
Seq. No.
                  LIB3431-046-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5668608
BLAST score
                  362
                  2.0e-34
E value
                  148
Match length
                  48 -
% identity
                  (AF115334) MenG [Pseudomonas fluorescens]
NCBI Description
```

Seq. No.

```
LIB3431-046-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  175
E value
                   1.0e-12
Match length
                   32
                   100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                   401735
Seq. No.
                  LIB3431-046-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1519249
                   697
BLAST score
E value
                  1.0e-73
Match length
                  146
                   95
% identity
NCBI Description
                   (U65956) GF14-b protein [Oryza sativa]
Seq. No.
                  401736
                  LIB3431-046-P1-K1-D9
Seq. ID
Method
                  BLASTX
                  q5738522
NCBI GI
BLAST score
                  180
E value
                   2.0e-13
Match length
                  50
                  72
% identity
                   (AL109846) putative pre-mrna splicing factor atp-dependent
NCBI Description
                  rna helicase [Schizosaccharomyces pombe]
                  401737
Seq. No.
                  LIB3431-046-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417260
BLAST score
                  381
E value
                  1.0e-36
Match length
                  121
                   64
% identity
                  LIGHT REGULATED PROTEIN PRECURSOR >qi 422003 pir S33632
NCBI Description
                  lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                  light-regulated gene [Oryza sativa]
                  401738
Seq. No.
                  LIB3431-046-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  540
                  2.0e-55
E value
                  123
Match length
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
```

[Oryza sativa]

E value

1.0e-41

```
Seq. No.
                  401739
Seq. ID
                  LIB3431-046-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  607
E value
                   4.0e-63
Match length
                  127
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  401740
Seq. ID
                  LIB3431-046-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g6063542
BLAST score
                  681
E value
                  8.0e-72
Match length
                  135
                  100
% identity
NCBI Description
                   (AP000615) EST C74302(E30840) corresponds to a region of
                  the predicted gene.; similar to glyceraldehyde-3-phosphate
                  dehydrogenase. (M64118) [Oryza sativa]
Seq. No.
                  401741
                  LIB3431-046-P1-K1-E5
Seq. ID
Method
                  BLASTX
                  g131205
NCBI GI
BLAST score
                  178
E value
                  9.0e-13
Match length
                  36
                  100
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I)
                  >gi_72677_pir__A1RZI photosystem I protein psaI - rice
                  chloroplast >gi_11996_emb_CAA33957_ (X15901) ORF36 [Oryza
                  sativa] >gi_226617_prf__1603356AP photosystem I small
                  peptide [Oryza sativa]
Seq. No.
                  401742
Seq. ID
                  LIB3431-046-P1-K1-E6
Method
                  BLASTX
                  g4530126
NCBI GI
BLAST score
                  236
E value
                  2.0e-19
Match length
                  90
% identity
                   (AF078082) receptor-like protein kinase homolog RK20-1
NCBI Description
                  [Phaseolus vulgaris]
                  401743
Seq. No.
                  LIB3431-046-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3334333
BLAST score
                  422
```

Method

BLASTX

```
103
Match length
                   76
% identity
                  SUPEROXIDE DISMUTASE-2 [CU-ZN] >qi 2660798 (AF034832)
NCBI Description
                   cytosolic copper/zinc superoxide dismutase
                   [Mesembryanthemum crystallinum]
Seq. No.
                  401744
                  LIB3431-046-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3789954
BLAST score
                  563
E value
                   4.0e-58
Match length
                  120
% identity
NCBI Description
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                  sativa]
                  401745
Seq. No.
                  LIB3431-046-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587556
BLAST score
                  284
                  2.0e-25
E value
Match length
                  103
                  53
% identity
NCBI Description
                   (AC006577) Similar to gi_1653162 (p)ppGpp
                  3-pyrophosphohydrolase from Synechocystis sp genome
                  gb D90911. EST gb W43807 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  401746
Seq. ID
                  LIB3431-046-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g115787
                  529
BLAST score
                  5.0e-54
E value
Match length
                  121
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                  401747
Seq. No.
                  LIB3431-046-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  707
                  7.0e-75
E value
Match length
                  151
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
Seq. No.
                  401748
                  LIB3431-046-P1-K1-F3
Seq. ID
```

NCBI GI

```
NCBI GI
                  g4415940
BLAST score
                  249
E value
                  3.0e-21
Match length
                  103
                  49
% identity
NCBI Description
                   (AC006418) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  401749
Seq. ID
                  LIB3431-046-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  412
                  3.0e-40
E value
                  117
Match length
                   68
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                  401750
Seq. No.
Seq. ID
                  LIB3431-046-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q1835731
BLAST score
                  507
E value
                  2.0e-51
Match length
                  123
% identity
                  81
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                  401751
Seq. No.
                  LIB3431-046-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512125
BLAST score
                  178
                   6.0e-13
E value
                  32
Match length
                  100
% identity
NCBI Description
                   (AF133340) putative chlorophyll a/b-binding protein
                   [Phalaenopsis sp. 'KCbutterfly']
                  401752
Seq. No.
                  LIB3431-046-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914603
BLAST score
                  680
E value
                  1.0e-71
Match length
                  131
                  99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                   (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
                  401753
Seq. No.
                  LIB3431-046-P1-K1-G1
Seq. ID
Method
                  BLASTX
```

q3789952

```
BLAST score
                  612
                  1.0e-63
E value
Match length
                  121
% identity
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
                  401754
Seq. No.
Seq. ID
                  LIB3431-046-P1-K1-G10
                  BLASTX
Method
NCBI GI
                  q132105
BLAST score
                  660
E value
                  2.0e-69
Match length
                  141
                  89
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401755
Seq. ID
                  LIB3431-046-P1-K1-G11
Method
                  BLASTX
                  q3914470
NCBI GI
BLAST score
                  311
                  6.0e-37
E value
                  115
Match length
                  71
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                  >gi_1321868_emb_CAA66373_ (X97771) 10kD PSII protein
                  [Hordeum vulgare]
Seq. No.
                  401756
Seq. ID
                  LIB3431-046-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g82080
                  438
BLAST score
                  2.0e-44
E value
Match length
                  138
                  68
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
Seq. No.
                  401757
Seq. ID
                  LIB3431-046-P1-K1-G3
                  BLASTX
Method
                  g131388
NCBI GI
BLAST score
                  352
E value
                  3.0e - 33
                  120
Match length
```

% identity

```
NCBI Description OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
                  33kDa oxygen evolving protein of photosystem II [Triticum
                  aestivum]
Seq. No.
                  401758
                  LIB3431-046-P1-K1-G6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6006355
BLAST score
                  108
                  8.0e-54
E value
Match length
                  164
                  100
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
                  401759
Seq. No.
                  LIB3431-046-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499417
BLAST score
                  467
                  1.0e-46
E value
Match length
                  111
% identity
                  80
NCBI Description
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
                  >gi_1085826_pir__S49248 H-protein - Flaveria anomala
                  >gi 547558 emb CAA85761 (Z37524) H-protein [Flaveria
                  anomala]
Seq. No.
                  401760
Seq. ID
                  LIB3431-046-P1-K1-G9
                  BLASTX
Method
NCBI GI
                  g4469020
BLAST score
                  602
                  2.0e-62
E value
Match length
                  132
% identity
                  (AL035602) putative protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                  401761
Seq. No.
                  LIB3431-046-P1-K1-H1
Seq. ID
                  BLASTX
Method
                  g115787
NCBI GI
BLAST score
                  544
                  9.0e-56
E value
Match length
                  124
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
```

Seq. No.

```
LIB3431-046-P1-K1-H10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3345477
BLAST score
                   564
E value
                   5.0e-58
Match length
                   106
% identity
                   100
NCBI Description
                   (AB016283) carbonic anhydrase [Oryza sativa]
                   401763
Seq. No.
                   LIB3431-046-P1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   9.0e-20
Match length
                   44
                   100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   401764
Seq. No.
Seq. ID
                   LIB3431-046-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   g399213
BLAST score
                   781
                   2.0e-83
E value
                   170
Match length
% identity
                   ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
NCBI Description
                   CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato
                   >gi 170435 (M32604) ATP-dependent protease (CD4B)
                   [Lycopersicon esculentum]
Seq. No.
                   401765
Seq. ID
                   LIB3431-046-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   q4079798
BLAST score
                   408
E value
                   8.0e-40
                   112
Match length
% identity
NCBI Description
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                   sativa]
Seq. No.
                   401766
Seq. ID
                   LIB3431-046-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   q118170
BLAST score
                   429
E value
                   4.0e-42
Match length
                   102
                   85
% identity
NCBI Description
                   CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I)
                   >gi_82491_pir__A28464 oryzacystatin - rice >gi_169784
(J03469) oryzacystatin [Oryza sativa] >gi_169807 (M29259)
                   oryzastatin [Oryza sativa] >gi 259137 bbs_120195 (S49967)
```

Seq. No.

401771

```
[Oryza sativa]
Seq. No.
                  401767
Seq. ID
                  LIB3431-046-P1-K1-H7
                  BLASTX
Method
                  g1173347
NCBI GI
                  883
BLAST score
                  2.0e-95
E value
                  173
Match length
                   93
% identity
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi 100803 pir S23452 sedoheptulose-bisphosphatase (EC
                   3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                   aestivum]
                   401768
Seq. No.
                  LIB3431-046-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2495180
BLAST score
                   396
E value
                   2.0e-38
Match length
                   94
                   83
% identity
NCBI Description
                   PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG)
                   (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN
                   SYNTHASE) >gi 421882 pir__S35873 hydroxymethylbilane
                   synthase (EC \overline{4.3.1.8}) - \overline{\text{garden pea}} >gi 541971 pir JQ2278
                  hydroxymethylbilane synthase (EC 4.3.1.8) precursor -
                   garden pea chloroplast >qi 313724 emb CAA51820 (X73418)
                  hydroxymethylbilane synthase [Pisum sativum]
Seq. No.
                   401769
Seq. ID
                  LIB3431-046-P1-N1-A1
Method
                   BLASTX
NCBI GI
                   g1353352
BLAST score
                   233
E value
                   2.0e-19
Match length
                   62
                   73
% identity
                   (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                   reinhardtii]
Seq. No.
                   401770
                   LIB3431-046-P1-N1-A10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q6006355
BLAST score
                   214
                   1.0e-117
E value
Match length
                   353
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
NCBI Description
```

oryzacystatin=cysteine protease inhibitor [Oryza=rice, Peptide, 102 aa] [Oryza] >gi 1280613 (U54702) oryzacystatin

```
LIB3431-046-P1-N1-A11
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4105560
BLAST score
                   101
E value
                   2.0e-49
Match length
                   164
                   90
% identity
                   Oryza sativa ribulose-5-phosphate-3-epimerase (RPE) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   401772
                   LIB3431-046-P1-N1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2288969
BLAST score
                   205
E value
                   5.0e-16
Match length
                   68
                   54
% identity
NCBI Description
                   (Y12862) glutathione transferase [Zea mays]
                   401773
Seq. No.
                   LIB3431-046-P1-N1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q115787
BLAST score
                   409
                   6.0e-40
E value
Match length
                   77
                   100
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   401774
Seq. No.
Seq. ID
                   LIB3431-046-P1-N1-A7
Method
                   BLASTX
                   g2326947
NCBI GI
BLAST score
                   224
E value
                   3.0e-18
Match length
                   44
% identity
                   (Z50801) Chlorophyll a/b-binding protein CP29 precursor
NCBI Description
                   [Zea mays]
                   401775
Seq. No.
                   LIB3431-046-P1-N1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q482311
BLAST score
                   244
E value
                   9.0e-21 ·
                   50
Match length
                   96
% identity
NCBI Description
                   photosystem II oxygen-evolving complex protein 1 - rice
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
```

complex protein 1 [Oryza sativa]

NCBI GI

```
Seq. No.
                   401776
Seq. ID
                   LIB3431-046-P1-N1-A9
Method
                   BLASTX
NCBI GI
                   g4158219
BLAST score
                   554
E value
                   6.0e-57
Match length
                   108
                   100
% identity
NCBI Description
                   (Y18623) amylogenin [Oryza sativa]
Seq. No.
                   401777
                   LIB3431-046-P1-N1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5932555
BLAST score
                   423
                   1.0e-41
E value
                   104
Match length
                   76
% identity
                   (AC009465) putative ribose 5-phosphate isomerase
NCBI Description
                   [Arabidopsis thaliana]
                   401778
Seq. No.
                   LIB3431-046-P1-N1-B6
Seq. ID
Method
                   BLASTX
                   g4138290
NCBI GI
BLAST score
                   239
E value
                   5.0e-20
                   48.
Match length
                   100
% identity
                   (AJ005841) thioredoxin M [Oryza sativa]
NCBI Description
                   401779
Seq. No.
Seq. ID
                   LIB3431-046-P1-N1-C10
Method
                   BLASTN
                   g1398998
NCBI GI
BLAST score
                   52
E value
                   3.0e-20
                   192
Match length
                   82
% identity
                   Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II,
NCBI Description
                   complete cds
Seq. No.
                   401780
Seq. ID
                   LIB3431-046-P1-N1-C11
Method
                   BLASTN
NCBI GI
                   g3063523
                   59
BLAST score
                   2.0e-24
E value
Match length
                   166
                   83
% identity
                   Oryza sativa ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   401781
Seq. No.
                   LIB3431-046-P1-N1-C4
Seq. ID
Method
                  BLASTX
```

g2072555

E value

7.0e-15

```
BLAST score
                   237
E value
                   9.0e-20
Match length
                   44
% identity
                   100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                   401782
Seq. ID
                  LIB3431-046-P1-N1-C6
Method
                  BLASTX
NCBI GI
                   q167097
BLAST score
                   165
                   4.0e-24
E value
Match length
                   70
% identity
                   (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                   [Hordeum vulgare]
                   401783
Seq. No.
                  LIB3431-046-P1-N1-C7
Seq. ID
Method
                  BLASTX
                  g671740
NCBI GI
BLAST score
                   299
E value
                   4.0e-27
Match length
                   61
% identity
                   95
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   401784
Seq. No.
                  LIB3431-046-P1-N1-D11
Seq. ID
Method
                  BLASTX
                  g829283
NCBI GI
BLAST score
                   203
E value
                   6.0e-16
Match length
                   48
% identity
                   (Z15018) heat shock protein hsp82 [Oryza sativa]
NCBI Description
                   401785
Seq. No.
                  LIB3431-046-P1-N1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3377841
BLAST score
                  182
                  1.0e-13
E value
Match length
                   47
% identity
                   (AF075598) contains similarity to phosphofructokinases
NCBI Description
                   (Pfam; PFK.hmm, score; 36.60) [Arabidopsis thaliana]
                   401786
Seq. No.
                  LIB3431-046-P1-N1-D2
Seq. ID
Method
                  BLASTN
                  g4099149
NCBI GI
BLAST score
                  43
```

```
91
Match length
                   87
% identity
NCBI Description
                   Hordeum vulgare vacuolar proton-translocating ATPase
                   subunit E (Ylp) mRNA, complete cds
                   401787
Seq. No.
                   LIB3431-046-P1-N1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5668608
BLAST score
                   192
E value
                   1.0e-14
Match length
                   83
% identity
                   42
NCBI Description
                   (AF115334) MenG [Pseudomonas fluorescens]
                   401788
Seq. No.
                   LIB3431-046-P1-N1-D4
Seq. ID
                   BLASTX
Method
                   g1835731
NCBI GI
                   340
BLAST score
E value
                   6.0e-32
                   80
Match length
                   84
% identity
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                   401789
Seq. No.
Seq. ID
                   LIB3431-046-P1-N1-D5
Method
                   BLASTX
NCBI GI
                   g829283
BLAST score
                   232
                   2.0e-19
E value
                   58
Match length
% identity
                   83
                   (Z15018) heat shock protein hsp82 [Oryza sativa]
NCBI Description
                   401790
Seq. No.
                   LIB3431-046-P1-N1-D6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2072554
BLAST score
                   390
                   0.0e + 00
E value
                   390
Match length
                  100
% identity
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                   401791
Seq. No.
                   LIB3431-046-P1-N1-D7
Seq. ID
Method
                   BLASTX
                   g4490317
NCBI GI
BLAST score
                   302
                   2.0e-27
E value
                   113
Match length
% identity
NCBI Description
                   (AL035678) putative protein [Arabidopsis thaliana]
```

Seq. No.

```
Seq. ID
                   LIB3431-046-P1-N1-E10
Method
                   BLASTX
NCBI GI
                   q729478
BLAST score
                   344
E value
                   2.0e-32
Match length
                   72
% identity
NCBI Description
                   FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
                   >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_
                   (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
                   a region of the predicted gene.; similar to
                   ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
Seq. No.
                   401793
                   LIB3431-046-P1-N1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g226263
BLAST score
                   247
E value
                   5.0e-21
Match length
                   46 .
                   100
% identity
                   chlorophyll a/b binding protein [Glycine max]
NCBI Description
Seq. No.
                   401794
                   LIB3431-046-P1-N1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131225
BLAST score
                   310
E value
                   2.0e-28
Match length
                   90
% identity
                   68
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                   precursor - barley >gi_167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
Seq. No.
                   401795
                   LIB3431-046-P1-N1-E3
Seq. ID
Method
                   BLASTX
                   q6063542
NCBI GI
BLAST score
                   512
E value
                   4.0e-52
                   96
Match length
                   99
% identity
                   (AP000615) EST C74302(E30840) corresponds to a region of
NCBI Description
                   the predicted gene.; similar to glyceraldehyde-3-phosphate
                   dehydrogenase. (M64118) [Oryza sativa]
Seq. No.
                   401796
Seq. ID
                   LIB3431-046-P1-N1-E5
Method
                   BLASTX
                   g11998
NCBI GI
BLAST score
                   292
                   4.0e-35
E value
                   76
Match length
```

% identity

```
NCBI Description
                   (X15901) ORF85 [Oryza sativa] >gi 226619 prf 1603356AR ORF
                  85A [Oryza sativa]
Seq. No.
                  401797
Seq. ID
                  LIB3431-046-P1-N1-E7
Method
                  BLASTX
NCBI GI
                  q3786214
BLAST score
                  295
E value
                  1.0e-26
Match length
                  74
% identity
                  74
                   (AJ002604) high pI CuZn-superoxide dismutase [Pinus
NCBI Description
                  sylvestris]
Seq. No.
                  401798
                  LIB3431-046-P1-N1-F1
Seq. ID
Method
                  BLASTX
                  g115772
NCBI GI
                  309
BLAST score
E value
                  3.0e-28
Match length
                  59
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding
                  protein 1R precursor - rice >gi_20178_emb_CAA32108
                   (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                   [Oryza sativa]
                  401799
Seq. No.
                  LIB3431-046-P1-N1-F11
Seq. ID
Method
                  BLASTN
                  g3345476
NCBI GI
BLAST score
                  173
                  1.0e-92
E value
                  248
Match length
                  92
% identity
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds
                  401800
Seq. No.
                  LIB3431-046-P1-N1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4415940
BLAST score
                  172
                  3.0e-12
E value
                  51
Match length
% identity
                  59
                  (AC006418) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  401801
                  LIB3431-046-P1-N1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115813
                  243
BLAST score
                  2.0e-20
E value
                  55
Match length
                  85
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
```

NCBI Description

```
chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  401802
Seq. No.
                  LIB3431-046-P1-N1-F5
Seq. ID
                  BLASTX
Method
                  g1835731
NCBI GI
                  371
BLAST score
                  2.0e-35
E value
Match length
                  82
                  88
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                  401803
Sèq. No.
                  LIB3431-046-P1-N1-F6
Seq. ID
                  BLASTX
Method
                  g421916
NCBI GI
                  178
BLAST score
                  6.0e-13
E value
                  32
Match length
                  100
% identity
                  chlorophyll a/b-binding protein - English ivy (fragment)
NCBI Description
                  >gi_12582_emb_CAA48410_ (X68333) light harvesting
                  chlorophyll a /b binding protein [Hedera helix]
                  401804
Seq. No.
                  LIB3431-046-P1-N1-F8
Seq. ID
Method
                  BLASTX
                  q100614
NCBI GI
                  196
BLAST score
                  3.0e-15
E value
                  50
Match length
                  78
% identity
                  ribulose-bisphosphate carboxylase activase A long form
NCBI Description
                  precursor - barley (fragment) >gi_167089 (M55446) ribulose
                  1,5-bisphosphate carboxylase activase [Hordeum vulgare]
                   401805
Seq. No.
Seq. ID
                  LIB3431-046-P1-N1-G10
Method
                  BLASTX
                  g347451
NCBI GI
                  236
BLAST score
                   9.0e-20
E value
                   47
Match length
% identity
                   98
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                   sativa]
                   401806
Seq. No.
                   LIB3431-046-P1-N1-G11
Seq. ID
                   BLASTX
Method
                   g3914470
NCBI GI
BLAST score
                   374
                   4.0e-39
E value
                   105
Match length
% identity
                   68
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
```

CAB-8) >gi_19182_emb_CAA33330 (X15258) Type III

```
[Hordeum vulgare]
                  401807
Seq. No.
                  LIB3431-046-P1-N1-G12
Seq. ID
                  BLASTN.
Method
                  q430946
NCBI GI
                  41
BLAST score
                  1.0e-13
E value
                  65
Match length
                  91
% identity
                  Arabidopsis thaliana PSI type III chlorophyll a/b-binding
NCBI Description
                  protein (Lhca3*1) mRNA, complete cds
                  401808
Seq. No.
                  LIB3431-046-P1-N1-G3
Seq. ID
                  BLASTX
Method
                  q482311
NCBI GI
                  364
BLAST score
                  8.0e-35
E value
                  73
Match length
                  99
% identity
                  photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
Seq. No.
                   401809
                  LIB3431-046-P1-N1-G6
Seq. ID
                   BLASTN
Method
                   q6006355
NCBI GI
                   162
BLAST score
                   4.0e-86
E value
                   220
Match length
                   93
% identity
                  Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
NCBI Description
                   401810
Seq. No.
                   LIB3431-046-P1-N1-G8
Seq. ID
Method
                   BLASTX
                   g2499417
NCBI GI
                   289
BLAST score
                   6.0e-26
E value
                   68
Match length
                   78
% identity
                   GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
NCBI Description
                   >gi_1085826_pir__S49248 H-protein - Flaveria anomala
                   >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria
                   anomala]
                   401811
Seq. No.
                   LIB3431-046-P1-N1-G9
Seq. ID
                   BLASTN
Method
                   g4680196
NCBI GI
                   56
BLAST score
                   2.0e-22
E value
                   108
Match length
                   88
% identity
```

>gi 1321868_emb_CAA66373_ (X97771) 10kD PSII protein

% identity

```
NCBI Description Sorghum bicolor BAC clone 25.M18, complete sequence
                  401812
Seq. No.
                  LIB3431-046-P1-N1-H10
Seq. ID
                  BLASTN
Method
NCBI GI
                  q606816
BLAST score
                  184
                  3.0e-99
E value
                  208
Match length
                  97
% identity
                  Oryza sativa chloroplast carbonic anhydrase mRNA, complete
NCBI Description
                  401813
Seq. No.
                  LIB3431-046-P1-N1-H4
Seq. ID
Method
                  BLASTN
                  q1398998
NCBI GI
BLAST score
                  165
                  9.0e-88
E value
                  272
Match length
                  97
% identity
                  Rice OSOEE2 gene for 23 kDa polypeptide of photosystem II,
NCBI Description
                  complete cds
Seq. No.
                  401814
                  LIB3431-046-P1-N1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173347
BLAST score
                  172
                  3.0e-12
E value
Match length
                  39
% identity
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7) P2ASE)
                  >gi 100803 pir S23452 sedoheptulose-bisphosphatase (EC
    ...
                  3.1.3.37) precursor - wheat >gi 14265 emb CAA46507
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  401815
Seq. ID
                  LIB3431-046-P1-N1-H9
Method
                  BLASTN
NCBI GI
                  g2661765
BLAST score
                  46
E value
                  1.0e-16
Match length
                  82
% identity
                  89
                  Zea mays mRNA for putative porphobilinogen deaminase
NCBI Description
Seq. No.
                  401816
Seq. ID
                  LIB3431-047-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g482311
BLAST score
                  649
                  4.0e-68
E value
Match length
                  129
```

BLAST score

```
NCBI Description photosystem II oxygen-evolving complex protein 1 - rice
                  (strain Nihonbare) >gi 739292 prf 2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
Seq. No.
                  401817
                  LIB3431-047-P1-K1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20262
BLAST score
                  252
E value
                  1.0e-139
Match length
                  252
                  100
% identity
NCBI Description O.sativa light-induced mRNA
                  401818
Seq. No.
                  LIB3431-047-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5912299
                  547
BLAST score
                  3.0e-56
E value
Match length
                  105
                  100
% identity
NCBI Description
                  (AJ133787) gigantea homologue [Oryza sativa]
Seq. No.
                  401819
Seq. ID
                  LIB3431-047-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  533
                  2.0e-54
E value
Match length
                  118
% identity
                  86
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >qi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401820
Seq. ID
                  LIB3431-047-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g22240
BLAST score
                  450
E value
                  7.0e-45
Match length
                  116
% identity
NCBI Description
                  (X07157) GADPH (383 AA) [Zea mays]
Seq. No.
                  401821
                  LIB3431-047-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6016875
```

Method

BLASTX

```
E value
                  2.0e-24
Match length
                  68
% identity
                  78
                  (AP000570) EST AU078302(C63241) corresponds to a region of
NCBI Description
                  the predicted gene.; hypothetical protein [Oryza sativa]
Seq. No.
                  401822
                  LIB3431-047-P1-K1-A8
Seq. ID
Method
                  BLASTN
                  q2072554
NCBI GI
BLAST score
                  47
E value
                  2.0e-17
Match length
                  147
% identity
                  83
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
Seq. No.
                  401823
Seq. ID
                  LIB3431-047-P1-K1-A9
Method
                  BLASTN
NCBI GI
                  q20369
BLAST `score
                  42
E value
                  9.0e-15
Match length
                  54
                  94
% identity
NCBI Description
                  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
                  synthetase (EC 6.3.1.2) (clone lambda-GS31)
                  >qi 2170909 dbj E02681 E02681 cDNA encoding precursor of
                  chloroplast localising glutamine synthetase
Seq. No.
                  401824
                  LIB3431-047-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  237
E value
                  1.0e-19
Match length
                  44
                  100
% identity
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  401825
                  LIB3431-047-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1709846
BLAST score
                  195
E value
                  7.0e-15
Match length
                  125
% identity
                  PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi 706853 (U04336)
NCBI Description
                  22 kDa component of photosystem II [Lycopersicon
                  esculentum]
Seq. No.
                  401826
Seq. ID
                  LIB3431-047-P1-K1-B12
```

```
NCBI GI
                  g132105
BLAST score
                  444
E value
                  4.0e-44
                  104
Match length
% identity
                  84
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  401827
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-B2
                  BLASTN
Method
NCBI GI
                  q1732362
BLAST score
                  35
                  4.0e-10
E value
                  43
Match length
                  95
% identity
NCBI Description
                  Malus domestica pAFD103 mRNA, partial cds
Seq. No.
                  401828
                  LIB3431-047-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4808833
BLAST score
                  311
                  7.0e-29
E value
                  63
Match length
% identity
                  (AF117125) endoplasmic reticulum-type calcium-transporting
NCBI Description
                  ATPase 4 [Arabidopsis thaliana]
                  401829
Seq. No.
                  LIB3431-047-P1-K1-B4
Seq. ID
                  BLASTN
Method
                  g5670155
NCBI GI
BLAST score
                  42
E value
                  2.0e-14
                  87
Match length
% identity
                  Oryza sativa subsp. japonica BAC clone 34K24, complete
NCBI Description
                  sequence
Seq. No.
                  401830
                  LIB3431-047-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407281
                  641
BLAST score
                  4.0e-67
E value
Match length
                  121
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
```

subunit [Oryza sativa]

```
Seq. No.
                  401831
Seq. ID
                  LIB3431-047-P1-K1-B7
                  BLASTX
Method
NCBI GI
                  g671740
BLAST score
                  354
E value
                  1.0e-33
Match length
                  65
% identity
                  100
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
Seq. No.
                  401832
Seq. ID
                  LIB3431-047-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g5921799
BLAST score
                  314
                  4.0e-29
E value
Match length
                  87
% identity
                  PUTATIVE ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT,
NCBI Description
                  MITOCHONDRIAL PRECURSOR (ENDOPEPTIDASE CLP)
                  >gi 3559935 emb CAA06443 (AJ005253) ClpP protease [Mus
                  musculus] >gi 4454289 emb CAA09966 (AJ012249) ClpP
                  protease [Mus musculus]
                  401833
Seq. No.
                  LIB3431-047-P1-K1-B9
Seq. ID
Method
                  BLASTN
                  g3885887
NCBI GI
                  41
BLAST score
                  3.0e-14
E value
Match length
                  45
% identity
NCBI Description
                  Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
Seq. No.
                  401834
                  LIB3431-047-P1-K1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5714761
BLAST score
                  54
E value
                  2.0e-21
Match length
                  78
% identity
                  92
                  Oryza sativa subsp. indica serine/threonine protein
NCBI Description
                  phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete
                  cds
                  401835
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-C11
Method
                  BLÁSTX
NCBI GI
                  g3478700
BLAST score
                  152
E value
                  4.0e-10
Match length
                  41
% identity
                  66
```

```
NCBI Description (AF034387) AFT protein [Arabidopsis thaliana]
                  401836
Seq. No.
                  LIB3431-047-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2370312
BLAST score
                  302
                  1.0e-27
E value
Match length
                  97
% identity
                  (AJ000995) DnaJ-like protein [Medicago sativa]
NCBI Description
                  >gi 3202020 gb AAC19391.1 (AF069507) DnaJ-like protein
                  MsJ1 [Medicago sativa]
                  401837
Seq. No.
                  LIB3431-047-P1-K1-C3
Seq. ID
Method
                  BLASTX
                  q462195
NCBI GI
BLAST score
                  211
                  5.0e-17
E value
                  48
Match length
                  83
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi_100682_pir__S21636 GOS2 protein - rice
                  >gi 20238 emb CAA36190 (X51910) GOS2 [Oryza sativa]
                  >gi_3789950 (AF094774) translation initiation factor [Oryza
                  satīva]
                  401838
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  ·g3345477
BLAST score
                  351
E value
                  3.0e-33
                  117
Match length
                  62
% identity
                  (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                  401839
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-C5
Method
                  BLASTX
                  g1350986
NCBI GI
BLAST score
                  458
E value
                  1.0e-45
                  97
Match length
                  93
% identity
                  40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
NCBI Description
                  >gi 483431 dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]
                  401840
Seq. No.
                  LIB3431-047-P1-K1-C6
Seq. ID
                  BLASTX
Method
                  g131283
NCBI GI
                  394
BLAST score
                  1.0e-39
E value
Match length
                  95
```

% identity

Seq. ID

NCBI GI BLAST score

Method

```
NCBI Description PHOTOSYSTEM II 44 KD REACTION CENTER PROTEIN (P6 PROTEIN)
                  (CP43) >gi_72710_pir__F2RZ44 photosystem II chlorophyll
                  a-binding protein psbC - rice chloroplast
                  >gi_11965_emb_CAA34014_ (X15901) PSII 43kDa protein [Oryza
                  sativa]
                  401841
Seq. No.
                  LIB3431-047-P1-K1-C7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g6103440
                  141
BLAST score
E value
                  2.0e-73
                  190
Match length
% identity
NCBI Description
                  Oryza sativa metallothionein-like protein (ML2) mRNA,
                  complete cds
Seq. No.
                  401842
Seq. ID
                  LIB3431-047-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  q3377792
BLAST score
                  106
E value
                  7.0e-53
Match length
                  106
                  100
% identity
                  Oryza sativa ribulose-1,5-bisphosphate
NCBI Description
                  carboxylase/oxygenase activase (rca) mRNA, complete cds
Seq. No.
                  401843
Seq. ID
                  LIB3431-047-P1-K1-D10
                  BLASTX
Method
NCBI GI
                  q534982
BLAST score
                  156
                  2.0e-19
E value
Match length
                  73
% identity
                  (X75898) phosphoglucomutase [Spinacia oleracea]
NCBI Description
                  401844
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q320618
BLAST score
                  465
                  1.0e-46
E value
                  110
Match length
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  401845
```

. .

LIB3431-047-P1-K1-D2

BLASTN g20181

```
E value
                  0.0e+00
Match length
                  369
                  98
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
Seq. No.
                  401846
                  LIB3431-047-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  532
                  2.0e-54
E value
Match length
                  122
                  83
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  401847
Seq. No.
                  LIB3431-047-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g534982
BLAST score
                  264
E value
                  5.0e-37
                  126
Match length
% identity
                  (X75898) phosphoglucomutase [Spinacia oleracea]
NCBI Description
                  401848
Seq. No.
                  LIB3431-047-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q729478
                  476
BLAST score
                  7.0e-48
E value
                  102
Match length
% identity
                  FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                  >gi 442481 dbj BAA04616 (D17790) ferredoxin-NADP+
                  reductase [Oryza sativa] >gi 6069649 dbj BAA85425.1
                  (AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to
                  a region of the predicted gene.; similar to
                  ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
                  401849
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  349
                  4.0e-33
E value
Match length
                  86
% identity
                  84
```

```
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   401850
                   LIB3431-047-P1-K1-E10
Seq. ID
                   BLASTX
Method
                   q3913018
NCBI GI
BLAST score
                   876
                   1.0e-94
E value
Match length
                   171
                   98
% identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi 218155 dbj_BAA02730_ (D13513) chloroplastic
                   aldolase [Oryza sativa]
Seq. No.
                   401851
                   LIB3431-047-P1-K1-E11
Seq. ID
                   BLASTX
Method
                   q6063542
NCBI GI
                   768
BLAST score
                   5.0e-82
E value
                   151
Match length
% identity
                   (APO00615) EST C74302(E30840) corresponds to a region of
NCBI Description
                   the predicted gene.; similar to glyceraldehyde-3-phosphate
                   dehydrogenase. (M64118) [Oryza sativa]
                   401852
Seq. No.
                   LIB3431-047-P1-K1-E12
Seq. ID
                   BLASTX
Method
                   q1617197
NCBI GI
BLAST score
                   304
                   1.0e-27
E value
                   76
Match length
% identity
                   (Z72488) CP12 [Nicotiana tabacum]
NCBI Description
                   401853
Seq. No.
Seq. ID
                   LIB3431-047-P1-K1-E2
                   BLASTN
Method
                   a6103440
NCBI GI
                    268
BLAST score
                   1.0e-149
E value
                    278
Match length
% identity
                   Oryza sativa metallothionein-like protein (ML2) mRNA,
NCBI Description
                    complete cds
                    401854
Seq. No.
Seq. ID
                    LIB3431-047-P1-K1-E3
                    BLASTN
Method
                    q6015437
NCBI GI
                    36
BLAST score
```

6.0e-11

E value

NCBI Description

```
Match length
                  36
                  100
% identity
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
                   401855
Seq. No.
                  LIB3431-047-P1-K1-E4
Seq. ID
Method
                  BLASTX
                  g2894534
NCBI GI
BLAST score
                   625
                   2.0e-65
E value
                   121
Match length
% identity
                   98
                   (AJ224327) aquaporin [Oryza sativa]
NCBI Description
                   401856
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-E6
Method
                  BLASTX
NCBI GI
                   q3288821
BLAST score
                   509
                   1.0e-51
E value
Match length
                   135
% identity
                   (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                   transaminase [Arabidopsis thaliana]
                   >gi 4733989 gb AAD28669.1 AC007209 5 (AC007209)
                   alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
                   401857
Seq. No.
Seq. ID
                   LIB3431-047-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   q4887131
                   432
BLAST score
                   7.0e-43
E value
                   101
Match length
% identity
                   77
                   (AF134732) 60S ribosomal protein L1 [Prunus armeniaca]
NCBI Description
                   401858
Seq. No.
                   LIB3431-047-P1-K1-E9
Seq. ID
Method
                   BLASTX
                   g1653089
NCBI GI
BLAST score
                   306
E value
                   7.0e-28
                   127
Match length
% identity
                   (D90911) hypothetical protein [Synechocystis sp.]
NCBI Description
                   401859
Seq. No.
Seq. ID
                   LIB3431-047-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g5541681
                   225
BLAST score
                   1.0e-18
E value
Match length
                   91
                   55
% identity
```

(AL096859) putative protein [Arabidopsis thaliana]

```
401860
Seq. No.
                   LIB3431-047-P1-K1-F2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3915131
BLAST score
                   242
                   9.0e-21
E value
Match length
                   48
% identity
                   100
                   THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1)
NCBI Description
                   >qi 426442 dbj BAA04864 (D21836) thioredoxin h [Oryza
                   satīva] >gī 454882 dbj BAA05546 (D26547) rice thioredoxin
                   h [Oryza sativa] > \overline{gi}_1 \overline{1930072} (U\overline{92541}) thioredoxin h [Oryza
                   sativa]
                   401861
Seq. No.
                   LIB3431-047-P1-K1-F4
Seq. ID
Method
                   BLASTN
                   q1103627
NCBI GI
BLAST score
                   57
                   3.0e-23
E value
                   85
Match length
                   92
% identity
                   Z.mays Fer1 gene
NCBI Description
Seq. No.
                   401862
Seq. ID
                   LIB3431-047-P1-K1-F5
Method
                   BLASTX
                   g3309269
NCBI GI
BLAST score
                   448
E value
                   2.0e-44
                   107
Match length
% identity
                   (AF074940) ferric leghemoglobin reductase-2 precursor
NCBI Description
                   [Glycine max]
Seq. No.
                   401863
Seq. ID
                   LIB3431-047-P1-K1-F6
Method
                   BLASTX
                   g4587615
NCBI GI
BLAST score
                   453
E value
                   1.0e-49
Match length
                   135
% identity
                   71
                   (AC006951) putative acyl-CoA synthetase [Arabidopsis
NCBI Description
                   thaliana] >gi 4689469 gb AAD27905.1 AC007213_3 (AC007213)
                   putative acyl-CoA synthetase [Arabidopsis thaliana]
                   401864
Seq. No.
Seq. ID
                   LIB3431-047-P1-K1-F8
                   BLASTX
Method
NCBI GI
                   g3789954
                   199
BLAST score
                   6.0e-16
E value
Match length
                   46
                   83
% identity
NCBI Description
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
```

sativa]

```
401865
Seq. No.
                  LIB3431-047-P1-K1-F9
Seq. ID
Method
                  BLASTX
                  q115787
NCBI GI
                  504
BLAST score
                  4.0e-51
E value
                  118
Match length
                  86
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -2\overline{8} to 235)
                  [Oryza sativa]
                  401866
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-G11
                  BLASTX
Method
NCBI GI
                  q132105
BLAST score
                  470
                  3.0e-47
E value
                  107
Match length
                  85
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  401867
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-G12
Method
                  BLASTX
                  g3345477
NCBI GI
BLAST score
                  315
                  5.0e-29
E value
Match length
                  109
% identity
                  59
                  (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
Seq. No.
                  401868
Seq. ID
                  LIB3431-047-P1-K1-G2
                  BLASTX
Method
                  g115771
NCBI GI
BLAST score
                  864
                  3.0e-93
E value
                  170
Match length
                  95
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-1) (LHCP) >gi 82682_pir__S04453 chlorophyll a/b-binding
                  protein precursor - maize >gi_22224_emb CAA32900_ (X14794)
                  chlorophyll a/b-binding preprotein (AA 1 - 262) [Zea mays]
```

Seq. No.

```
LIB3431-047-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q4204276
BLAST score
                  421
                  1.0e-41
E value
Match length
                  107
                  75
% identity
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  401870 -
Seq. No.
                  LIB3431-047-P1-K1-G5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2570511
                  506
BLAST score
                  2.0e-51
E value
                  105
Match length
                  99
% identity
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  401871
                  LIB3431-047-P1-K1-G6
Seq. ID
Method
                  BLASTN
                  g6015437
NCBI GI
BLAST score
                  35
E value
                  2.0e-10
Match length
                  35
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  401872
                  LIB3431-047-P1-K1-G7
Seq. ID
Method
                  BLASTX
                  g3126854
NCBI GI
BLAST score
                  478
                  3.0e-48
E value
Match length
                  90
                  99
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   401873
Seq. No.
                  LIB3431-047-P1-K1-G8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3126854
BLAST score
                  306
                  7.0e-48
E value
Match length
                  119
                  85
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   401874
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g224293
BLAST score
                   406
                  1.0e-39
E value
Match length
                  82
```

% identity

Match length

```
NCBI Description histone H4 [Triticum aestivum]
Seq. No.
                  401875
                  LIB3431-047-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2739375
BLAST score
                  161
E value
                  5.0e-11
                  93
Match length
                  - 42
% identity
NCBI Description (AC002505) unknown protein [Arabidopsis thaliana]
Seq. No.
                  401876
                  LIB3431-047-P1-K1-H11
Seq. ID
                  BLASTN
Method
NCBI GI
                  q536895
BLAST score
                  139
                  4.0e-72
E value
Match length
                  195
% identity
                  93
NCBI Description Wheat mRNA for protein H2A, complete cds, clone wcH2A-10
                  401877
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  443
                  4.0e-45
E value
Match length
                  123
% identity
                  75
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxy\overline{l}ase (\overline{EC} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401878
Seq. ID
                  LIB3431-047-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g5679336 -
BLAST score
                  193
                  1.0e-14
E value
Match length
                  78
% identity
NCBI Description (AF171223) putative zinc finger protein [Oryza sativa]
                  401879
Seq. No.
Seq. ID
                  LIB3431-047-P1-K1-H3
                  BLASTX
Method
NCBI GI
                  g4884370
BLAST score
                  147
E value
                  2.0e-09
```

Seq. ID

```
% identity
                  41
                  (AL050157) hypothetical protein [Homo sapiens]
NCBI Description
                  401880
Seq. No.
                  LIB3431-047-P1-K1-H4
Seq. ID
                  BLASTX
Method
                  g4079798
NCBI GI
                  398
BLAST score
                  9.0e-39
E value
                  108
Match length
                  73
% identity
                  (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
                  401881
Seq. No.
                  LIB3431-047-P1-K1-H5
Seq. ID
                  BLASTX
Method
                  q3292829
NCBI GI
                  185
BLAST score
                  5.0e-14
E value
Match length
                  86
% identity
                   44
                  (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
                   401882
Seq. No.
                   LIB3431-047-P1-K1-H6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1419090
BLAST score
                   484
                   7.0e-49
E value
Match length
                   118
% identity
                   (X94968) 37kDa chloroplast inner envelope membrane
NCBI Description
                   polypeptide precursor [Nicotiana tabacum]
Seq. No.
                   401883
                   LIB3431-047-P1-K1-H7
Seq. ID
                   BLASTX
Method
                   g3953471
NCBI GI
BLAST score
                   276
                   1.0e-24
E value
Match length
                   75
% identity
                   (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   401884
                   LIB3431-047-P1-K1-H8
Seq. ID
                   BLASTX
Method
                   g629858
NCBI GI
BLAST score
                   587
                   7.0e-61
E value
                   124
Match length
                   90
% identity
                   protein kinase C inhibitor - maize
NCBI Description
                   401885
Seq. No.
```

LIB3431-047-P1-K1-H9

```
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  37
                  4.0e-11
E value
                  37
Match length
                  100
% identity
NCBI Description
                  Human butyrophilin (BTF5) mRNA, complete cds
Seq. No.
                  401886
                  LIB3431-047-P1-N1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5912298
BLAST score
                  156
                  4.0e-82
E value
Match length
                  170
                  98
% identity
NCBI Description
                  Oryza sativa mRNA for gigantea homologue, partial
Seq. No.
                  401887
                  LIB3431-047-P1-N1-A4
Seq. ID
Method
                  BLASTX
                  g132105
NCBI GI
                  354
BLAST score
E value
                  2.0e-33
Match length
                  65
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  401888
Seq. No.
                  LIB3431-047-P1-N1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g120661
BLAST score
                  268
                  2.0e-23
E value
Match length
                  52
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
NCBI Description
                  PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
                  dehydrogenase A-subunit precursor [Nicotiana tabacum]
                  401889
Seq. No.
                  LIB3431-047-P1-N1-A8
Seq. ID
Method
                  BLASTX
                  g2072555
NCBI GI
BLAST score
                  226
                  2.0e-18
E value
Match length
                  44
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
```

Match length

```
>gi 6103441_gb_AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  401890
                  LIB3431-047-P1-N1-A9
Seq. ID
                  BLASTN
Method
                  q20369
NCBI GI
BLAST score
                  291
                  1.0e-163
E value
                  326
Match length
% identity
                  98
                  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
NCBI Description
                  synthetase (EC 6.3.1.2) (clone lambda-GS31)
                  >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of
                  chloroplast localising glutamine synthetase
                  401891
Seq. No.
                  LIB3431-047-P1-N1-B1
Seq. ID
Method
                  BLASTN
                  q2072554
NCBI GI
                  386
BLAST score
                  0.0e+00
E value
                  408
Match length
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  cds
                  401892
Seq. No.
                  LIB3431-047-P1-N1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q6103011
BLAST score
                  451
                  7.0e-45
E value
                  97
Match length
                  51
% identity
                  (X84225) precursor of photosystem II subunit (22KDa)
NCBI Description
                  [Nicotiana tabacum]
                  401893
Seq. No.
Seq. ID
                  LIB3431-047-P1-N1-B12
Method
                  BLASTN
                  g218207
NCBI GI
BLAST score
                  181
                  3.0e-97
E value
                  217
Match length
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
                  401894
Seq. No.
Seq. ID
                  LIB3431-047-P1-N1-B3
                  BLASTN
Method
NCBI GI
                  g2160711.
BLAST score
                  320
                  1.0e-180
E value
                  356
```

% identity

```
% identity
                  98
NCBI Description Oryza sativa Ca2+-ATPase gene, complete cds
                   401895
                  LIB3431-047-P1-N1-B5
Seq. ID
                  BLASTX
Method
                   q671740
NCBI GI
                   243
BLAST score
                   2.0e-20
E value
Match length
                   47
                   100
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
Seq. No.
                   401896
                   LIB3431-047-P1-N1-B7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g218209
                   59
BLAST score
                   2.0e-24
E value
Match length
                   75
                   95
% identity
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS2106
                   401897
Seq. No.
                   LIB3431-047-P1-N1-B9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3885887
BLAST score
                   298
                   1.0e-167
E value
                   349
Match length
                   96
% identity
                   Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                   complete cds
                   401898
Seq. No.
                   LIB3431-047-P1-N1-C10
Seq. ID
Method
                   BLASTN
                   q5714761.
NCBI GI
BLAST score
                   54
                   2.0e-21
E value
                   78
Match length
                   92
% identity
                   Oryza sativa subsp. indica serine/threonine protein
NCBI Description
                   phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete
                   cds
                   401899
Seq. No.
Seq. ID
                   LIB3431-047-P1-N1-C11
                   BLASTN
Method
                   q3819352
NCBI GI
BLAST score
                   58
E value
                   8.0e-24
Match length
                   82
```

```
NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0813.rev
                  401900
Seq. No.
                  LIB3431-047-P1-N1-C2
Seq. ID
                  BLASTN
Method
                  q20369
NCBI GI
BLAST score
                  122
                  5.0e-62
E value
                  270
Match length
% identity
                  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
NCBI Description
                  synthetase (EC 6.3.1.2) (clone lambda-GS31)
                  >gi 2170909 dbj E02681 E02681 cDNA encoding precursor of
                  chloroplast localising glutamine synthetase
                  401901
Seq. No.
                  LIB3431-047-P1-N1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3334346
BLAST score
                  232
                  3.0e-19
E value
                  47
Match length
                  91
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG
NCBI Description
                  >gi_2852445_dbj_BAA24697_ (AB003378) SUI1 homolog [Salix
                  bakko]
                  401902
Seq. No.
Seq. ID
                  LIB3431-047-P1-N1-C4
Method
                  BLASTN
NCBI GI
                  q3345476
                  250
BLAST score
                  1.0e-138
E value
                  304
Match length
% identity
                  95
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds
                  401903
Seq. No.
                  LIB3431-047-P1-N1-C5
Seq. ID
Method
                  BLASTX
                  g1350986
NCBI GI
BLAST score
                  412
E value
                  2.0e-40
Match length
                  83
% identity
                  100
                  40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
NCBI Description
                  >gi 483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]
                  401904
Seq. No.
Seq. ID
                  LIB3431-047-P1-N1-C6
                  BLASTN
Method
NCBI GI
                  g11957
BLAST score
                  107
                  4.0e-53
E value
                  301
Match length
% identity
                  83
NCBI Description Rice complete chloroplast genome
```

```
401905
Seq. No.
Seq. ID
                   LIB3431-047-P1-N1-C7
Method
                   BLASTX
                   g2072555
NCBI GI
                   230
BLAST score
                   6.0e-19
E value
                   44
Match length
                   98
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                 401906
Seq. No.
Seq. ID
                   LIB3431-047-P1-N1-C8
Method
                   BLASTX
NCBI GI
                   q167097
BLAST score
                   189
                   6.0e-26
E value
Match length
                   74
                   82
% identity
                   (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                   [Hordeum vulgare]
Seq. No.
                   401907
Seq. ID
                   LIB3431-047-P1-N1-D11
Method
                   BLASTN
NCBI GI
                   q2570514
BLAST score
                   312
E value
                   1.0e-175
Match length
                   370
                   96
% identity
                  Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
NCBI Description
Seq. No.
                   401908
                   LIB3431-047-P1-N1-D2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g20181 .
BLAST score
                   142
E value
                   5.0e-74
Match length
                   156
% identity
                   97
                   Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                   a/b-binding protein
Seq. No.
                   401909
Seq. ID
                   LIB3431-047-P1-N1-D3
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   360
E value
                   4.0e-34
Match length
                   67
                   99
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4.\overline{1}.1.39) small chain
```

precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

```
401910
Seq. No.
Sea. ID
                  LIB3431-047-P1-N1-D4
                  BLASTX
Method
NCBI GI
                  g534982
BLAST score
                  214
                  2.0e-32
E value
Match length
                  106
% identity
                  (X75898) phosphoglucomutase [Spinacia oleracea]
NCBI Description
                  401911
Seq. No.
                  LIB3431-047-P1-N1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  a114622
BLAST score
                  249
                  4.0e-21
E value
                  53
Match length
                  92
% identity
```

NCBI Description ATP SYNTHASE B CHAIN (SUBUNIT I) >gi_67929_pir__LWRZ1
H+-transporting ATP synthase (EC 3.6.1.34) chain I - rice
chloroplast >gi_669080_emb_CAA33992_ (X15901) ATPase I
subunit [Oryza sativa] >gi_226695_prf__1603356W ATPase I
[Oryza sativa]

Seq. No. 401912

Seq. ID LIB3431-047-P1-N1-D7

Method BLASTX
NCBI GI 9729478
BLAST score 398
E value 1.0e-38
Match length 81
% identity 90

NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)

>gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_

(AP000616) ESTs AU078647(E1557), C72400(E1557) correspond to

a region of the predicted gene.; similar to

ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No. 401913

Seq. ID LIB3431-047-P1-N1-D8

Method BLASTX
NCBI GI g5911312
BLAST score 466
E value 1.0e-46
Match length 105
% identity 80

NCBI Description (AF026167) ankyrin repeat protein EMB506 [Arabidopsis

thaliana]

Seq. No. 401914

NCBI GI

```
LIB3431-047-P1-N1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q218154
BLAST score
                  58
E value
                  8.0e-24
Match length
                  114
                  99
% identity
                  Oryza sativa gene for cytoplasmic aldolase, complete cds,
NCBI Description
                  clone:Aldp
                  401915
Seq. No.
                  LIB3431-047-P1-N1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g6063530
                  337
BLAST score
                  0.0e + 00
E value
                  381
Match length
                  97
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
                  401916
Seq. No.
                  LIB3431-047-P1-N1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617197
                  224
BLAST score
                  3.0e-18
E value
                  47
Match length
% identity
                  87
NCBI Description
                  (Z72488) CP12 [Nicotiana tabacum]
                  401917
Seq. No.
                  LIB3431-047-P1-N1-E2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2072554
BLAST score
                  270
                   1.0e-150
E value
Match length
                  294
                  99
% identity
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                  401918
Seq. No.
                  LIB3431-047-P1-N1-E3
Seq. ID
Method
                  BLASTN
                  g3126853
NCBI GI
BLAST score
                  168
                   2.0e-89
E value
Match length
                  222
                  98
% identity
                  Oryza sativa chlorophyll a/b binding protein (RCABP89)
NCBI Description
                  mRNA, nuclear gene encoding chloroplast protein, complete
                  cds
                   401919
Seq. No.
                  LIB3431-047-P1-N1-E4
Seq. ID
Method
                  BLASTX
                  q2696804
```

Match length

```
306
BLAST score
                  6.0e-28
E value
                  57
Match length
                  98
% identity
NCBI Description
                  (AB009665) water channel protein [Oryza sativa]
                  401920
Seq. No.
                  LIB3431-047-P1-N1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2754849
                  250
BLAST score
                  3.0e-21
E value
                  57
Match length
                  84
% identity
                  (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                  [Fritillaria agrestis]
Seq. No.
                  401921
                  LIB3431-047-P1-N1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5541681
BLAST score
                  213
E value
                  5.0e-17
                  93
Match length
% identity
                  55
                  (AL096859) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  401922
Seq. ID
                  LIB3431-047-P1-N1-F11
Method
                  BLASTX
NCBI GI
                  q693920
BLAST score
                  347
E value
                  1.0e-32
Match length
                  66
% identity
                  100
NCBI Description
                  (U21113) chlorophyll a/b binding protein [Solanum
                  tuberosum]
Seq. No.
                  401923
Seq. ID
                  LIB3431-047-P1-N1-F12
Method
                  BLASTX
NCBI GI
                  q517500
BLAST score
                  389
E value
                  1.0e-37
Match length
                  93
% identity
NCBI Description
                  (M87435) precursor of the oxygen evolving complex 17 kDa
                  protein [Zea mays] >qi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
Seq. No.
                  401924
                  LIB3431-047-P1-N1-F2
Seq. ID
                  BLASTN
Method
NCBI GI
                  q454881
BLAST score
                  213
                  1.0e-116
E value
```

Method

BLASTN

```
% identity
                  96
NCBI Description Rice gene for thioredoxin h, complete cds
                  401925
Seq. No.
                  LIB3431-047-P1-N1-F4
Seq. ID
Method
                  BLASTN
                  g455510
NCBI GI
BLAST score
                  132
                  7.0e-68
E value
Match length
                  136
                  99
% identity
NCBI Description Rice mRNA for ferritin, partial sequence
                  401926
Seq. No.
                  LIB3431-047-P1-N1-F6
Seq. ID
Method
                  BLASTX
                  q4587615
NCBI GI
BLAST score
                  282
                  5.0e-25
E value
                  80
Match length
% identity
                  66
                  (AC006951) putative acyl-CoA synthetase [Arabidopsis
NCBI Description
                  thaliana] >gi 4689469 gb AAD27905.1_AC007213_3 (AC007213)
                  putative acyl-CoA synthetase [Arabidopsis thaliana]
Seq. No.
                  401927
                  LIB3431-047-P1-N1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3789954
BLAST score
                  332
E value
                  6.0e - 31
Match length
                  63
% identity
NCBI Description
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
Seq. No.
                  401928
                  LIB3431-047-P1-N1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  393
E value
                  5.0e-38
Match length
                  73
                  99
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >qi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401929
Seq. ID
                  LIB3431-047-P1-N1-G12
```

NCBI GI

g122106

```
NCBI GI
                  g3345476
BLAST score
                  244
                  1.0e-135
E value
                  307
Match length
                  95
% identity
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds
                  401930
Seq. No.
                  LIB3431-047-P1-N1-G2
Seq. ID
                  BLASTN
Method
                  g20181
NCBI GI
                  56
BLAST score
                  7.0e-23
E value
Match length
                  67
                  96
% identity
NCBI Description
                  Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
                  401931
Seq. No.
                  LIB3431-047-P1-N1-G4
Seq. ID
                  BLASTX
Method
                  g4204276
NCBI GI
BLAST score
                  226
                  2.0e-18
E value
                  73
Match length
% identity
                  (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  401932
                  LIB3431-047-P1-N1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4689380
BLAST score
                  260
E value
                  9.0e-23
                  55
Match length
% identity
                  (AF139465) LHCII type III chlorophyll a/b binding protein
NCBI Description
                  [Vigna radiata]
Seq. No.
                  401933
Seq. ID
                  LIB3431-047-P1-N1-G7
Method
                  BLASTX
NCBI GI
                  q115802
BLAST score
                  187
E value
                  3.0e-14
Match length
                  36
                  97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll
                  a/b-binding protein (cab-36) - common tobacco
                  >qi 19827 emb CAA41188 (X58230) chlorophyll a/b binding
                  protein [Nicotiana tabacum]
Seq. No.
                  401934
Seq. ID
                  LIB3431-047-P1-N1-G9
Method
                  BLASTX
```

```
375
BLAST score
                   5.0e-36
E value
                   77
Match length
                   97
% identity
                   HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize
NCBI Description
                   >qi 81642 pir S06904 histone H4 - Arabidopsis thaliana
                   >gi_21190\overline{2}8_p\overline{ir}_560475 histone H4 - garden pea
                   >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum
                   aestivum] >gi 166740 (M17132) histone H4 [Arabidopsis
                   thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis
                   thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays]
                   >gi_168501 (M\overline{1}3370) histone H4 [Zea mays] >gi_168503
                   (M1\overline{3}377) histone H4 [Zea mays] >gi_498898 (U10042) histone
                   H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_
                   (Z79638) histone H4 homologue [Sesbania rostrata]
                   >gi 3927823 (AC005727) histone H4 [Arabidopsis thaliana]
                   >gi 4580385 gb AAD24364.1_AC007184_4 (AC007184) histone H4
                   [Arabidopsis thaliana] >gi 6009915 dbj BAA85120.1
                   (AB018245) histone H4-like protein [Solanum melongena]
                   >qi 225838 prf 1314298A histone H4 [Arabidopsis thaliana]
Seq. No.
                   401935
Seq. ID
                   LIB3431-047-P1-N1-H12
Method
                   BLASTX
NCBI GI
                   q1419090
BLAST score
                   320
                   2.0e-29
E value
Match length
                   85
% identity
                   72
                   (X94968) 37kDa chloroplast inner envelope membrane
NCBI Description
                   polypeptide precursor [Nicotiana tabacum]
Seq. No.
                   401936
Seq. ID
                   LIB3431-047-P1-N1-H4
Method
                   BLASTN
                   g4079797
NCBI GI
BLAST score
                   51
E value
                   1.0e-19
Match length
                   106
% identity
                   Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
NCBI Description
                   complete cds .
Seq. No.
                   401937
Seq. ID
                   LIB3431-048-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   149
E value
                   4.0e-10
Match length
                   36
% identity
                   83
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4\overline{.1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
```

NCBI Description

```
401938
Seq. No.
                  LIB3431-048-P1-K1-B1 .
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3252813
                  219
BLAST score
                  9.0e-18
E value
                  92
Match length
% identity
                  43
                   (AC004705) vacuolar sorting receptor-like protein
NCBI Description
                   [Arabidopsis thaliana] >gi 3810586 (AC005398) vacuolar
                  sorting receptor-like protein [Arabidopsis thaliana]
Seq. No.
                  401939
Seq. ID
                  LIB3431-048-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q4324967
BLAST score
                  195
E value
                  2.0e-15
Match length
                  38
% identity
NCBI Description
                  (AF114796) ADP-ribosylation factor [Glycine max]
                  401940
Seq. No.
Seq. ID
                  LIB3431-048-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q4689390
BLAST score
                  260
                   4.0e-23
E value
Match length
                  55
% identity
NCBI Description
                   (AF139470) chlorophyll a/b-binding protein CP24 precursor
                   [Vigna radiata]
                  401941
Seq. No.
                  LIB3431-048-P1-K1-B2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4959460
BLAST score
                  35
                  4.0e-10
E value
                  35
Match length
                  100
% identity
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
                  401942
Seq. No.
                  LIB3431-048-P1-K1-B3
Seq. ID
                  BLASTN
Method
NCBI GI
                  q18957
BLAST score
                  39
                  9.0e-13
E value
Match length
                  55
% identity
                  93
```

carboxylase S [Oryza sativa]

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

Hordeum vulgare gene for CP29 precursor for core

chlorophyll a/b binding (CAB) protein of photosystem II

Match length

```
(PSII)
                   401943
 Seq. No.
                   LIB3431-048-P1-K1-B4
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g130274
                   277
 BLAST score
                   5.0e-25
· E value
                   56
 Match length
                   95
 % identity
 NCBI Description
                   PLASTOCYANIN >gi 82500 pir S06105 plastocyanin - rice
                   401944
 Seq. No.
                   LIB3431-048-P1-K1-B5
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   q20369
                   143
 BLAST score
                   7.0e-75
 E value
                   158
 Match length
                   97
 % identity
                   Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
 NCBI Description
                   synthetase (EC 6.3.1.2) (clone lambda-GS31)
                   >gi 2170909 dbj E02681 E02681 cDNA encoding precursor of
                   chloroplast localising glutamine synthetase
 Seq. No.
                   401945
 Seq. ID
                   LIB3431-048-P1-K1-B7
 Method
                   BLASTX
 NCBI GI
                   g3789954
 BLAST score
                   518
 E value
                   7.0e-53
                   97
 Match length
 % identity
                   99
 NCBI Description
                    (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                   sativa]
 Seq. No.
                   401946
                   LIB3431-048-P1-K1-B8
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g115772
 BLAST score
                   174
 E value
                   5.0e-13
Match length
                   40
 % identity
 NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
                   CAB-1) (LHCP) >qi 82460 pir S03705 chlorophyll a/b-binding
                   protein 1R precursor - rice >gi 20178 emb CAA32108
                    (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                    [Oryza sativa]
 Seq. No.
                   401947
 Seq. ID
                   LIB3431-048-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   q2894534
BLAST score
                   314
 E value
                   2.0e-29
```

```
% identity
                   95
NCBI Description
                   (AJ224327) aquaporin [Oryza sativa]
                   401948
Seq. No.
                  LIB3431-048-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1917019
BLAST score
                  252
                   4.0e-22
E value
                  51
Match length
% identity
                  92
                  (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
NCBI Description
                   401949
Seq. No.
Seq. ID
                  LIB3431-048-P1-K1-C2
Method
                  BLASTX
                  g2583133
NCBI GI
BLAST score
                  230
E value
                   5.0e-19
Match length
                  127
% identity
                  38
                   (AC002387) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   401950
Seq. ID
                  LIB3431-048-P1-K1-C4
Method
                  BLASTX
NCBI GI
                   g4678261
BLAST score
                  330
E value
                   3.0e-31
Match length
                  66
% identity
                  91
NCBI Description
                   (AL049657) putative proteasome regulatory subunit
                   [Arabidopsis thaliana]
                  401951
Seq. No.
Seq. ID
                  LIB3431-048-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  g1245938
BLAST score
                  35
E value
                  7.0e-11
Match length
                  35
% identity
NCBI Description
                  rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
                  heart atrium, mRNA, 2998 nt]
Seq. No.
                  401952
Seq. ID
                  LIB3431-048-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g20340
BLAST score
                  42
E value
                  9.0e-15
                  94
Match length
% identity
                  86
NCBI Description
                  Rice rbcS gene for ribulose 1,5-bisphosphate
                  carboxylase/oxygenase small subunit (EC 4.1.1.39)
```

Seq. No.

NCBI GI

```
Seq. ID
                  LIB3431-048-P1-K1-D10
                  BLASTX
Method
                  g1181331
NCBI GI
BLAST score
                  213
                  1.0e-17
E value
                  57
Match length
                  77
% identity
                   (X77569) calnexin [Zea mays]
NCBI Description
                  401954
Seq. No.
                  LIB3431-048-P1-K1-D2
Seq. ID
Method
                  BLASTX
                  q6014904
NCBI GI
                  145
BLAST score
E value
                   3.0e-09
Match length
                  54
                  52
% identity
                  DAG PROTEIN, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi_1200205_emb_CAA65064_ (X95753) DAG [Antirrhinum majus]
Seq. No.
                   401955
                  LIB3431-048-P1-K1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3869067
BLAST score
                  35
                   2.0e-10
E value
Match length
                   47
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCK7, complete sequence
                  401956
Seq. No.
Seq. ID
                   LIB3431-048-P1-K1-D5
Method
                   BLASTN
NCBI GI
                   g5257255
BLAST score
                   157
                   4.0e-83
E value
Match length
                   178
                   98
% identity
                  Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
NCBI Description
Seq. No.
                   401957
                   LIB3431-048-P1-K1-D6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q5734713
BLAST score
                   152
                   2.0e-10
E value
Match length
                   37
                   86
% identity
                   (AC008075) Is a member of PF 01169 Uncharacterized
NCBI Description
                   (transmembrane domain) protein family. [Arabidopsis
                   thaliana]
Seq. No.
                   401958
Seq. ID
                   LIB3431-048-P1-K1-D8
                   BLASTX
Method
```

g1729971

```
BLAST score
                  258
                  7.0e-23
E value
Match length
                  54
% identity
                  94
NCBI Description
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                  rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                  sativa]
                  401959
Seq. No.
                  LIB3431-048-P1-K1-E1
Seq. ID
Method
                  BLASTX
                  q5630087
NCBI GI
BLAST score
                  200
                  1.0e-15
E value
Match length
                  111
                  41
% identity
NCBI Description
                   (AC004876) similar to predicted proteins AAB54240
                   (PID:g2088822) and S67138 (PID:g2132925) [Homo sapiens]
                  401960
Seq. No.
                  LIB3431-048-P1-K1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g304219
BLAST score
                  80
E value
                  4.0e-37
                  199
Match length
% identity
NCBI Description
                  Hordeum vulgare chloroplast photosystem I PSK-I subunit
                  mRNA, complete cds
Seq. No.
                  401961
                  LIB3431-048-P1-K1-E2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4959460
BLAST score
                  38
E value
                  3.0e-12
Match length
                  38
% identity
                  100
                  Zea mays RACB small GTP binding protein mRNA, complete cds
NCBI Description
Seq. No.
                  401962
Seq. ID
                  LIB3431-048-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  222
E value
                  1.0e-18
Match length
                  63
% identity
                  73
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
```

sativa] >gi 226375 prf 1508256A ribulose bisphosphate

Seq. ID

carboxylase S [Oryza sativa]

```
Seq. No.
                   401963
                  LIB3431-048-P1-K1-E5
Seq. ID
Method
                  BLASTX
                   g4105131
NCBI GI
BLAST score
                   139
                   6.0e-09
E value
Match length
                   31
% identity
                   94
                 (AF043539) ClpC protease [Spinacia oleracea]
NCBI Description
Seq. No.
                   401964
                   LIB3431-048-P1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5733874
BLAST score
                   351
                   2.0e-33
E value
Match length
                   112
% identity
                  (AC007932) F11A17.8 [Arabidopsis thaliana]
NCBI Description
                   401965
Seq. No.
Seq. ID
                   LIB3431-048-P1-K1-F10
Method
                   BLASTX
NCBI-GI
                   q671740
BLAST score
                   315
                   1.0e-29
E value
Match length
                   68
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   401966
Seq. No.
Seq. ID
                   LIB3431-048-P1-K1-F4
                   BLASTN
Method
NCBI GI
                   q2306980 ·
BLAST score
                   99
                   1.0e-48
E value
Match length
                   112
                   97
% identity
NCBI Description
                  Oryza sativa photosystem I antenna protein (Lhca) mRNA,
                   complete cds
                   401967
Seq. No.
Seq. ID
                  LIB3431-048-P1-K1-F6
                  BLASTN
Method
                   g21843
NCBI GI
BLAST score
                   39
                   1.0e-12
E value
Match length
                   76
% identity
                  Wheat PsbO mRNA for 33kDa oxygen evolving protein of
NCBI Description
                  photosystem II
                   401968
Seq. No.
```

LIB3431-048-P1-K1-F7

```
BLASTX
Method
NCBI GI
                  g3126854
                  151
BLAST score
                  4.0e-10
E value
Match length
                  33
                  91
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  401969
Seq. No.
                  LIB3431-048-P1-K1-G10
Seq. ID
                  BLASTX
Method
                  g733454
NCBI GI
BLAST score
                  266
                  2.0e-23
E value
                  74
Match length
                  73
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
                  401970
Seq. No.
                  LIB3431-048-P1-K1-G12
Seq. ID
                  BLASTX
Method
                  q2501189
NCBI GI
BLAST score
                   444
                  2.0e-44
E value
                  90
Match length
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
                   401971
Seq. No.
                   LIB3431-048-P1-K1-G4
Seq. ID
Method
                   BLASTX
                   q671740
NCBI GI
BLAST score
                   416
                   6.0e-41
E value
                   75
Match length
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   401972
Seq. No.
                   LIB3431-048-P1-K1-G9
Seq. ID
Method
                   BLASTN
                   g218207
NCBI GI
                   104
BLAST score
E value
                   9.0e-52
                   112
Match length
                   98
% identity
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   pOSSS1139
                   401973
Seq. No.
                   LIB3431-048-P1-K1-H1
Seq. ID
```

```
BLASTX
Method
                  g320618
NCBI GI
BLAST score
                  275
                  8.0e-25
E value
Match length
                  51
                  96
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf __1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  401974
Seq. No.
                  LIB3431-048-P1-K1-H10
Seq. ID
                  BLASTX
Method
                  g3891918
NCBI GI
BLAST score
                  339
                  2.0e-32
E value
                  67
Match length
                  93
% identity
                  Ferredoxin:nadp+ Oxidoreductase (Ferredoxin Reductase)
NCBI Description
                  Mutant E3121
                  401975
Seq. No.
                  LIB3431-048-P1-K1-H2
Seq. ID
Method
                  BLASTX
                  q606817
NCBI GI
BLAST score
                  143
E value
                  2.0e-09
                  36
Match length
                  78
% identity
                   (U08404) carbonic anhydrase [Oryza sativa]
NCBI Description
                  >qi 5917783 gb AAD56038.1 AF182806 1 (AF182806) carbonic
                  anhydrase 3 [Oryza sativa]
Seq. No.
                  401976
                  LIB3431-048-P1-K1-H3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1235663
BLAST score
                  103
E value
                  4.0e-51
Match length
                  115
                  97
% identity
                  Oryza sativa clone pFDRSC61 novel calmodulin-like protein
NCBI Description
                  mRNA, complete cds
Seq. No.
                  401977
                  LIB3431-048-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063710
BLAST score
                  188
                  1.0e-14
E value
Match length
                  54
% identity
                   (AL022537) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

NCBI GI

g115813

```
Seq. ID
                  LIB3431-048-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g2244786
BLAST score
                  158
                  4.0e-11
E value
                  39
Match length
                  69
% identity
                  (Z97335) ribonucleoprotein like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  401979
                  LIB3431-048-P1-N1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  385
E value
                  4.0e-37
                  72
Match length
% identity
                  97
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  401980
                  LIB3431-048-P1-N1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115813
BLAST score
                  257
E value
                  4.0e-22
Match length
                  61
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                  401981
                  LIB3431-048-P1-N1-A2
Seq. ID
Method
                  BLASTX
NCBI GI -
                  g2499417
BLAST score
                  370
                  2.0e-35
E value
Match length
                  91
% identity
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
NCBI Description
                  >qi 1085826 pir S49248 H-protein - Flaveria anomala
                  >gi 547558 emb CAA85761_ (Z37524) H-protein [Flaveria
                  anomala]
Seq. No.
                  401982
                  LIB3431-048-P1-N1-A3
Seq. ID
Method
                  BLASTX
```

E value

2.0e-27

```
257
BLAST score
                  3.0e-22
E value
                  61
Match length
                  82
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi 19182 emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  401983
Seq. No.
                  LIB3431-048-P1-N1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1663724
                  357
BLAST score
                  9.0e - 34
E value
Match length
                  105
% identity
                  66
                  (U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
NCBI Description
Seq. No.
                  401984
                  LIB3431-048-P1-N1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  63
                  1.0e-26
E value
Match length
                  174
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  cds
Seq. No.
                  401985
Seq. ID
                  LIB3431-048-P1-N1-A8
Method
                  BLASTN
NCBI GI
                  q3789953
BLAST score
                  184
                   4.0e-99
E value
Match length
                  255
                  93
% identity
                  Oryza sativa chlorophyll a/b-binding protein precursor
NCBI Description
                   (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
Seq. No.
                   401986
Seq. ID
                  LIB3431-048-P1-N1-B11
                  BLASTX
Method
NCBI GI
                  q2293566
BLAST score
                  166
                   2.0e-11
E value
Match length
                  30
                  100
% identity
                  (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
NCBI Description
                   401987
Seq. No.
                  LIB3431-048-P1-N1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q481190
BLAST score
                   301
```

BLAST score

195



```
Match length
% identity
                   95
                  plastocyanin precursor - barley >gi 22705 emb CAA68696_
NCBI Description
                   (Y00704) plastocyanin precursor [Hordeum vulgare]
                   >gi 431920 emb CAA82201 (Z28347) plastocyanin [Hordeum
                   vulgare]
                   401988
Seq. No.
                   LIB3431-048-P1-N1-B5
Seq. ID
                   BLASTN
Method
NCBI GI
                   g20369
                   321
BLAST score
                   0.0e + 00
E value
                   355
Match length
                   98
% identity
                  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
NCBI Description
                   synthetase (EC 6.3.1.2) (clone lambda-GS31)
                   >gi_2170909_dbj_E02681 E02681 cDNA encoding precursor of
                  -chloroplast localising glutamine synthetase
                   401989
Seq. No.
                   LIB3431-048-P1-N1-B7
Seq. ID
Method
                   BLASTX
                  g3789954
NCBI GI
                   299
BLAST score
                   5.0e-27
E value
                   57
Match length
% identity
NCBI Description
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                   sativa]
                   401990
Seq. No.
Seq. ID
                   LIB3431-048-P1-N1-B8
Method
                   BLASTX
NCBI GI
                   g3036946
BLAST score
                   301
E value
                   2.0e-27
Match length
                   61
                 - 95
% identity
NCBI Description
                   (AB012637) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
Seq. No.
                   401991
                   LIB3431-048-P1-N1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2696804
BLAST score
                   406
E value
                   1.0e-39
Match length
                   79
% identity
NCBI Description
                   (AB009665) water channel protein [Oryza sativa]
Seq. No.
                   401992
Seq. ID
                   LIB3431-048-P1-N1-C12
Method
                   BLASTX
NCBI GI
                   g1917019 .
```

```
E value
                  5.0e-15
Match length
                  67
                  69
% identity
                  (U92045) ribosomal protein S6 RPS6-1 [Zea mays]
NCBI Description
                  401993
Seq. No.
                  LIB3431-048-P1-N1-C3
Seq. ID
                  BLASTN
Method
                  g4138289
NCBI GI
                  243
BLAST score
                  1.0e-134
E value
                  343
Match length
                  93
% identity
NCBI Description Oryza sativa mRNA for thioredoxin M
Seq. No.
                  401994
                  LIB3431-048-P1-N1-C4
Seq. ID
Method
                  BLASTX
                  q4678261
NCBI GI
                  388
BLAST score
                  2.0e-37
E value
                  85
Match length
% identity
                  92
                  (AL049657) putative proteasome regulatory subunit
NCBI Description
                  [Arabidopsis thaliana]
                  401995
Seq. No.
Seq. ID
                  LIB3431-048-P1-N1-C5
Method
                  BLASTX
                  g4585875
NCBI GI
                  395
BLAST score
                  3.0e-38
E value
                  89
Match length
% identity
NCBI Description (AC005850) Unknown protein [Arabidopsis thaliana]
                  401996
Seq. No.
                  LIB3431-048-P1-N1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g671740.
BLAST score
                  155
                  2.0e-10
E value
                  33
Match length
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  401997
Seq. No.
                  LIB3431-048-P1-N1-C9
Seq. ID
Method
                  BLASTN
                  g3345476
NCBI GI
BLAST score
                  235
E value
                  1.0e-129
                  305
Match length
                  95
% identity
```

NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds

Method

BLASTX

```
Seq. No.
                   401998
                   LIB3431-048-P1-N1-D3
Seq. ID
Method
                  BLASTX
                   g3256035
NCBI GI
BLAST score
                   222
                   5.0e-18
E value
                  81
Match length
                   52
% identity
                   (Y14274) putative serine/threonine protein kinase [Sorghum
NCBI Description
                  bicolor]
                   401999
Seq. No.
                   LIB3431-048-P1-N1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5257277
BLAST score
                   331
                   7.0e-31
E value
Match length
                   68
                   99
% identity
                   (AP000364) ESTs C98431(E0144),C71728(E0144) correspond to a
NCBI Description
                   region of the predicted gene.; Similar to Medicago sativa
                   S-adenosyl-L-methionine. (U20736) [Oryza sativa]
Seq. No.
                   402000
                   LIB3431-048-P1-N1-D8
Seq. ID
Method'
                   BLASTN
NCBI GI
                   g435648
BLAST score
                   69
E value
                   2.0e-30
Match length
                   105
% identity
                   91
                  Rice mRNA for gamma-Tip, complete cds
NCBI Description
Seq. No.
                   402001
                   LIB3431-048-P1-N1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1651922
BLAST score
                   175
E value
                   2.0e-12
Match length
                   60
% identity
                   (D90901) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                   402002
Seq. ID
                   LIB3431-048-P1-N1-E10
Method
                   BLASTN
NCBI GI
                   g19565
BLAST score
                   35
E value
                   4.0e-10
Match length
                   47
% identity
                   94
                  M.liliiflora GADPH mRNA for glycolytic
NCBI Description
                   glyceraldehyde-3-phosphate
                                                         dehydrogenase
                   402003
Seq. No.
                   LIB3431-048-P1-N1-E11
Seq. ID
```

BLAST score

```
g548605
NCBI GI
BLAST score
                  162
                  2.0e-11
E value
                  37
Match length
                  89
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) .(PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
                  402004
Seq. No.
                  LIB3431-048-P1-N1-E2
Seq. ID
                  BLASTX
Method
                  g131176
NCBI GI
BLAST score
                  260
                  1.0e-22
E value
Match length
                  62
                  85
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                  >gi 72683 pir F1BH4 photosystem I chain IV precursor -
                  barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
                  -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A
                  10.8kD photosystem I protein [Hordeum vulgare var.
                  distichum]
Seq. No.
                  402005
Seq. ID
                  LIB3431-048-P1-N1-E4
Method
                  BLASTX
                  q347451
NCBI GI
                  359
BLAST score
                  5.0e-34
E value
Match length
                  72
                  92
% identity
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
Seq. No.
                  402006
Seq. ID
                  LIB3431-048-P1-N1-E5
Method
                  BLASTX
                  q461753
NCBI GI
                  321
BLAST score
                  1.0e-29
E value
Match length
                  87
% identity
                  ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG
NCBI Description
                  PRECURSOR >gi 419773 pir S31164 ATP-dependent ClpB
                  proteinase regulatory chain homolog precursor, chloroplast
                  - garden pea >gi_169128 (L09547) nuclear encoded precursor
                  to chloroplast protein [Pisum sativum]
Seq. No.
                  402007
                  LIB3431-048-P1-N1-E6
Seq. ID
                  BLASTN
Method
                  q2196541
NCBI GI
                  161
```

```
2.0e-85
E value
Match length
                  221
                  93
% identity
NCBI Description Oryza sativa glycine-rich protein mRNA, complete cds
                  402008
Seq. No.
                  LIB3431-048-P1-N1-E7
Seq. ID
Method
                  BLASTX
                  g5733874
NCBI GI
BLAST score
                  243
E value
                  1.0e-20
                  75
Match length
                  56
% identity
                  (AC007932) F11A17.8 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  402009
                  LIB3431-048-P1-N1-F1
Seq. ID
Method
                  BLASTX
                  q131176
NCBI GI
BLAST score
                  288
                  8.0e-26
E value
                  60
Match length
% identity
                  93
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
NCBI Description
                  (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                  >gi 72683 pir F1BH4 photosystem I chain IV precursor -
                  barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA
                  -46 to 101) [Hordeum vulgare] >gi 226163 prf 1413233A
                  10.8kD photosystem I protein [Hordeum vulgare var.
                  distichum]
                  402010
Seq. No.
                  LIB3431-048-P1-N1-F10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  164
                  3.0e-87
E value
                  249
Match length
% identity
                  92
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
                  402011
Seq. No.
Seq. ID
                  LIB3431-048-P1-N1-F12
Method
                  BLASTX
NCBI GI
                  q115807
BLAST score
                  234
                  1.0e-19
E value
Match length
                  61
                  75
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN E PRECURSOR (LHCII TYPE I
                  CAB-E) (LHCP) >gi 72736 pir CDNTEC chlorophyll a/b-binding
                  protein type I precursor (cab-E) - curled-leaved tobacco
                  >gi 170212 (M21398) chlorophyll a/b-binding protein-E
```

[Nicotiana plumbaginifolia]

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```
402012
Seq. No.
                   LIB3431-048-P1-N1-F4
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2306980
BLAST score
                   74
                   1.0e-33
E value
                   88
Match length
                   97
% identity,
                   Oryza sativa photosystem I antenna protein (Lhca) mRNA,
NCBI Description
                   complete cds
                   402013
Seq. No.
                   LIB3431-048-P1-N1-F6
Seq. ID
Method
                   BLASTX
                   g482311
NCBI GI
                   298
BLAST score
                   6.0e-27
E value
                   69
'Match length
                   90
% identity
                   photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                   complex protein 1 [Oryza sativa]
                   402014
Seq. No.
                   LIB3431-048-P1-N1-F7
Seq. ID
Method
                   BLASTN
                   g3126853
NCBI GI
BLAST score
                   122
E value
                   4.0e-62
                   188
Match length
                   96
% identity
                   Oryza sativa chlorophyll a/b binding protein (RCABP89)
NCBI Description
                   mRNA, nuclear gene encoding chloroplast protein, complete
                   cds
                   402015
Seq. No.
                   LIB3431-048-P1-N1-F8
Seq. ID
                   BLASTN
Method
NCBI GI
                   q430946
BLAST score
                   37
E value
                   3.0e-11
                   65
Match length
                   89
% identity
                   Arabidopsis thaliana PSI type III chlorophyll a/b-binding
NCBI Description
                   protein (Lhca3*1) mRNA, complete cds
                   402016
Seq. No.
                   LIB3431-048-P1-N1-G1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g733454
                   402
BLAST score
                   4.0e-39
E value
Match length
                   81
% identity
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
```

[Zea mays]

```
402017
Seq. No.
Seq. ID
                   LIB3431-048-P1-N1-G2
Method
                   BLASTX
NCBI GI
                   g4105794
BLAST score
                   175
                   2.0e-12
E value
Match length
                   47
% identity
                   60
NCBI Description
                   (AF049928) PGP224 [Petunia x hybrida]
                   402018
Seq. No.
                   LIB3431-048-P1-N1-G4
Seq. ID
Method
                   BLASTN
                   g3063523
NCBI GI
BLAST score
                   39
E value
                   1.0e-12
Match length
                   59
% identity
                   92
                   Oryza sativa ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit mRNA, complete cds
                   402019
Seq. No.
Seq. ID
                   LIB3431-048-P1-N1-G8
Method
                   BLASTX
NCBI GI
                   g4757718
                   190
BLAST score
E value
                   4.0e-14
                   53
Match length
                   66
% identity
                   actin-like 6 > gi 4001803 (AF041474) BAF53a [Homo sapiens]
NCBI Description
                   >gi 4218064 dbj BAA74577 (AB015907) actin-related protein
                   [Homo sapiens]
                   402020
Seq. No.
                   LIB3431-048-P1-N1-G9
Seq. ID
                   BLASTN
Method
NCBI GI
                   g218207
BLAST score
                   34
E value
                   1.0e-09
                   98
Match length
                   84
% identity
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   p0SSS1139
                   402021
Seq. No.
                   LIB3431-048-P1-N1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g729478
BLAST score
                   171
                   2.0e-12
E value
Match length
                   39
% identity
                   79
NCBI Description
                   FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
                   >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1
```

(AP000616) ESTs AU078647(E15 $\overline{5}$ 7),C724 $\overline{0}$ 0(E $\overline{1}$ 557) correspond to

NCBI Description

a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

402022 Seq. No. LIB3431-048-P1-N1-H12 Seq. ID Method BLASTX g1170937 NCBI GI BLAST score 189 3.0e-14 E value Match length 33 100 % identity NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi 450549 emb CAA81481 (Z26867) S-adenosyl methionine synthetase [Oryza sativa] Seq. No. 402023 LIB3431-048-P1-N1-H2 Seq. ID Method BLASTX NCBI GI q3345477 346 BLAST score E value 2.0e-32 Match length 66 % identity (AB016283) carbonic anhydrase [Oryza sativa] NCBI Description 402024 Seq. No. Seq. ID LIB3431-048-P1-N1-H3 Method BLASTX NCBI GI q1235664 314 BLAST score 7.0e-29 E value 88 Match length % identity (U37936) novel calmodulin-like protein [Oryza sativa] NCBI Description >gi 3171148 (AF064456) calmodulin-like protein [Oryza sativa subsp. indica] Seq. No. 402025 LIB3431-048-P1-N1-H5 Seq. ID Method BLASTX : g3063710 NCBI GI BLAST score 175 2.0e-12 E value Match length 35 % identity (AL022537) putative protein [Arabidopsis thaliana] NCBI Description 402026 Seq. No. Seq. ID LIB3431-049-P1-K1-A10 Method BLASTN NCBI GI g20181 BLAST score 71 4.0e-32 E value Match length 113 % identity

Rice cab2R gene for light harvesting chlorophyll

a/b-binding protein

```
402027
Seq. No.
                  LIB3431-049-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4510363
                  242
BLAST score
                  5.0e-21
E value
                  50
Match length
                  86
% identity
                  (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  402028
Seq. No.
                  LIB3431-049-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g445116
BLAST score
                  226
                  2.0e-28
E value
                  71
Match length
                  92
% identity
                  light-harvesting complex IIa protein; [Hordeum vulgare]
NCBI Description
                  402029
Seq. No.
                  LIB3431-049-P1-K1-B12
Seq. ID
Method
                  BLASTX
                  g606817
NCBI GI
BLAST score
                  295
E value
                  2.0e-32
Match length
                  87
                  86
% identity
                  (U08404) carbonic anhydrase [Oryza sativa]
NCBI Description
                  >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic
                  anhydrase 3 [Oryza sativa]
                  402030
Seq. No.
                  LIB3431-049-P1-K1-B2
Seq. ID
                  BLASTN
Method
NCBI GI
                  g20181
BLAST score
                  74
                  7.0e-34
E value
                  81
Match length
                  99
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
                  402031
Seq. No.
                  LIB3431-049-P1-K1-B3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g20181
                  48
BLAST score
                  2.0e-18
E value
Match length
                  72
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
```

a/b-binding protein

```
402032
Seq. No.
                  LIB3431-049-P1-K1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4079797
BLAST score
                  144
                  2.0e-75
E value
                  155
Match length
                  99
% identity
                  Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
NCBI Description
                  complete cds
                  402033
Seq. No.
                  LIB3431-049-P1-K1-B7
Seq. ID
Method
                  BLASTX
                  g549063
NCBI GI
                  276
BLAST score
                  5.0e-37
E value
                  82
Match length
                  99
% identity
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                  >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
                  factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                  21kd polypeptide [Oryza sativa]
                  402034
Seq. No.
                  LIB3431-049-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q606817
BLAST score
                  661
                  4.0e-81
E value
                  155
Match length
% identity
                   (U08404) carbonic anhydrase [Oryza sativa]
NCBI Description
                  >qi 5917783 gb AAD56038.1 AF182806 1 (AF182806) carbonic
                  anhydrase 3 [Oryza sativa]
                  402035
Seq. No.
                  LIB3431-049-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1805617
BLAST score
                  163
                  5.0e-20
E value
                  56
Match length
% identity
                   (D49704) OSH44 transcript; homeobox gene [Oryza sativa]
NCBI Description
                  402036
Seq. No.
                  LIB3431-049-P1-K1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3885885
BLAST score
                  191
                  1.0e-103
E value
Match length
                  226
% identity
                  Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA,
NCBI Description
                  complete cds
```

```
402037
Seq. No.
                  LIB3431-049-P1-K1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218171
                  83
BLAST score
                  4.0e-39
E value
                  138
Match length
                  91
% identity
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                  a/b binding protein of photosystem II (LHCPII), complete
                  402038
Seq. No.
                  LIB3431-049-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2739360
BLAST score
                  152
                  6.0e-18
E value
                  102
Màtch length
                  51
% identity
                   (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3075385 (AC004484) unknown protein [Arabidopsis
                  thaliana]
                  402039
Seq. No.
Seq. ID
                  LIB3431-049-P1-K1-D1
Method
                  BLASTN -
NCBI GI
                  g4218534
BLAST score
                  45
E value
                  2.0e-16
                  45
Match length
                  100
% identity
                  Triticum sp. mRNA for GRAB1 protein
NCBI Description
                  402040
Seq. No.
                  LIB3431-049-P1-K1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3789954
BLAST score
                  367
E value
                  4.0e-45
                  100
Match length
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  402041
Seq. No.
                  LIB3431-049-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3676294
                  151
BLAST score
E value
                  5.0e-21
Match length
                  66
                  77
% identity
                  (U96496) mitochondrial ATPase beta subunit [Nicotiana
NCBI Description
                  sylvestris]
```

Seq. No.

```
LIB3431-049-P1-K1-D4
Seq. ID
                  BLASTX
Method
                  g3126854
NCBI GI
                  345
BLAST score
                   6.0e-35
E value
                  78
Match length
                   97
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   402043
Seq. No.
                  LIB3431-049-P1-K1-E10
Seq. ID
                  BLASTN
Method
                  g3126853
NCBI GI
BLAST score
                  150
                   6.0e-79
E value
Match length
                  222
                  93
% identity
                  Oryza sativa chlorophyll a/b binding protein (RCABP89)
NCBI Description
                  mRNA, nuclear gene encoding chloroplast protein, complete
                   402044
Seq. No.
                   LIB3431-049-P1-K1-E11
Seq. ID
                  BLASTN
Method
                   g4138289
NCBI GI
BLAST score
                  68
                   4.0e-30
E value
Match length
                  72
% identity
                   99
                  Oryza sativa mRNA for thioredoxin M
NCBI Description
                   402045
Seq. No.
                  LIB3431-049-P1-K1-E9
Seq. ID
Method
                   BLASTN
                   g3885891
NCBI GI
                   80
BLAST score
                  7.0e-37
E value
                  95
Match length
% identity
                   97
                  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
NCBI Description
                   mRNA, complete cds
                   402046
Seq. No.
                   LIB3431-049-P1-K1-F12
Seq. ID
Method
                   BLASTX
                   g3885894
NCBI GI
                   266
BLAST score
                   9.0e-34
E value
                  91
Match length
% identity
                   (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
                   402047
Seq. No.
                   LIB3431-049-P1-K1-F2
Seq. ID
                   BLASTX
Method
                   q2130089
NCBI GI
```

BLAST score

```
E value
                   4.0e-18
                   49
Match length
                   90
% identity
NCBI Description
                   2-oxoglutarate/malate translocator (clone OMT103),
                   mitochondrial membrane - proso millet >gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate
                   translocator [Panicum miliaceum]
                   402048
Seq. No.
                   LIB3431-049-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   332
                   1.0e-33
E value
Match length
                   95
                   75
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   402049
                   LIB3431-049-P1-K1-F6
Seq: ID
Method
                   BLASTN
NCBI GI
                   q409581
BLAST score
                   38
E value
                   1.0e-12
Match length
                   62
                   90
% identity
                   Rice mRNA for serine carboxypeptidase-like protein
NCBI Description
Seq. No.
                   402050
                   LIB3431-049-P1-K1-F8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g218207
BLAST score
                   107
E value
                   2.0e-53.
Match length
                   142
% identity
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   p0SSS1139
                   402051
Seq. No.
                   LIB3431-049-P1-K1-F9
Seq. ID
                   BLASTN
Method
NCBI GI
                   g218132
BLAST score
                   137
E value
                   3.0e-71
Match length
                   162
                   96
% identity
NCBI Description
                   Rice mRNA for Heat shock protein
                   402052
Seq. No.
                   LIB3431-049-P1-K1-G7
Seq. ID
```

BLASTX

Method

```
NCBI GI
                   g4741940
BLAST score
                   255
                   1.0e-30
E value
                   75
Match length
% identity
                   88
                   (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
                   402053
Seq. No.
                   LIB3431-049-P1-K1-H10
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2062705
BLAST score
                   35
                   2.0e-10
E value
Match length
                   35
                   100
% identity
                  Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
Seq. No.
                   402054
                   LIB3431-049-P1-K1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4262142
BLAST score
                   157
E value
                   1.0e-10
Match length
                   61
% identity
                   54
                   (AC005275) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   402055
                   LIB3431-049-P1-K1-H7
Seq. ID
                   BLASTN
Method
                   g21840
NCBI GI
BLAST score
                   34
                   1.0e-09
E value
                   50
Match length
                   92
% identity
                  Triticum aestivum RNA for phosphoribulokinase
NCBI Description
Seq. No.
                   402056
                   LIB3431-049-P1-N1-A2
Seq. ID
Method
                   BLASTX
                   g4510363
NCBI GI
BLAST score
                   175
                   2.0e-12
E value
Match length
                   36
% identity
                   (AC007017) putative DNA-binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   402057
                   LIB3431-049-P1-N1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3158476
BLAST score
                   317
                   5.0e-29
E value
Match length
                   76
```

% identity

```
NCBI Description
                  (AF067185) aquaporin 2 [Samanea saman]
                  402058
Seq. No.
                  LIB3431-049-P1-N1-A7
Seq. ID
                  BLASTX
Method
                  g115813
NCBI GI
BLAST score
                  248
E value
                  4.0e-21
Match length
                  56
% identity
                  86
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi 19182 emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  402059
Seq. No.
Seq. ID
                  LIB3431-049-P1-N1-A8
Method
                  BLASTX -
                  g563235
NCBI GI
BLAST score
                  513
                  4.0e-52
E value
Match length
                  117
% identity
                  (U15964) xyloglucan endo-transglycosylase homolog; similar
NCBI Description
                  to Triticum aestivum endo-xyloglucan transferase, PIR
                  Accession Number E49539 [Zea mays] >gi_563927 (U15781)
                  xyloglucan endo-transglycosylase homolog [Zea mays]
                  >gi 1097378 prf 2113418A xyloglucan endotransglycosylase
                  homolog [Zea mays]
Seq. No.
                  402060
                  LIB3431-049-P1-N1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2326947
BLAST score
                  153
                  6.0e-10
E value
Match length
                  34
                  91
% identity
NCBI Description
                 (Z50801) Chlorophyll a/b-binding protein CP29 precursor
                  [Zea mays]
Seq. No.
                  402061
                  LIB3431-049-P1-N1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3036949
                  309 -
BLAST score
                  3.0e-28
E value
                  59
Match length
% identity
NCBI Description
                  (AB012638) light harvesting chlorophyll a/b-binding protein
                  [Nicotiana sylvestris]
                  402062
Seq. No.
Seq. ID
                  LIB3431-049-P1-N1-B5
Method
                  BLASTX
NCBI GI
                  q4079798
BLAST score
                  385
```

4.0e-37

E value

```
76
Match length
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
                  402063
Seq. No.
                  LIB3431-049-P1-N1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g549063
BLAST score
                  283
                  3.0e-25
E value
Match length
                  53
                  98
% identity
                  TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
NCBI Description
                  >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
                  factor homolog - rice >gi 303835 dbj BAA02151 (D12626)
                  21kd polypeptide [Oryza sativa]
                  402064
Seq. No.
                  LIB3431-049-P1-N1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2624325
                  150
BLAST score
                  5.0e-79
E value
                  201
Match length
% identity
                  Oryza sativa mRNA for glycine-rich RNA-binding protein
NCBI Description
                  (OsGRP1)
                  402065
Seq. No.
                  LIB3431-049-P1-N1-C10
Seq. ID
Method
                  BLASTX
                  g400879
NCBI GI
BLAST score
                  257
                  2.0e-22
E value
                  53
Match length
                  83
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                  (PSI-N) >gi 479690 pir S35159 photosystem I chain psaN -
                  barley >gi 19095 emb CAA47056 (X66428) photosystem I
                  subunit N [Hordeum vulgare]
                  402066
Seq. No.
                  LIB3431-049-P1-N1-C2
Seq. ID
Method
                  BLASTX
                  g2130069
NCBI GI
                  200
BLAST score
                  2.0e-15
E value
Match length
                  39
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  402067
                  LIB3431-049-P1-N1-C4
Seq. ID
Method
                  BLASTN
```

q1805615

NCBI GI

```
BLAST score
                   345
E value
                   0.0e + 00
Match length
                   432
                   94
% identity
NCBI Description
                  Rice OSH45 gene for OSH42, OSH44 and OSH45 transcripts,
                   exon 2, 3, 4, 5, 6 and 7, complete cds
                   402068
Seq. No.
                   LIB3431-049-P1-N1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3885885
BLAST score
                   195
E value
                   1.0e-105
                   202
Match length
                   100
% identity
                  Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA,
NCBI Description
                   complete cds
                   402069
Seq. No.
                   LIB3431-049-P1-N1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g289920
                   284
BLAST score
                   3.0e-25
E value
                   56
Match length
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   402070
Seq. No.
                   LIB3431-049-P1-N1-C8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2739360
BLAST score
                   261
                   1.0e-22
E value
                   111
Match length
                   52
% identity
                   (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3075385 (AC004484) unknown protein [Arabidopsis
                   thaliana]
                   402071
Seq. No.
                   LIB3431-049-P1-N1-C9
Seq. ID
                   BLASTN
Method
                   g2970050
NCBI GI
BLAST score
                   38
                   7.0e-12
E value
                  102
Match length
                  84
% identity
NCBI Description
                  Vigna radiata mRNA for ARG10, complete cds
Seq. No.
                   402072
Seq. ID
                  LIB3431-049-P1-N1-D1
                  BLASTN
Method
                   g398603
NCBI GI
BLAST score
                   39
```

2.0e-12

E value

```
Match length
                  63
                  90
% identity
                  A.thaliana ATAF1 mRNA
NCBI Description
Seq. No.
                  402073
                  LIB3431-049-P1-N1-D10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3789954
                  184
BLAST score
                  1.0e-13
E value
Match length
                  47
                  79
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                  402074
Seq. No.
                  LIB3431-049-P1-N1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  389
                  1.0e-37
E value
Match length
                  82
% identity
                  90
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   402075
Seq. ID
                  LIB3431-049-P1-N1-D6
Method
                  BLASTX
NCBI GI
                  q5478797
BLAST score
                   415
E value
                   9.0e-41
Match length
                   91
% identity
NCBI Description
                   (AB021310) chlorophyll b synthase [Oryza sativa]
Seq. No.
                   402076
Seq. ID
                  LIB3431-049-P1-N1-D9
Method
                  BLASTX_
NCBI GI
                  q1617197
BLAST score
                  177
E value
                  7.0e-13
Match length
                  36
                  89
% identity
NCBI Description
                   (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                  402077
Seq. ID
                  LIB3431-049-P1-N1-E10
Method
                  BLASTN
NCBI GI
                  q3126853
BLAST score
                  63
E value
                  5.0e-27
Match length
                  98
                  91
% identity
NCBI Description
                  Oryza sativa chlorophyll a/b binding protein (RCABP89)
                  mRNA, nuclear gene encoding chloroplast protein, complete
```

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402078
Seq. No.
Seq. ID
                   LIB3431-049-P1-N1-E11
Method
                   BLASTN
NCBI GI
                   g4138289
BLAST score
                   163
                   2.0e-86
E value
Match length
                   324
                   87
% identity
NCBI Description
                   Oryza sativa mRNA for thioredoxin M
                   402079
Seq. No.
Seq. ID
                   LIB3431-049-P1-N1-E2
Method
                   BLASTX
NCBI GI
                   g128690
BLAST score
                   529
E value
                   8.0e-54
Match length
                   116
% identity
NCBI Description
                   NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST
                   >gi_66161_pir__DERZN3 NADH dehydrogenase (ubiquinone) (EC
                   1.6.5.3) Chain 3 - rice chloroplast >gi_11989_emb_CAA34001_
                   (X15901) ndhC; NADH dehydrogenase ND3 [Oryza sativa]
                   >gi_226610_prf__1603356AG NADH dehydrogenase ND3 [Oryza
                   sativa]
                   402080
Seq. No.
Seq. ID
                   LIB3431-049-P1-N1-E9
Method
                   BLASTX
NCBI GI
                   q3885892
                   200
BLAST score
                   1.0e-15
E value
Match length
                   49
                   82
% identity
                   (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
                   402081
Seq. No.
Seq. ID
                   LIB3431-049-P1-N1-F12
Method
                   BLASTX
NCBI GI
                   g3885894
BLAST score
                   178
E value
                   5.0e-13
Match length
                   59
% identity
                   68
                   (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
                   402082
Seq. No.
                   LIB3431-049-P1-N1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2130089
BLAST score
                   439
                   2.0e-43
E value
                   88
Match length
                   90
% identity
                   2-oxoglutarate/malate translocator (clone OMT103),
NCBI Description
                   mitochondrial membrane - proso millet
>gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate
                   translocator [Panicum miliaceum]
```

. . . .

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402083
Seq. No.
Seq. ID
                  LIB3431-049-P1-N1-F4
Method
                  BLASTX
NCBI GI
                  q320618
BLAST score
                  241
                  2.0e-20
E value
Match length
                  54
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza satīva]
Seq. No.
                  402084
                  LIB3431-049-P1-N1-F6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g409581
BLAST score
                  416
E value.,
                  0.0e + 00
                  452
Match length
                  98
% identity
                  Rice mRNA for serine carboxypeptidase-like protein
NCBI Description
Seq. No.
                  402085
Seq. ID
                  LIB3431-049-P1-N1-F8
Method
                  BLASTX
                  q671740
NCBI GI
BLAST score
                  252
E value
                  1.0e-21
Match length
                  57
                  82
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                  402086
Seq. ID
                  LIB3431-049-P1-N1-F9
Method
                  BLASTX
NCBI GI
                  q829283
BLAST score
                  273
                  5.0e-24
E value
Match length
                  68
% identity
                  (Z15018) heat shock protein hsp82 [Oryza sativa]
NCBI Description
                  402087
Seq. No.
Seq. ID
                  LIB3431-049-P1-N1-G2
Method
                  BLASTX
NCBI GI
                  g3885892
BLAST score
                  389
                  1.0e-37
E value
Match length
                  75
% identity
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
```

Seq. No.

Method

```
Seq. ID
                  LIB3431-049-P1-N1-G3
                  BLASTN
Method
                  g3885891
NCBI GI
                  34
BLAST score
                  5.0e-10
E value
                  58
Match length
                  90
% identity
NCBI Description Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                  mRNA, complete cds
Seq. No.
                  402089
                  LIB3431-049-P1-N1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g6006283
BLAST score
                  162
                  3.0e-11
E value
Match length
                  41
                  71
% identity
                  (AB015861) photosystem I subunit PSI-L [Arabidopsis
NCBI Description
                  thaliana]
                  402090
Seq. No.
                  LIB3431-049-P1-N1-G7
Seq. ID
Method
                  BLASTX
                  g551047
NCBI GI
                  243
BLAST score
                  2.0e-20
E value
Match length
                  55
% identity
                  85
                  (X79277) type II LHCI [Lolium temulentum]
NCBI Description
Seq. No.
                  402091
                  LIB3431-049-P1-N1-G8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  180
                  1.0e-96
E value
Match length
                  279
% identity
                  90
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS1139
                  402092
Seq. No.
Seq. ID
                  LIB3431-049-P1-N1-H5
Method
                  BLASTX
                  g4262142
NCBI GI
BLAST score
                  145
                  5.0e-09
E value
Match length
                  69
% identity
                  49
                  (AC005275) putative alcohol dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
                  402093
Seq. No.
                  LIB3431-049-P1-N1-H6
Seq. ID
                  BLASTX
```

1.150

```
g671740
NCBI GI
                  380
BLAST score
E value
                  2.0e-36
Match length
                  69
% identity
                  100
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
                  402094
Seq. No.
                  LIB3431-049-P1-N1-H7
Seq. ID
Method
                  BLASTX
                  g21839
NCBI GI
BLAST score
                  336
E value
                  2.0e-31
                  75
Match length
                  87
% identity
                  (X57952) phosphoribulokinase [Triticum aestivum]
NCBI Description
                  402095
Seq. No.
                  LIB3431-050-P1-K1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2062705
                  35
BLAST score
                  5.0e-10
E value
                  35
Match length
                  100
% identity .
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  402096
Seq. No.
                  LIB3431-050-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131192
BLAST score
                  449
                  1.0e-44
E value
                  97
Match length
                  87
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_100606_pir__S20937
                  photosystem I chain V precursor - barley
                  >gi_19091_emb_CAA42727_ (X60158) photosystem I polypeptide
                  PSI-G precursor [Hordeum vulgare]
                  402097
Seq. No.
                  LIB3431-050-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
                  339
BLAST score
                  4.0e-32
E value
                  79
Match length
                  86
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
```

Match length

116

```
carboxylase S [Oryza sativa]
Seq. No.
                  402098
                  LIB3431-050-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  449
E value
                  1.0e-44
Match length
                  83
                  99
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                  402099
Seq. ID
                  LIB3431-050-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  6.0e-20
Match length
                  44
                  100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  402100
                  LIB3431-050-P1-K1-A7
Seq. ID
Method
                  BLASTX
                  g1170507
NCBI GI
BLAST score
                  627
E value
                  2.0e-65
                  130
Match length
                  92
% identity
                  EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3)
NCBI Description
                  >gi_100276_pir__S22579 translation initiation factor eIF-4A
                  - curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206)
                  nicotiana eukaryotic translation initiation factor 4A
                   [Nicotiana plumbaginifolia]
                  402101
Seq. No.
                  LIB3431-050-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3080391
BLAST score
                  526
                  1.0e-53
E value
                  125
Match length
% identity
                  (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  402102
                  LIB3431-050-P1-K1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  101
                  2.0e-49
E value
```

sativa] >gi 226375 prf 1508256A ribulose bisphosphate

```
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
                  402103
Seq. No.
                  LIB3431-050-P1-K1-B10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20262
                  268
BLAST score
E value
                  1.0e-149
Match length
                  308
                  97
% identity
NCBI Description
                  O.sativa light-induced mRNA
                  402104
Seq. No.
                  LIB3431-050-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  290
E value
                  3.0e-26
                  70
Match length
                  79
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
                  402105
Seq. No.
Seq. ID
                  LIB3431-050-P1-K1-B3
                  BLASTX
Method
                  g3367596
NCBI GI
BLAST score
                  311
                  6.0e-32
E value
                  98
Match length
                  70
% identity >
NCBI Description
                   (AL031135) putative protein [Arabidopsis thaliana]
                  402106
Seq. No.
                  LIB3431-050-P1-K1-B7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2924785
                  165
BLAST score
                  2.0e-11
E value
                  79
Match length
                  47
% identity
NCBI Description
                   (AC002334) similar to disease resistance protein
                   [Arabidopsis thaliana]
                  402107
Seq. No.
Seq. ID
                  LIB3431-050-P1-K1-C1
                  BLASTX
Method
NCBI GI
                  q3236242
                  435
BLAST score
                  4.0e-43
E value
```

Match length

```
% identity
NCBI Description
                  (AC004684) putative ribosomal protein L36 [Arabidopsis
                  402108
Seq. No.
                  LIB3431-050-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  364
                  8.0e-35
E value
Match length
                  103
% identity
                  70
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  402109
Seq. No.
                  LIB3431-050-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3036953
BLAST score
                  273
                  5.0e-24
E value
                  51
Match length
                  100
% identity
                  (AB012640) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
Seq. No.
                  402110
                  LIB3431-050-P1-K1-C7
Seq. ID
Method
                  BLASTX
                  g3808101
NCBI GI
BLAST score
                  335
E value
                  2.0e-33
                  99
Match length
                  70
% identity
                  (AJ012165) chloroplast protease [Capsicum annuum]
NCBI Description
Seq. No.
                  402111
                  LIB3431-050-P1-K1-C9
Seq. ID
Method
                  BLASTX
                  g132105
NCBI GI
BLAST score
                  480
                  2.0e-48
E value
Match length
                  112
                  82
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

LIB3431-050-P1-K1-D1

Seq. No.

Seq. ID

Method

BLASTX

```
Method
                  BLASTX
NCBI GI
                  q3929924
BLAST score
                  210
E value
                  4.0e-17
Match length
                  41
                  100
% identity
NCBI Description (AB020502) catalase [Oryza sativa]
Seq. No.
                  402113
                  LIB3431-050-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q462195
BLAST score
                  281
                  5.0e-25
E value
Match length
                  69
% identity
                  81
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi 100682 pir__S21636 GOS2 protein - rice
                  >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                  >gi_3789950 (AF094774) translation initiation factor [Oryza
                  satīva]
                  402114
Seq. No.
Seq. ID
                  LIB3431-050-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
                  7.0e-20
E value
Match length
                  44
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  402115
Seq. No.
                  LIB3431-050-P1-K1-D2
Seq. ID
Method
                  BLASTN
                  g6015437
NCBI GI
                  36
BLAST score
                  8.0e-11
E value
                  36
Match length
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  402116
Seq. No.
                  LIB3431-050-P1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1370188
BLAST score
                  304
E value
                  5.0e-28
                  71
Match length
% identity
                  79
                  (Z73943) RAB7D [Lotus japonicus]
NCBI Description
                  402117
Seq. No.
                  LIB3431-050-P1-K1-D6
Seq. ID
```

```
NCBI GI
                   q733454
BLAST score
                   317
                   4.0e-29
E value
Match length
                   66
                   94
% identity
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
Seq. No.
                   402118
                  LIB3431-050-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q5541681
                   225
BLAST score
                   3.0e-18
E value
Match length
                   165
                   39
% identity
                   (AL096859) putative protein [Arabidopsis thaliana]
NCBI Description
                   402119
Seq. No.
                  LIB3431-050-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g6015065
                   308
BLAST score
                   9.0e-29
E value
Match length
                   64
                   92
% identity
                  ELONGATION FACTOR 2 (EF-2) >gi 2369714 emb_CAB09900_
NCBI Description
                   (Z97178) elongation factor 2 [Beta vulgaris]
                   402120
Seq. No.
                   LIB3431-050-P1-K1-E1
Seq. ID
Method
                   BLASTX
                   g1835731
NCBI GI
                   357
BLAST score
                   5.0e-34
E value
                   81
Match length
                   89
% identity
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                   402121
Seq. No.
                   LIB3431-050-P1-K1-E10
Seq. ID
                   BLASTN
Method
                   g6015437
NCBI GI
                   36
BLAST score
                   1.0e-10
E value
                   47
Match length
                   65
% identity
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
                   402122
Seq. No.
                   LIB3431-050-P1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2346966
BLAST score
                   144
                   8.0e-09
E value
                   57
Match length
```

% identity

```
(AB004871) CPC [Arabidopsis thaliana]
NCBI Description
                   >qi 4559383 qb AAD23043.1 AC006526 8 (AC006526) putative
                   DNA binding protein CPC [Arabidopsis thaliana]
Seq. No.
                   402123
                   LIB3431-050-P1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3915186
BLAST score
                   231
E value
                   4.0e-19
Match length
                   86
% identity
NCBI Description
                   UBIQUITIN-CONJUGATING ENZYME E2-21 KD (UBIQUITIN-PROTEIN
                   LIGASE) (UBIQUITIN CARRIER PROTEIN) (PEROXIN-4) >gi 3128447
                   (AF061604) ubiquitin-conjugating enzyme homolog peroxin 4
                   [Pichia angusta]
                   402124
Seq. No.
                   LIB3431-050-P1-K1-E7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   36
E value
                   9.0e-11
Match length
                   36
% identity
                   100
NCBI Description
                   Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   402125
Seq. ID
                   LIB3431-050-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   g3036946
BLAST score
                   281
E value
                   3.0e-25
Match length
                   56
                   95
% identity
                   (AB012637) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                   402126
Seq. No.
                   LIB3431-050-P1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q125580
BLAST score
                   155
                   8.0e-11
E value
Match length
                   48
                   73
% identity
                   PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
NCBI Description
                   (PRK) >gi_100839_pir__S15743 phosphoribulokinase (EC 2.7.1.19) - wheat >gi_5924030_emb_CAB56544.1_ (X51608)
                   phosphoribulokinase [Triticum aestivum]
Seq. No.
                   402127
                   LIB3431-050-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4572679
BLAST score
                   161
                   2.0e-11
E value
```



```
Match length
% identity
NCBI Description
                   (AC006954) RSZp22 splicing factor; contains RNA recognition
                  motif [Arabidopsis thaliana]
                  402128
Seq. No.
Seq. ID
                  LIB3431-050-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  q1172558
BLAST score
                  201
E value
                  7.0e-16
Match length
                  79
                  47
% identity
                  OUTER PLASTIDIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT
NCBI Description
                  ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                  >gi_480122_pir__S36454 porin por1 - garden pea
                  >gi 396819 emb CAA80988 (Z25540) Porin [Pisum sativum]
Seq. No.
                  402129
                  LIB3431-050-P1-K1-F4
Seq. ID
Method
                  BLASTX
                  g115787
NCBI GI
BLAST score
                  344
E value
                  1.0e-32
Match length
                  80
% identity
                  91
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                  402130
Seq. ID
                  LIB3431-050-P1-K1-F6
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  36
                  4.0e-11
E value
                  36
Match length
                  100
% identity
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
                  402131
Seq. No.
                  LIB3431-050-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3688182
BLAST score
                  367
E value
                  2.0e-37
                  92
Match length
% identity
                  (AL031804) P-Protein - like protein [Arabidopsis thaliana]
NCBI Description
                  402132
Seq. No.
```

LIB3431-050-P1-K1-F9 Seq. ID

Method BLASTX NCBI GI q3789952 BLAST score 497

```
2.0e-50
E value
Match length
                  102
% identity
                  96
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
                  402133
Seq. No.
Seq. ID
                  LIB3431-050-P1-K1-G1
Method
                  BLASTN
NCBI GI
                  q6006355
                  125
BLAST score
                  8.0e-64
E value
Match length
                  260
% identity
                  100
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
                  402134
Seq. No.
                  LIB3431-050-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4680501
BLAST score
                  216
                  2.0e-17
E value .
Match length
                  91
% identity
                  (AF119222) hypothetical protein [Oryza sativa]
NCBI Description
Seq. No.
                  402135
                  LIB3431-050-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q21693
BLAST score
                  450
                  5.0e-45
E value
Match length
                  83
% identity
NCBI Description (X66012) cathepsin B [Triticum aestivum]
Seq. No.
                  402136
                  LIB3431-050-P1-K1-G4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4959460
BLAST score
                  38
E value
                  9.0e-12
                  38
Match length
                  100
% identity
                  Zea mays RACB small GTP binding protein mRNA, complete cds
NCBI Description
Seq. No.
                  402137
Seq. ID
                  LIB3431-050-P1-K1-G5
Method
                  BLASTX
                  q3687440
NCBI GI
                  310
BLAST score
                  1.0e-28
E value
Match length
                  107
% identity
                   (AL022577) dJ353H6.2.1 (SW1/SNF related, matrix associated,
NCBI Description
                  actin dependent regulator of chromatin, subfamily a, member
```

1 (SNF2L1)) [Homo sapiens]

```
Seq. No.
                   402138
                  LIB3431-050-P1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g417260 .
BLAST score
                   349
E value
                   5.0e-33
Match length
                   110
% identity
                   66
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                   lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                   light-regulated gene [Oryza sativa]
                   402139
Seq. No.
                  LIB3431-050-P1-K1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1944407
BLAST score
                   265
E. value
                   3.0e-23
Match length
                   65
                   72
% identity
NCBI Description
                   (D86988) KIAA0221 [Homo sapiens]
                   402140
Seq. No.
                  LIB3431-050-P1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   233
                   2.0e-19
E value
Match length
                   44
                   98
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                   402141
Seq. No.
                   LIB3431-050-P1-K1-H2
Seq. ID
                                                      3
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   406
                   9.0e-40
E value
                   96
Match length
                   80
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi 218172 dbj BAA00536 (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   402142
Seq. ID
                  LIB3431-050-P1-K1-H3
Method
                  BLASTX
                   g430947
NCBI GI
                   390
BLAST score
                   6.0e-38
E value
Match length
                   104
                   72
% identity
```

(U01103) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No. 402143

NCBI Description

Seq. ID LIB3431-050-P1-K1-H4

Method BLASTX
NCBI GI g132105
BLAST score 251
E value 8.0e-22
Match length 67

% identity 76

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

Seq. No. 402144

Seq. ID LIB3431-050-P1-K1-H5

Method BLASTX
NCBI GI g2570515
BLAST score 488
E value 3.0e-49
Match length 110

Match length 110 % identity 86

NCBI Description (AF022740) glycolate oxidase [Oryza sativa]

Seq. No. 402145

Seq. ID LIB3431-050-P1-K1-H9

Method BLASTX
NCBI GI g2072555
BLAST score 237
E value 7.0e-20
Match length 44
% identity 100

NCBI Description (AF001396) metallothionein-like protein [Oryza sativa]

>gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like

protein [Oryza sativa]

Seq. No. 402146

Seq. ID LIB3431-050-P1-N1-A11

Method BLASTX
NCBI GI g131192
BLAST score 359
E value 3.0e-34
Match length 74
% identity 89

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR

(PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi 100606 pir S20937

photosystem I chain V precursor - barley

>gi 19091 emb CAA42727 (X60158) photosystem I polypeptide

PSI-G precursor [Hordeum vulgare]

```
402147
Seq. No.
                   LIB3431-050-P1-N1-A2
Seq. ID
Method
                   BLASTX
                   g347451
NCBI GI
                   291
BLAST score
                   4.0e-26
E value
                   57
Match length
% identity
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                   sativa]
                   402148
Seq. No.
                   LIB3431-050-P1-N1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   279
E value
                   1.0e-24
Match length
                   54
                   93
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   402149
Seq. No.
                   LIB3431-050-P1-N1-A9
Seq. ID
Method
                   BLASTX
                   g2499417
NCBI GI
                   277
BLAST score
                   1.0e-24
E value
Match length
                   62
                   82
% identity
NCBI Description
                   GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
                   >gi 1085826 pir S49248 H-protein - Flaveria anomala
                   >gi 547558 emb CAA85761 (Z37524) H-protein [Flaveria
                   anomala]
                   402150
Seq. No.
Seq. ID
                   LIB3431-050-P1-N1-B10
Method
                   BLASTN
                   g20262
NCBI GI
                   146
BLAST score
                   2.0e-76
E value
Match length
                   274
% identity
                   89
                  O.sativa light-induced mRNA
NCBI Description
                   402151
Seq. No.
                   LIB3431-050-P1-N1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4587570
BLAST score
                   144
                   8.0e-09
E value
                   66
Match length
% identity
                   (AC006550) Strong similarity to gi 2244833 centromere
NCBI Description
                   protein homolog from Arabidopsis thaliana chromosome 4
                   contig gb_Z97337. ESTs gb_T20765 and gb_AA586277 come from
```

this gene Seq. No. 402152 Seq. ID LIB3431-050-P1-N1-B2 Method BLASTX NCBI GI g115787 480 BLAST score 3.0e-48E value Match length 92 99 % identity CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_ (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] 402153 Seq. No. Seq. ID LIB3431-050-P1-N1-B5 Method BLASTX NCBI GI g1429226 BLAST score 228 1.0e-18 E value 47 Match length 85 % identity (X98861) TFIIA [Arabidopsis thaliana] NCBI Description Seq. No. 402154 LIB3431-050-P1-N1-B8 Seq. ID Method BLASTX NCBI GI g5729802 452 BLAST score E value 6.0e-45 91 Match length 89 % identity NCBI Description similar to S. pombe dim1+ >gi_2565275 (AF023611) Dim1p homolog [Homo sapiens] 402155 Seq. No. LIB3431-050-P1-N1-C1 Seq. ID BLASTX Method g3236242 NCBI GI 334 BLAST score E value 4.0e-31 98 Match length % identity 69 (AC004684) putative ribosomal protein L36 [Arabidopsis NCBI Description thaliana]

Seq. No. 402156

Seq. ID LIB3431-050-P1-N1-C11

Method BLASTX
NCBI GI g131176
BLAST score 203
E value 6.0e-16
Match length 47
% identity 87

NCBI Description PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR

NCBI GI

```
barley >gi 19087 emb_CAA68782 (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163 prf_1413233A
                   10.8kD photosystem I protein [Hordeum vulgare var.
                   distichum]
Seq. No.
                   402157
Seq. ID
                   LIB3431-050-P1-N1-C12
Method
                   BLASTX
NCBI GI
                   g115813
BLAST score
                   201
E value
                   1.0e-15
Match length
                   46
% identity
                   80
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                   CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                   402158
                   LIB3431-050-P1-N1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g289920
BLAST score
                   267
                    3.0e-23
E value
Match length
                   51
% identity
                    (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
Seq. No.
                   402159
                   LIB3431-050-P1-N1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2492487
                   330
BLAST score
E value
                   1.0e-30
Match length
                   76
% identity
                   87
                   14-3-3-LIKE PROTEIN B (14-3-3B) >qi 1070354 emb CAA63658
NCBI Description
                    (X93170) Hv14-3-3b [Hordeum vulgare]
                   402160
Seq. No.
                   LIB3431-050-P1-N1-C9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g218207
BLAST score
                   124
E value
                   2.0e-63
Match length
                   231
                   88
% identity
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                   p0SSS1139
                   402161
Seq. No.
Seq. ID
                   LIB3431-050-P1-N1-D1
Method
                   BLASTN
```

(PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)

>qi 72683 pir F1BH4 photosystem I chain IV precursor -

g3868755

```
BLAST score
                   150
E value
                  8.0e-79
Match length
                  250
% identity
                   91
                  Oryza sativa CatC gene for catalase, complete cds
NCBI Description
                   402162
Seq. No.
                  LIB3431-050-P1-N1-D10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3789949
BLAST score
                   186
                   1.0e-100
E value
                   298
Match length
                   91
% identity
                  Oryza sativa translation initiation factor (GOS2) mRNA,
NCBI Description
                   complete cds
                   402163
Seq. No.
                  LIB3431-050-P1-N1-D11
Seq. ID
Method
                  BLASTX
                   g2072555
NCBI GI
                   333
BLAST score
                   5.0e-31
E value
                   62
Match length
                   97
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   402164
Seq. No.
                   LIB3431-050-P1-N1-D4
Seq. ID
Method
                   BLASTX
                   g4680212
NCBI GI
                   187
BLAST score
                   7.0e-14
E value
                   53
Match length
                  66.
% identity
                   (AF114171) hypothetical protein [Sorghum bicolor]
NCBI Description
                   402165
Seq. No.
                   LIB3431-050-P1-N1-D7
Seq. ID
                   BLASTX
Method
                   g5541681
NCBI GI
                   212
BLAST score
                   7.0e-17
E value
                   92
Match length
                   55
% identity
                   (AL096859) putative protein [Arabidopsis thaliana]
NCBI Description
                   402166
Seq. No.
                   LIB3431-050-P1-N1-E1
Seq. ID
                   BLASTX
Method
                   q1835731
NCBI GI
BLAST score
                   187
                   1.0e-28
E value
                   88
Match length
```

% identity

```
(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                  402167
Seq. No.
                  LIB3431-050-P1-N1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g11957
BLAST score
                  323
E value
                  0.0e+00
Match length
                  431
% identity
                  99
NCBI Description Rice complete chloroplast genome
                  402168
Seq. No.
                  LIB3431-050-P1-N1-E9
Seq. ID
                  BLASTN
Method
                  g20181
NCBI GI
                  43
BLAST score
                  6.0e-15
E value
                  146
Match length
                  82
% identity
                  Rice cab2R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
                  402169
Seq. No.
                  LIB3431-050-P1-N1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g21839
BLAST score
                  340
                  8.0e-32
E value
                  73
Match length
                  93
% identity
                  (X57952) phosphoribulokinase [Triticum aestivum]
NCBI Description
                  402170
Seq. No.
                  LIB3431-050-P1-N1-F12
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3273244
BLAST score
                  46
                  1.0e-16
E value
Match length
                  62
                  94
% identity
NCBI Description Oryza sativa DNA for NLS receptor, complete cds
Seq. No.
                  402171
                  LIB3431-050-P1-N1-F3
Seq. ID
                  BLASTX
Method
                  g1172555
NCBI GI
BLAST score
                  184
                  2.0e-13
E value
                  61
Match length
                  57
% identity
                  34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN
NCBI Description
                  (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC)
                  (POM 34) >gi_629720_pir__S46936 34K porin - potato
                  >gi 1076682 pir A55364 porin (clone pPOM-34) - potato
                  mitochondrion >gi 516166 emb CAA56599 (X80386) 34 kDA
                  porin [Solanum tuberosum]
```

```
402172
Seq. No.
                  LIB3431-050-P1-N1-F8
Seq. ID
Method
                  BLASTX
                  g710308
NCBI GI
BLAST score
                  174
E value
                  2.0e-12
Match length
                  49
                  67
% identity
NCBI Description
                  (U11693) victorin binding protein [Avena sativa]
                  402173
Seq. No.
Seq. ID
                  LIB3431-050-P1-N1-G1
Method
                  BLASTN
NCBI GI
                  g6006355
BLAST score
                  265
                  1.0e-147
E value
                  360
Match length
                  93
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.
                  402174
                  LIB3431-050-P1-N1-G10
Seq. ID
                  BLASTX
Method
                  g4680338
NCBI GI
                  194
BLAST score
E value
                  8.0e-15
                  51
Match length
                  73
% identity
                  (AF128457) hypothetical protein [Oryza sativa subsp.
NCBI Description
                  indica]
Seq. No.
                  402175
                  LIB3431-050-P1-N1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1362615
BLAST score
                  256
                  6.0e-22
E value
                  99
Match length
                  54
% identity
                  iswi protein - fruit fly (Drosophila melanogaster)
NCBI Description
                  >gi 439197 (L27127) ISWI protein [Drosophila melanogaster]
Seq. No.
                  402176
                  LIB3431-050-P1-N1-G7
Seq. ID
                  BLASTN
Method
                  g20262
NCBI GI
BLAST score
                  78
                  3.0e-36
E value
Match length
                  121
                  92
% identity
NCBI Description O.sativa light-induced mRNA
                  402177
Seq. No.
                  LIB3431-050-P1-N1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2570514
```

E value

8.0e-29

```
BLAST score
                  38
                  5.0e-12
E value
                  42
Match length
% identity
                  98
NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
                  402178
Seq. No.
                  LIB3431-050-P1-N1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g421916
BLAST score
                  168
                  1.0e-11
E value
Match length
                  31
                  100
% identity
                  chlorophyll a/b-binding protein - English ivy (fragment)
NCBI Description
                  >gi_12582_emb_CAA48410_ (X68333) light harvesting
                  chlorophyll a /b binding protein [Hedera helix]
                  402179
Seq. No.
                  LIB3431-050-P1-N1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  72
                  3.0e-32
E value
Match length
                  174
% identity
                  85
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
                  402180
Seq. No.
Seq. ID
                  LIB3431-050-P1-N1-H5
Method
                  BLASTN
NCBI GI
                  g2570514
BLAST score
                  240
                  1.0e-132
E value
                  335
Match length
% identity
                  93
NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
                  402181
Seq. No.
                  LIB3431-050-P1-N1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  135
E value
                  6.0e-70
                  183
Match length
                  93
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                  cds
                  402182
Seq. No.
                  LIB3431-051-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  313
```

E value

5.0e-50

```
62
Match length
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  402183
Seq. No.
                  LIB3431-051-P1-K1-A3
Seq. ID
Method
                  BLASTN
                  g20177
NCBI GI
BLAST score
                  102
E value
                  2.0e-50
Match length
                  123
% identity
                  Rice cab1R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
                  402184
Seq. No.
                  LIB3431-051-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5103807
BLAST score
                  349
                  5.0e-33
E value
                  93
Match length
                  69
% identity
                   (AC007591) Contains similarity to gb AF014403 type-2
NCBI Description
                  phosphatidic acid phosphatase alpha-2 (PAP2_a2) from Homo
                  sapiens. ESTs gb T88254 and gb AA394650 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  402185
Seq. ID
                  LIB3431-051-P1-K1-A6
Method
                  BLASTN
NCBI GI
                  g5456937
BLAST score
                  54
E value
                  1.0e-21
Match length
                  54
                  100
% identity
                  Oryza sativa rps9 mRNA for ribosomal protein S9, complete
NCBI Description
                  cds
                  402186
Seq. No.
Seq. ID
                  LIB3431-051-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g3885886
BLAST score
                  642
                  2.0e-67
E value
Match length
                  125
% identity
                  100
NCBI Description
                  (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
Seq. No.
                  402187
                  LIB3431-051-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3913018
BLAST score
                  494
```

```
Match length
                  101
% identity
                  99
NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                  (ALDP) >gi 218155_dbj_BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  402188
Seq. No.
                  LIB3431-051-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                  450
E value
                  8.0e-45
Match length
                  108
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
                  402189
Seq. No.
                  LIB3431-051-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  517
                  1.0e-52
E value
                  107
Match length
                  93
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  402190
Seq. No.
                  LIB3431-051-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  534
                  8.0e-55
E value
                  102
Match length
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  402191
                  LIB3431-051-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q606817
BLAST score
                  489
                  2.0e-49
E value
Match length
                  93
% identity
                  (U08404) carbonic anhydrase [Oryza sativa]
NCBI Description
                  >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic
                  anhydrase 3 [Oryza sativa]
Seq. No.
                  402192
                  LIB3431-051-P1-K1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2624327
BLAST score
                  141
                  2.0e-73
E value
                  201
Match length
```

Seq. No.

Seq. ID

NCBI GI

BLAST score

Method

```
% identity
                  Oryza sativa mRNA for glycine rich RNA-binding protein 2
NCBI Description
                  (OsGRP2)
                  402193
Seq. No.
                  LIB3431-051-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2499932
BLAST score
                  479
                  2.0e-48
E value
Match length
                  105
% identity
                  ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305
NCBI Description
                  (U22442) adenine phosphoribosyltransferase form 1 [Triticum
                  aestivum]
                  402194
Seq. No.
                  LIB3431-051-P1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2982453
BLAST score
                  474
                  9.0e-48
E value
                  109
Match length
                  83
% identity
                  (AL022223) fructose-bisphosphate aldolase-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  402195
Seq. No.
                  LIB3431-051-P1-K1-C10
Seq. ID
                  BLASTX
Method
                  g124224
NCBI GI
BLAST score
                  511
                  9.0e-55
E value
                  121
Match length
                  90
% identity
                  INITIATION FACTOR 5A-1 (EIF-5A) (EIF-4D)
NCBI Description
                  >gi_100345_pir__S21060 translation initiation factor eIF-5A
                  - common tobacco >gi_19887_emb_CAA45105_ (X63543)
                  eukaryotic initiatin factor 5A (3) [Nicotiana tabacum]
                  402196
Seq. No.
                  LIB3431-051-P1-K1-C11
Seq. ID
Method
                  BLASTX
                  g2492514
NCBI GI
                  525
BLAST score
                  1.0e-53
E value
                  110
Match length
                  94
% identity
                  CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
NCBI Description
                  >gi_1483215_emb_CAA68141_ (X99808) chloroplast FtsH
                  protease [Arabidopsis thaliana]
                  402197
```

LIB3431-051-P1-K1-C12

BLASTX

272

q115825

Method

BLASTN

```
7.0e-24
E value
Match length
                  56
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 3C PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-3C) (LHCP) >gi_72734_pir__CDT03C chlorophyll
                  a/b-binding protein 3C precursor - tomato
                  >gi_224932_prf__1204205G protein 3C,chlorophyll binding
                  [Lycopersicon esculentum]
Seq. No.
                  402198
Seq. ID
                  LIB3431-051-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g2130069
BLAST score
                  513
E value
                  3.0e-52
Match length
                  115
                  85
% identity
                  catalase (EC 1.11.1.6) catA - rice
NCBI Description
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
Seq. No.
                  402199
                  LIB3431-051-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914603
BLAST score
                  468
                  4.0e-47
E value
Match length
                  87
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                  (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  activase [Oryza sativa]
                  402200
Seq. No.
                  LIB3431-051-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  ig3075488
BLAST score
                  718.
E value
                  4.0e-76
                  143
Match length
% identity
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  402201
                  LIB3431-051-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                  464
E value
                  2.0e-46
Match length
                  112
% identity
                  79
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
Seq. No.
                  402202
                  LIB3431-051-P1-K1-D11
Seq. ID
```

NCBI GI

g132166

```
NCBI GI
                  g304219
BLAST score
                  80
E value
                  4.0e-37
Match length
                  179
% identity
                  86
                  Hordeum vulgare chloroplast photosystem I PSK-I subunit
NCBI Description
                  mRNA, complete cds
                  402203
Seq. No.
                  LIB3431-051-P1-K1-D12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5106774
BLAST score
                  63
                  7.0e-27
E value
                  188
Match length
                  84
% identity
                  Hordeum vulgare ribosomal protein S12 (rps12) mRNA,
NCBI Description
                  complete cds
                  402204
Seq. No.
Seq. ID
                  LIB3431-051-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g4585882
BLAST score
                  532
                  2.0e-54
E value
Match length
                  119
                  80
% identity
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                  402205
Seq. No.
                  LIB3431-051-P1-K1-D3
Seq. ID
Method
                  BLASTN
                  g3789951
NCBI GI
BLAST score
                  111
                  2.0e-55
E value
                  252
Match length
                  92
% identity
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  402206
Seq. No.
Seq. ID
                  LIB3431-051-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  g20181
                  123
BLAST score
                  1.0e-62
E value
Match length
                  130
% identity
NCBI Description
                  Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
                  402207
Seq. No.
Seq. ID
                  LIB3431-051-P1-K1-D5
Method
                  BLASTX
```

```
BLAST score
                  160
E value
                  6.0e-11
Match length
                  31
                  87
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                  >gi 81660 pir S04048 ribulose-bisphosphate carboxylase
                  activase precursor - Arabidopsis thaliana
                  >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 -
                  473) [Arabidopsis thaliana]
Seq. No.
                  402208
Seq. ID
                  LIB3431-051-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  150
                  3.0e-10
E value
                  30
Match length
                  90
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  402209
Seq. No.
                  LIB3431-051-P1-K1-D7
Seq. ID
Method
                  BLASTN -
NCBI GI
                  g3377792
BLAST score
                  106
                  2.0e-52
E value
                  309
Match length
                  84
% identity
                  Oryza sativa ribulose-1,5-bisphosphate
NCBI Description
                  carboxylase/oxygenase activase (rca) mRNA, complete cds
Seq. No.
                  402210
                  LIB3431-051-P1-K1-D8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  36
E value
                  1.0e-10
                  47
Match length
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
Seq. No.
                  402211
                  LIB3431-051-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131388
BLAST score
                  264
                  5.0e-23
E value
                  108
Match length
% identity
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi 21844 emb CAA40670 (X57408)
```

```
aestivuml
Seq. No.
                   402212
                   LIB3431-051-P1-K1-E1
Seq. ID
Method
                   BLASTX
                   q320618
NCBI GI
                   205
BLAST score
E value
                   2.0e-16
                   68
Match length
                   66
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611 prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza satīva]
                   402213
Seq. No.
                   LIB3431-051-P1-K1-E10
Seq. ID
Method '
                   BLASTX
NCBI GI
                   g3345477
BLAST score
                   576
                   1.0e-59
E value
Match length
                   111
                   98
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
Seq. No.
                   402214
                   LIB3431-051-P1-K1-E11
Seq. ID
Method
                   BLASTX
                   g115772
NCBI GI
BLAST score
                   523
                   2.0e-53
E value
                   99
Match length
                   100
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding
                   protein 1R precursor - rice >gi_20178_emb_CAA32108
                   (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                   [Oryza sativa]
                   402215
Seq. No.
                   LIB3431-051-P1-K1-E12
Seq. ID
Method
                   BLASTX
                   g671740
NCBI GI
BLAST score
                   420
                   4.0e-41
E value
Match length
                   78
% identity
                   97
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   402216
Seq. No.
                   LIB3431-051-P1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2961176
```

33kDa oxygen evolving protein of photosystem II [Triticum

356

BLAST score

```
E value
                     6.0e-34
  Match length
                     104
                     73
  % identity
  NCBI Description
                     (AF050674) ribosomal protein L27 precursor [Oryza sativa]
  Seq. No.
                     402217
                     LIB3431-051-P1-K1-E5
  Seq. ID
  Method
                     BLASTX
NCBI GI
                     q4512707
  BLAST score
                     419
  E value.
                     5.0e-41
  Match length
                     151
  % identity
  NCBI Description
                     (AC006569) hypothetical protein [Arabidopsis thaliana]
  Seq. No.
                     402218
                     LIB3431-051-P1-K1-E6
  Seq. ID
                     BLASTN
  Method
  NCBI GI
                     g505134
  BLAST score
                     63
  E value
                     5.0e-27
                     163
  Match length
  % identity
                     85
                    Rice mRNA for ferredoxin, complete cds
  NCBI Description
                     402219
  Seq. No.
                     LIB3431-051-P1-K1-E8
  Seq. ID
  Method
                     BLASTX
                     g320618
  NCBI GI
  BLAST score
                     303
  E value
                     4.0e-28
  Match length
                     61
  % identity
                     92
                     chlorophyll a/b-binding protein I precursor - rice
  NCBI Description
                     >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                     chlorophyll a/b-binding protein [Oryza sativa]
                     >gi_227611_prf_:1707316A chlorophyll a/b binding protein 1
                     [Oryza sativa]
                     402220
  Seq. No.
                     LIB3431-051-P1-K1-E9
  Seq. ID
  Method
                     BLASTX
                     g1617197
  NCBI GI
  BLAST score
                     292
  E value
                     2.0e-26
                     76
  Match length
                     74
  % identity
  NCBI Description
                     (Z72488) CP12 [Nicotiana tabacum]
  Seq. No.
                     402221
  Seq. ID
                     LIB3431-051-P1-K1-F1
  Method
                     BLASTX
                     q115808
  NCBI GI
                     472
  BLAST score
                     1.0e-47
  E value
                     92
  Match length
```

% identity

```
CHLOROPHYLL A-B BINDING PROTEIN 91R PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-91R) (LHCP) >gi_72732_pir__CDPJ91 chlorophyll a/b-binding protein 91R precursor - petunia
                   >gi_20487_emb_CAA26209_ (X02356) cab 91R precursor polypeptide (aa -34 to 233) [Petunia sp.]
Seq. No.
                   402222
                   LIB3431-051-P1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
                   1.0e-19
E value
Match length
                   44
                   100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   402223
                   LIB3431-051-P1-K1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g320618
                   542
BLAST score
E value
                   2.0e-56
Match length
                   133
% identity
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   402224
                   LIB3431-051-P1-K1-F3
Seq. ID
Method
                   BLASTN
                   g3789951
NCBI GI
                   254
BLAST score
E value
                   1.0e-141
                   297
Match length
% identity
                   Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
                   402225
Seq. No.
                   LIB3431-051-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3913018
                   565
BLAST score
                   2.0e-58
E value
                   116
Match length
% identity
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                   aldolase [Oryza sativa]
```

Seq. No.

```
LIB3431-051-P1-K1-F7
Seq. ID
                  BLASTX
Method
                  g4582787
NCBI GI
BLAST score
                  373
E value
                  5.0e-36
Match length
                  96
                  79
% identity
                   (AJ012281) adenosine kinase [Zea mays]
NCBI Description
                  402227
Seq. No.
                  LIB3431-051-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115813
BLAST score
                  304
                  1.0e-27
E value
                  93
Match length -
                   69
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >qi 19182 emb CAA33330 (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  402228
Seq. No.
                  LIB3431-051-P1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2306981
BLAST score
                  170
                   3.0e-12
E value
Match length
                  78
% identity
                   45
                   (AF010321) photosystem I antenna protein [Oryza sativa]
NCBI Description
                   402229
Seq. No.
                  LIB3431-051-P1-K1-G1
Seq. ID
Method
                  BLASTX
                  g3126854
NCBI GI
BLAST score
                   348
                   5.0e-33
E value
Match length
                   69
% identity
                   97
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   402230
Seq. No.
                  LIB3431-051-P1-K1-G10
Seq. ID
Method
                  BLASTX
                  q4091129
NCBI GI
BLAST score
                  198
                   4.0e-15
E value
Match length
                  154
                   31
% identity
                   (AF050165) protein phosphatase 2A regulatory subunit PR59;
NCBI Description
                   PP2A regulatory subunit PR59 [Mus musculus]
                  402231
Seq. No.
                  LIB3431-051-P1-K1-G11
Seq. ID
Method
                  BLASTX
                  q3126854
NCBI GI
```

BLAST score

```
E value
                  2.0e-55
Match length
                  112
                  92
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  402232
Seq. No.
                  LIB3431-051-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  268
E value
                  9.0e-43
Match length
                  109
                  82
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  402233
Seq. ID
                  LIB3431-051-P1-K1-G3
Method
                  BLASTX
                  g5523862
NCBI GI
BLAST score
                  367
E value
                  3.0e-35
Match length
                  99
% identity
                  (AF085169) LRk-type protein [Triticum aestivum]
NCBI Description
                  402234
Seq. No.
                  LIB3431-051-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3789954
BLAST score
                  458
                  1.0e-45
E value
                  109
Match length
% identity
NCBI Description
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                  sativa]
                  402235
Seq. No.
                  LIB3431-051-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  230
                  3.0e-19
E value
Match length
                  76
% identity
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
```

Seq. No.

```
LIB3431-051-P1-K1-G7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  35
E value
                  3.0e-10
                  35
Match length
                  100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                  402237
Seq. No.
                  LIB3431-051-P1-K1-H11
Seq. ID
Method
                  BLASTX
                  g133936
NCBI GI
BLAST score
                  674
                  5.0e-71
E value
Match length
                  134
                  100
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70867_pir__R3RZ3
NCBI Description
                  ribosomal protein S3 - rice chloroplast
                  >qi 12025 emb CAA33934 (X15901) ribosomal protein S3
                  [Oryza sativa] >gi_226646_prf__1603356BW ribosomal protein
                  S3 [Oryza sativa]
                  402238
Seq. No.
                  LIB3431-051-P1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g320618
BLAST score
                  241
                  1.0e-20
E value
Match length
                  63
                  76
% identity
                  chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                  >gi 218172 dbj BAA00536 (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  402239
                  LIB3431-051-P1-K1-H2
Seq. ID
                  BLASTX
Method
                  g1519251
NCBI GI
                  490
BLAST score
                  9.0e-50
E value
Match length
                  101
                  99
% identity
                  (U65957) GF14-c protein [Oryza sativa]
NCBI Description
                  402240
Seq. No.
                  LIB3431-051-P1-K1-H3
Seq. ID
                  BLASTX
Method
                  g417260
NCBI GI
BLAST score
                  248
                  3.0e-21
E value
                  105
Match length
% identity
                  50
NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
                  lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
```

Match length

60

light-regulated gene [Oryza sativa]

```
Seq. No.
                  402241
Seq. ID
                  LIB3431-051-P1-K1-H4
Method
                  BLASTN
NCBI GI
                  g3345476
BLAST score
                  260
E value
                  1.0e-144
Match length
                  282
% identity
                  99
NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds
                  402242
Seq. No.
                  LIB3431-051-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4678947
BLAST score
                  353
                  2.0e-33
E value
                  101
Match length
                  65
% identity
                 (AL049711) putative protein [Arabidopsis thaliana]
NCBI Description
                  402243
Seq. No.
                  LIB3431-051-P1-N1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170606
BLAST score
                  159
E value
                  1.0e-10
                  49
Match length
                  65
% identity
                  ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                  >gi 629863 pir S45634 adenylate kinase (EC 2.7.4.3),
                  chloroplast - maize >gi 3114421 pdb 1ZAK A Chain A,
                  Adenylate Kinase From Maize In Complex With The Inhibitor
                  P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)
                  >gi 3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize
                  In Complex With The Inhibitor
                  P1, P5-Bis (Adenosine-5'-) pentaphosphate (Ap5a)
Seq. No.
                  402244
                  LIB3431-051-P1-N1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  164
                  4.0e-87
E value
                  296
Match length
                  89
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
Seq. No.
                  402245
                  LIB3431-051-P1-N1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2864617
BLAST score
                  179
                  4.0e-13
E value
```

NCBI Description

```
% identity
NCBI Description
                   (AL021811) H+-transporting ATP synthase chain9 - like
                  protein [Arabidopsis thaliana] >gi_5730141_emb_CAB52473.1
                   (AJ245574) ATP synthase beta chain precursor (subunit II)
                   [Arabidopsis thaliana]
                  402246
Seq. No.
Seq. ID
                  LIB3431-051-P1-N1-A2
Method
                  BLASTX
NCBI GI
                  g693920
BLAST score
                  356
E value
                  8.0e-34
Match length
                   68
                  100
% identity
NCBI Description
                   (U21113) chlorophyll a/b binding protein [Solanum
                  tuberosum]
                  402247
Seq. No.
                  LIB3431-051-P1-N1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5456937
BLAST score
                  329
E value
                  0.0e + 00
Match length
                  329
% identity
                  100
NCBI Description
                  Oryza sativa rps9 mRNA for ribosomal protein S9, complete
                  402248
Seq. No.
                  LIB3431-051-P1-N1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4508079
BLAST score
                  350
                   4.0e-33
E value
                  95
Match length
% identity
                   66
                   (AC005882) 66284 [Arabidopsis thaliana]
NCBI Description
                   402249
Seq. No.
Seq. ID
                  LIB3431-051-P1-N1-A9
Method
                  BLASTN
NCBI GI
                  g18266
BLAST score
                  35
E value
                   3.0e-10
Match length
                   47
% identity
NCBI Description
                  C.stellata mRNA for ribosomal protein L27
Seq. No.
                  402250
Seq. ID
                  LIB3431-051-P1-N1-B1
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  537
E value
                   5.0e-55
Match length
                  99
                   99
% identity
```

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

Seq. No.

Seq. ID

Method

402255

BLASTX

LIB3431-051-P1-N1-B5

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

```
Seq. No.
                  402251
                  LIB3431-051-P1-N1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3036951
BLAST score
                  323
                  5.0e-30
E value
                  63
Match length
                  98
% identity
                  (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
Seq. No.
                  402252
                  LIB3431-051-P1-N1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4538963
BLAST score
                  169
                  5.0e-12
E value
                  48
Match length
% identity
NCBI Description
                  (AL049488) chlorophyll a/b-binding protein-like
                  [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129 1
                  (AF134129) Lhcb5 protein [Arabidopsis thaliana]
Seq. No.
                  402253
Seq. ID
                  LIB3431-051-P1-N1-B12
Method
                  BLASTX
NCBI GI
                  g733456
BLAST score
                  335
                                                              · .
                  2.0e-31
E value
Match length
                  73
% identity
NCBI Description
                  (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
                  [Zea mays]
Seq. No.
                  402254
Seq. ID
                  LIB3431-051-P1-N1-B4
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  134
E value
                  4.0e-69
Match length
                  354
% identity
                  85
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
```

E value

Match length

7.0e-16

88

```
g3345477
NCBI GI
                   172
BLAST score
E value
                   3.0e-12
Match length
                   32
                   97
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                   402256
Seq. No.
Seq. ID
                   LIB3431-051-P1-N1-B6
Method
                   BLASTN
NCBI GI
                   g2624327
BLAST score
                   240
E value
                   1.0e-132
Match length
                   284
% identity
                   96
NCBI Description
                   Oryza sativa mRNA for glycine rich RNA-binding protein 2
                   (OsGRP2)
                   402257
Seq. No.
Seq. ID
                   LIB3431-051-P1-N1-B8
Method
                   BLASTX
NCBI GI
                   q2440046
BLAST score
                   163
E value
                   3.0e-11
Match length
                   40
                   70
% identity
NCBI Description
                   (AJ001294) major intrinsic protein PIPC [Craterostigma
                   plantagineum]
                   402258
Seq. No.
Seq. ID
                   LIB3431-051-P1-N1-C1
Method
                   BLASTN
NCBI GI
                   g20191
BLAST score
                   215
E value
                   1.0e-117
Match length
                   279
% identity
                   9.4
NCBI Description
                   O.sativa mRNA for catalase
                   402259
Seq. No.
Seq. ID
                   LIB3431-051-P1-N1-C10
Method
                   BLASTX
                   g5734790
NCBI GI
BLAST score
                   373
E value
                   9.0e-36
Match length
                   80
                   90
% identity
NCBI Description
                   (AC007980) ATP-dependent metalloprotease [Arabidopsis
                   thaliana]
                   402260
Seq. No.
Seq. ID
                   LIB3431-051-P1-N1-C11
Method
                   BLASTN
                   g20177
NCBI GI
BLAST score
                   44
```

```
% identity
                  Rice cab1R gene for light harvesting chlorophyll
NCBI Description
                  a/b-binding protein
                  402261
Seq. No.
Seq. ID
                  LIB3431-051-P1-N1-C12
Method
                  BLASTX
NCBI GI
                  q3036951
BLAST score
                  323
                  5.0e-30
E value
Match length
                  63
% identity
                  (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                  [Nicotiana sylvestris]
Seq. No.
                  402262
                  LIB3431-051-P1-N1-C6
Seq. ID
Method
                  BLASTN
                  g3377792
NCBI GI
BLAST score
                  94
E value
                  1.0e-45
Match length
                  149
                  92
% identity
                  Oryza sativa ribulose-1,5-bisphosphate
NCBI Description
                  carboxylase/oxygenase activase (rca) mRNA, complete cds
Seq. No.
                  402263
                  LIB3431-051-P1-N1-C7
Seq. ID
Method
                  BLASTN
                  g3075487
NCBI GI
                  244
BLAST score
E value
                  1.0e-135
Match length
                  260
% identity
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  402264
                  LIB3431-051-P1-N1-D1
Seq. ID
Method
                  BLASTX
                  q430947
NCBI GI
BLAST score
                  198
E value
                  4.0e-15
                  63
Match length
                  57
% identity
                  (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                  [Arabidopsis thaliana]
                  402265
Seq. No.
Seq. ID
                  LIB3431-051-P1-N1-D10
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                  363
E value
                  1.0e-34
Match length
                  77
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
```

E value

Match length % identity

NCBI Description



[Zea mays]

```
Seq. No.
                  402266
Seq. ID
                  LIB3431-051-P1-N1-D11
Method
                  BLASTX
                  g5106775
NCBI GI
BLAST score
                  363
                  1.0e-34
E value
                  71
Match length
                  96
% identity
                   (AF067732) ribosomal protein S12 [Hordeum vulgare]
NCBI Description
                  402267
Seq. No.
                  LIB3431-051-P1-N1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g5106775
BLAST score
                  259
                  2.0e-22
E value
                  52
Match length
                  92
% identity
                  (AF067732) ribosomal protein S12 [Hordeum vulgare]
NCBI Description
                  402268
Seq. No.
                  LIB3431-051-P1-N1-D4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g132166
BLAST score
                  160
E value
                  5.0e-11
Match length
                  31
                  87
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
NCBI Description
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                  >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase
                  activase precursor - Arabidopsis thaliana
                  >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 -
                   473) [Arabidopsis thaliana]
                  402269
Seq. No.
Seq. ID
                  LIB3431-051-P1-N1-D5
Method
                  BLASTX
NCBI GI
                  q167097
                  142
BLAST score
                  7.0e-09
E value
Match length
                  30
% identity
                  83
                   (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                   [Hordeum vulgare]
                   402270
Seq. No.
Seq. ID
                  LIB3431-051-P1-N1-D6
Method
                  BLASTN
NCBI GI
                  g3377792
                  97
BLAST score
```

Oryza sativa ribulose-1,5-bisphosphate

4.0e-47

267

carboxylase/oxygenase activase (rca) mRNA, complete cds 402271 Seq. No. LIB3431-051-P1-N1-D8 Seq. ID Method BLASTN NCBI GI g416266 211 BLAST score 1.0e-115 E value 269 Match length 94 % identity NCBI Description Rice mRNA for oxygen-evolving protein, partial sequence 402272 Seq. No. LIB3431-051-P1-N1-D9 Seq. ID BLASTX Method g733454 NCBI GI BLAST score 158 8.0<u>e-11</u> E value 45 Match length 69 % identity (U23188) chlorophyll a/b-binding apoprotein CP26 precursor NCBI Description [Zea mays] 402273 Seq. No. LIB3431-051-P1-N1-E1 Seq. ID BLASTX Method q2961176 NCBI GI BLAST score 322 7.0e-30 E value 81 Match length 80 % identity (AF050674) ribosomal protein L27 precursor [Oryza sativa] NCBI Description Seq. No. 402274 LIB3431-051-P1-N1-E10 Seq. ID Method BLASTX g3928140 NCBI GI BLAST score 166 E value 1.0e-11 Match length 34 % identity 88 (AJ131044) chlorophyll a/b binding protein [Cicer NCBI Description arietinum] 402275 Seq. No. LIB3431-051-P1-N1-E5 Seq. ID BLASTX Method g1070408 NCBI GI BLAST score 166 E value 1.0e-11 Match length 47 74 % identity NCBI Description ferredoxin [2Fe-2S] I - rice

402276

BLASTX

LIB3431-051-P1-N1-E7

Seq. No.

Seq. ID

Method

```
q115786
 NCBI GI
 BLAST score
                    202
                    8.0e-16
 E value
 Match length
                    52
                    75
 % identity
 NCBI Description
                    CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I
                    CAB) (LHCP) >gi_82680_pir__A29119 chlorophyll a/b-binding
                    protein - maize >gi_22357_emb_CAA68451_ (Y00379) LHCP [Zea
                    mays]
 Seq. No.
                    402277
                    LIB3431-051-P1-N1-E9
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    q5917782
 BLAST score
                    139
 E value
                    2.0e-72
                    228
 Match length
                    89
 % identity
                    Oryza sativa carbonic anhydrase 3 mRNA, complete cds
 NCBI Description
 Seq. No.
                    402278
                    LIB3431-051-P1-N1-F10
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3036949
 BLAST score
                    262
                    7.0e-23
 E value
 Match length
                    53
                    94
 % identity
                    (AB012638) light harvesting chlorophyll a/b-binding protein
 NCBI Description
                    [Nicotiana sylvestris]
 Seq. No.
                    402279
 Seq. ID
                    LIB3431-051-P1-N1-F2
 Method
                    BLASTN
 NCBI GI
                    g3789951
 BLAST score
                    136
 E value
                    2.0e-70
Match length
                    311
                    99
 % identity
                    Oryza sativa chlorophyll a/b-binding protein presursor
 NCBI Description
                    (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                    complete cds
                    402280
 Seq. No.
                    LIB3431-051-P1-N1-F8
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g551047
 BLAST score
                    241.
 E value
                    2.0e-20
                    50
 Match length
 % identity
                    (X79277) type II LHCI [Lolium temulentum]
 NCBI Description
```

Seq. No. 402281

Seq. ID LIB3431-051-P1-N1-F9

Method BLASTN NCBI GI g2306980

```
BLAST score
                   180
                   9.0e-97
E value
Match length
                   240
% identity
                   94
NCBI Description
                   Oryza sativa photosystem I antenna protein (Lhca) mRNA,
                   complete cds
                   402282
Seq. No.
Seq. ID
                   LIB3431-051-P1-N1-G10
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   270
                   1.0e-23
E value
Match length
                   52
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   402283
Seq. No.
                   LIB3431-051-P1-N1-G11
Seq. ID
Method
                   BLASTX
                   g671740
NCBI GI
BLAST score
                   170
E value
                   5.0e-12
Match length
                   41
% identity
                   83
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
Seq. No.
                   402284
                   LIB3431-051-P1-N1-G12
Seq. ID
Method
                   BLASTX
                   g132105
NCBI GI
BLAST score
                   167
E value
                   1.0e-11
Match length
                   33
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   402285
Seq. ID
                   LIB3431-051-P1-N1-G2
Method
                   BLASTX
NCBI GI
                   g5679314
BLAST score
                   317
E value
                   3.0e-29
Match length
                   100
% identity
                   (AF164021) receptor kinase [Oryza sativa]
NCBI Description
```

Seq. No.

```
Seq. ID
                  LIB3431-051-P1-N1-G3
Method
                  BLASTN
NCBI GI
                  q3789953
BLAST score
                  39
E value
                  1.0e-12
Match length
                  43
                  98
% identity
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein precursor
                   (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                   402287
Seq. No.
Seq. ID
                  LIB3431-051-P1-N1-G6
Method
                  BLASTX
NCBI GI
                  a1617197
BLAST score
                  225
                   2.0e-18
E value
                  47
Match length
                  87
% identity
                   (Z72488) CP12 [Nicotiana tabacum]
NCBI Description
                  402288
Seq. No.
                  LIB3431-051-P1-N1-G8
Seq. ID
Method
                  BLASTN
                  g20369
NCBI GI
BLAST score .
                  292
E value
                   1.0e-163
Match length
                  308
                   99
% identity
                  Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
NCBI Description
                   synthetase (EC 6.3.1.2) (clone lambda-GS31)
                  >gi 2170909 dbj E02681 E02681 cDNA encoding precursor of
                  chloroplast localising glutamine synthetase
                   402289
Seq. No.
                  LIB3431-051-P1-N1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1519250
                  385
BLAST score
                  0.0e + 00
E value
Match length
                   421
                   98
% identity
                  Oryza sativa GF14-c protein mRNA, complete cds
NCBI Description
                   402290
Seq. No.
                  LIB3431-051-P1-N1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g133936
BLAST score
                   610
                   1.0e-63
E value
                  125
Match length
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70867_pir__R3RZ3
NCBI Description
                  ribosomal protein S3 - rice chloroplast
                  >gi 12025 emb CAA33934 (X15901) ribosomal protein S3
                   [Oryza sativa] >gi 226646 prf 1603356BW ribosomal protein
                  S3 [Oryza sativa]
```

```
402291
Seq. No.
                  LIB3431-051-P1-N1-H11
Seq. ID
                  BLASTN
Method
                  g218171
NCBI GI
                  128
BLAST score
                  1.0e-65
E value
                  184
Match length
                  92
% identity
NCBI Description
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
                  a/b binding protein of photosystem II (LHCPII), complete
                  402292
Seq. No.
                  LIB3431-051-P1-N1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2804572
BLAST score
                  186
                  7.0e-14
E value
                  36
Match length
                  94
% identity
NCBI Description
                   (AB006081) chlorophyll a/b-binding protein [Fagus crenata]
Seq. No.
                  402293
                  LIB3431-051-P1-N1-H2
Seq. ID
Method
                  BLASTN
                  q5091597
NCBI GI
BLAST score
                  152
E value
                  8.0e-80
                  252
Match length
                  27
% identity
                  Oryza sativa chromosome 1 BAC 10A19I, complete sequence
NCBI Description
Seq. No.
                  402294
                  LIB3431-051-P1-N1-H5
Seq. ID
Method
                  BLASTX
                  g1174778
NCBI GI
BLAST score
                  215
E value
                  2.0e-17
Match length
                  41
% identity
                  98
                  TRYPTOPHAN SYNTHASE BETA CHAIN 1 (ORANGE PERICARP 1)
NCBI Description
                  >gi_320136_pir__PQ0449 tryptophan synthase (EC 4.2.1.20)
                  beta-1 chain - maize (fragment) >gi 168572 (M76684)
                  tryptophan synthase beta-subunit [Zea mays]
                  402295
Seq. No.
                  LIB3431-052-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g710626
BLAST score
                  188
                  3.0e-14
E value
Match length
                  45
% identity
                   (D30719) ERD15 protein [Arabidopsis thaliana] >gi 3241941
NCBI Description
                   (AC004625) dehydration-induced protein ERD15 [Arabidopsis
                  thaliana] >gi 3894181 (AC005662) ERD15 protein [Arabidopsis
```

Seq. ID

```
thaliana]
                   402296
Seq. No.
                   LIB3431-052-P1-K1-A12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   41
                   6.0e-14
E value
Match length
                   52
                   68
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                   402297
Seq. No.
                   LIB3431-052-P1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q131225
                   308
BLAST score
                   2.0e-28
E value
                   70
Match length
                   87
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                   V) (PSI-L) >gi_100605_pir_ A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
                   402298
Seq. No.
                   LIB3431-052-P1-K1-A8
Seq. ID
                   BLASTX
Method
                   q168643
NCBI GI
                   260
BLAST score
E value
                    7.0e-23
                   83
Match length
                    65
% identity
NCBI Description
                   (L02540) NADPH HC-toxin reductase [Zea mays]
                    402299
Seq. No.
Seq. ID
                   LIB3431-052-P1-K1-B11
Method
                   BLASTN
                    g2062705
NCBI GI
                    36
BLAST score
                    9.0e-11
E value
                    36
Match length
                    100
% identity
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
                    402300
Seq. No.
                   LIB3431-052-P1-K1-B12
Seq. ID
Method
                   BLASTX
                    g3158476
NCBI GI
BLAST score
                    230
                    2.0e-19
E value
                    62
Match length
                    71
% identity
                   (AF067185) aquaporin 2 [Samanea saman]
NCBI Description
                    402301
Seq. No.
```

LIB3431-052-P1-K1-B4

```
Method
                  BLASTX
NCBI GI
                  q131225
BLAST score
                  300
E value
                   8.0e-28
Match length
                   67
                  88
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                   402302
Seq. No.
                  LIB3431-052-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4835588
                   400
BLAST score
E value
                   6.0e-39
                  77
Match length
                                                        100
% identity
NCBI Description
                   (AB027054) nitrilase-like protein [Oryza sativa]
                  402303
Seq. No.
                  LIB3431-052-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4678311
BLAST score
                  212
E value
                   4.0e-17
                   63
Match length
% identity
                   67
                   (AL049655) aquaporin/MIP-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  402304
Seq. No.
                  LIB3431-052-P1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2570494
BLAST score
                  109
E value
                  1.0e-54
Match length
                  140
% identity
                  Oryza sativa glyceralehyde-3-phosphate dehydrogenase
NCBI Description
                  subunit (GAPDH) mRNA, partial cds
Seq. No.
                  402305
                  LIB3431-052-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g416869
BLAST score
                  301
                  2.0e-27
E value
Match length
                  93
                  61
% identity
                  CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYLSERINE
NCBI Description
                  SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                  >gi_303902_dbj_BAA03542_ (D14722) cysteine synthase
                  [Spinacia oleracea]
```

Seq. No.

Method

BLASTX

```
Seq. ID
                   LIB3431-052-P1-K1-C6
Method
                   BLASTX
 NCBI GI
                   g2501189
 BLAST score
                   152
E value
                   2.0e-10
Match length
                   51
 % identity
                   59
NCBI Description
                   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                   >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
Seq. No.
                   402307
Seq. ID
                   LIB3431-052-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g6041792
BLAST score
                   311
E value
                   1.0e-28
Match length
                   127.
% identity
                   52
NCBI Description
                  (AC009755) unknown protein [Arabidopsis thaliana]
Seq. No.
                   402308
Seq. ID
                  LIB3431-052-P1-K1-D11
Method
                   BLASTN
NCBI GI
                   g11957
BLAST score
                   212
E value
                   1.0e-116
Match length
                   316
% identity
                  90
NCBI Description Rice complete chloroplast genome
Seq. No.
                  402309
Seq. ID
                  LIB3431-052-P1-K1-D12
Method
                  BLASTN
NCBI GI
                  q20262
BLAST score
                  254
E value
                  1.0e-141
Match length
                  254
% identity
                  100
NCBI Description O.sativa light-induced mRNA
Seq. No.
                  402310
Seq. ID
                  LIB3431-052-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q2765817
BLAST score
                  163
E value
                  3.0e-11
Match length
                  63
% identity
NCBI Description
                  (Z95352) AtMlo-h1 [Arabidopsis thaliana]
                  >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1
                  [Arabidopsis thaliana]
Seq. No.
                  402311
Seq. ID
                  LIB3431-052-P1-K1-D4
```

NCBI GI

g132105

```
BLAST score
                   629
E value
                   1.0e-65
                                             ٠<u>;</u>.
Match length
                   142
% identity
                   85
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   402312
Seq. ID
                   LIB3431-052-P1-K1-D6
Method
                   BLASTN
NCBI GI
                   g20340
BLAST score
                   90
E value
                   2.0e-43
Match length
                   105
% identity
                   96
NCBI Description
                  Rice rbcS gene for ribulose 1,5-bisphosphate
                  carboxylase/oxygenase small subunit (EC 4.1.1.39)
Seq. No.
                   402313
Seq. ID
                  LIB3431-052-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q4566614
BLAST score
                  375
E value
                  3.0e-36
Match length
                  81
% identity
                  85
NCBI Description
                  (AF112887) actin depolymerizing factor [Populus alba x
                  Populus tremula]
Seq. No.
                  402314
Seq. ID
                  LIB3431-052-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2244781
BLAST score
                  170
E value
                  5.0e-12
Match length
                  97
% identity
                  39
NCBI Description
                  (Z97335) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  402315
Seq. ID
                  LIB3431-052-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g5230785
BLAST score
                  185
E value
                  7.0e-14
Match length
                  51
% identity
                  67
```

NCBI Description (AF107024) histone H1 WH1B.1 [Triticum aestivum]

```
Seq. No.
                   402316
 Seq. ID
                   LIB3431-052-P1-K1-E2
 Method
                   BLASTX
 NCBI GI
                   g2947060
 BLAST score
                   469
 E value
                   4.0e-47
Match length
                   118
 % identity
                   75
NCBI Description
                  (AC002521) putative membrane protein [Arabidopsis thaliana]
 Seq. No.
                   402317
 Seq. ID
                   LIB3431-052-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   q671740
BLAST score
                   405
E value
                   1.0e-39
Match length
                   77
% identity
                   96
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
                   402318
Seq. No.
Seq. ID
                   LIB3431-052-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   487
E value
                   2.0e-53
Match length
                   107
% identity
                   94
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                  402319
Seq. ID
                  LIB3431-052-P1-K1-E5
Method
                  BLASTN
NCBI GI
                  g1519252
BLAST score
                  54
E value
                  6.0e-22
Match length
                  102
% identity
                  88
NCBI Description
                  Oryza sativa GF14-d protein mRNA, complete cds
Seq. No.
                  402320
Seq. ID
                  LIB3431-052-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  293
E value
                  1.0e-26
Match length
                  76
% identity
                  79
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
```

```
(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

402321
```

```
Seq. No.
                   402321
Seq. ID
                   LIB3431-052-P1-K1-E9
Method
                   BLASTX `
NCBI GI
                   g1173347
BLAST score
                   401
E value
                   3.0e-39
Match length
                   80
% identity
NCBI Description
                   SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                   >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                   3.1.3.37) precursor - wheat >gi 14265 emb CAA46507
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                   aestivum]
Seq. No.
                   402322
Seq. ID
                   LIB3431-052-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   q733454
BLAST score ·
                   382
E value
                   6.0e-37
Match length
                   95
% identity
                   79
NCBI Description
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
Seq. No.
                  402323
Seq. ID
                  LIB3431-052-P1-K1-F10
Method
                  BLASTN
NCBI GI
                  g3789951
BLAST score
                  70
E value
                  1.0e-31
Match length
                  81
% identity
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein presursor
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
Seq. No.
                  402324
Seq. ID
                  LIB3431-052-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g21839
BLAST score
                  368
E value
                  2.0e-35
Match length
                  84
% identity
NCBI Description
                  (X57952) phosphoribulokinase [Triticum aestivum]
```

Seq. No. 402325

Seq. ID LIB3431-052-P1-K1-F12

Method BLASTX

% identity

-77

```
g3789952
NCBI GI
BLAST score
                  341
E value
                  5.0e-32
Match length
                  66
% identity
NCBI Description
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                  sativa]
Seq. No.
                  402326
Seq. ID
                  LIB3431-052-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q3075488
BLAST score
                  303
E value
                  9.0e-28
Match length
                  82
                  72
% identity
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
                  402327
Seq. No.
Seq. ID
                  LIB3431-052-P1-K1-F4
Method
                  BLASTN
NCBI GI
                  g4959460
BLAST score
                  33
E value
                  3.0e-09
                  33
Match length
% identity
                  100
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
Seq. No.
                  402328
                  LIB3431-052-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3360289
                  230
BLAST score
E value
                  4.0e-19
                  59
Match length
% identity
                  76
NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase
             1 [Zea mays]
                  402329
Seq. No.
                  LIB3431-052-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5302772
BLAST score
                  148
E value
                  1.0e-09
Match length
                  83
% identity
                  40
NCBI Description (Z97336) SNF1 like protein kinase [Arabidopsis thaliana]
                  402330
Seq. No.
Seq. ID
                  LIB3431-052-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  q2129622
BLAST score
                  296
E value
                  5.0e-27
Match length
                  71
```

```
NCBI Description immunophilin FKBP15-1 - Arabidopsis thaliana >gi 1272406
                   (U52046) immunophilin [Arabidopsis thaliana]
Seq. No.
                   402331
Seq. ID
                   LIB3431-052-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   g3126854
BLAST score
                   203
E value
                   2.0e-16
Match length
                   47
% identity
                   85
NCBI Description
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   402332
Seq. ID
                   LIB3431-052-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   590
E value
                   3.0e-61
Match length
                   111
% identity
                   99
NCBI Description
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   402333
Seq. ID
                  LIB3431-052-P1-K1-G11
Method
                  BLASTX
NCBI GI
                   q115813
BLAST score
                   164
E value
                   1.0e-11
Match length
                   61
% identity
                   64
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                  CAB-8) >gi 19182 emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                  402334
                  LIB3431-052-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2501189
BLAST score
                  261
E value
                  6.0e-23.
Match length
                  78
% identity
                  72
NCBI Description
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                  >gi_2130146_pir S61419 thiamine biosynthetic enzyme thi1-1
                  - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  402335
Seq. ID
                  LIB3431-052-P1-K1-G4
Method
                  BLASTN
NCBI GI
                  q2062705
BLAST score
                  34
E value
                  4.0e-10
Match length
                  34
% identity
                  100
NCBI Description Human butyrophilin (BTF5) mRNA, complete cds
```

NCBI GI

g82080

```
Seq. No.
                   402336
Seq. ID
                  LIB3431-052-P1-K1-G5
Method
                  BLASTN
NCBI GI
                   g3885893
                   99
BLAST score
E value
                   2.0e-48
Match length
                  127
% identity
                   94
NCBI Description
                  Oryza sativa photosystem-1 H subunit GOS5 (PSI-H) mRNA,
                  complete cds
Seq. No.
                  402337
Seq. ID
                  LIB3431-052-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q125580
BLAST score
                  173
E value
                  1.0e-12
Match length
                  37
% identity
                  95
NCBI Description
                  PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
                   (PRK) >gi_100839_pir__S15743 phosphoribulokinase (EC
                  2.7.1.19) - wheat >gi 5924030 emb CAB56544.1 (X51608)
                  phosphoribulokinase [Triticum aestivum]
                  402338
Seq. No.
Seq. ID
                  LIB3431-052-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  279
E value
                  7.0e-25
Match length
                  77
% identity
                  77
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  402339
Seq. No.
               LIB3431-052-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g320618
BLAST score
                  259
                  2.0e-22
E value
Match length
                  67
% identity
                  76
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611 prf __1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  402340
Seq. ID
                  LIB3431-052-P1-K1-H10
Method
                  BLASTX
```

```
BLAST score
                   161
E value
                   3.0e-11
Match length
                   83
% identity
                   47
NCBI Description
                   chlorophyll a/b-binding protein type III precursor - tomato
                   >gi_226872_prf__1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                   402341
Seq. ID
                   LIB3431-052-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   g2494261
BLAST score
                   299
E value
                   3.0e-27
Match length
                   98
% identity
                   62
NCBI Description
                   ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
                   >gi_99903 pir S21567 translation elongation factor Tu
                   precursor - soybean chloroplast >gi_18776 emb CAA46864
                   (X66062) EF-Tu [Glycine max] >gi_44\overline{8}921_prf_ \overline{1}918220A
                   elongation factor Tu [Glycine max]
Seq. No.
                   402342
Seq. ID
                   LIB3431-052-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   418
E value
                   4.0e-41
Match length
                   112
% identity
                   79
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi 82461 pir S03706 chlorophyll a/b-binding
                   protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   402343
Seq. ID
                   LIB3431-052-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   g1652848
BLAST score
                   143
E value
                   2.0e-09
Match length
                   36
% identity
NCBI Description
                   (D90909) DNA photolyase [Synechocystis sp.]
Seq. No.
                   402344
Seq. ID
                  LIB3431-052-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g131176
BLAST score
                  293
E value
                  1.0e-26
Match length
                  . 55
% identity
                  100
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
                   (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
```

>gi_72683_pir__F1BH4 photosystem I chain IV precursor -

E value

```
barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A
                   10.8kD photosystem I protein [Hordeum vulgare var.
                   distichum]
                   402345
Seq. No.
                   LIB3431-052-P1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3183079
BLAST score
                   413
E value
                   4.0e-44
Match length
                   107
% identity
                   84
                   MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
NCBI Description
                   >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate
                   dehydrogenase [Oryza sativa]
                   402346
Seq. No.
                   LIB3431-052-P1-N1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2289010
BLAST score
                   389
E value
                   2.0e-37
Match length
                   86
% identity
                   86
NCBI Description
                   (AC002335) FKBP type peptidyl-prolyl cis-trans isomerase
                   isolog [Arabidopsis thaliana]
Seq. No.
                   402347
                   LIB3431-052-P1-N1-B1
Seq. ID
Method
                   BLASTN
                   q6069643
NCBI GI
BLAST score
                   120
                   6.0e-61
E value
                   207
Match length
% identity
NCBI Description
                   Oryza sativa genomic DNA, chromosome 6, clone:P0514G12
                   402348
Seq. No.
Seq. ID
                   LIB3431-052-P1-N1-B4
Method
                   BLASTX
NCBI GI
                   g131225
BLAST score
                   514
                   4.0e-52
E value
Match length
                   127
% identity
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                   precursor - barley >gi_167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
                   402349
Seq. No.
Seq. ID
                   LIB3431-052-P1-N1-B5
Method
                   BLASTX
NCBI GI
                   g126896
BLAST score
                   392
                   6.0e-38
```

Method

BLASTX

```
    Match length

                   91
                   87
 % identity
                   MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR
 NCBI Description
                   >gi 319831 pir DEPUMW malate dehydrogenase (EC 1.1.1.37)
                   precursor, mitochondrial - watermelon
                   >gi 18297 emb CAA35239 (X17362) precursor protein (AA -27
                   to 320) [Citrullus lanatus]
 Seq. No.
                   402350
 Seq. ID
                   LIB3431-052-P1-N1-B6
 Method
                   BLASTX
 NCBI GI
                   g115813
 BLAST score
                   163
                   2.0e-11
 E value
Match length
                   41
 % identity
                   76
 NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                   CAB-8) >gi 19182 emb CAA33330 (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
 Seq. No.
                   402351
 Seq. ID
                   LIB3431-052-P1-N1-B7
Method
                   BLASTN
NCBI GI
                   g4835587
 BLAST score
                   93
E value
                   1.0e-44
Match length
                   93
 % identity
                   100
NCBI Description
                   Oryza sativa ONIT4 mRNA for nitrilase-like protein,
                   complete cds
Seq. No.
                   402352
Seq. ID
                   LIB3431-052-P1-N1-B8
Method
                   BLASTN
NCBI GI
                   g3885891
BLAST score
                   58
E value
                   7.0e-24
Match length
                   110
% identity
                   88
NCBI Description
                   Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                   mRNA, complete cds
Seq. No.
                   402353
Seq. ID
                   LIB3431-052-P1-N1-B9
Method
                   BLASTX
NCBI GI
                   g120661
BLAST score
                   264
E value
                   3.0e-23
Match length
                   56
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST
NCBI Description
                   PRECURSOR >gi_170237 (M14417) glyceraldehyde-3-phosphate
                   dehydrogenase A-subunit precursor [Nicotiana tabacum]
Seq. No.
                   402354
                   LIB3431-052-P1-N1-C11
Seq. ID
```

NCBI GI

```
q6056418
NCBI GI
BLAST score
                  287
                  1.0e-25
E value
Match length
                  94
                  59
% identity
                  (AC009525) Similar to beta-glucosidases [Arabidopsis
NCBI Description
                  thaliana]
                  402355
Seq. No.
                  LIB3431-052-P1-N1-C12
Seq. ID
                  BLASTX
Method
                  q3328221
NCBI GI
BLAST score
                  443
                  7.0e-44
E value
Match length
                  96
% identity
                  (AF076920) thioredoxin peroxidase [Secale cereale]
NCBI Description
Seq. No.
                  402356
                  LIB3431-052-P1-N1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2982456
                  312
BLAST score
                  2.0e-28
E value
                  90
Match length
% identity
                  (AL022223) putative protein [Arabidopsis thaliana]
NCBI Description
                  402357
Seq. No.
Seq. ID
                  LIB3431-052-P1-N1-C3
Method
                  BLASTX
                  q2754849
NCBI GI
                  280
BLAST score
                  9.0e-25
E value
Match length
                  65
% identity
                   (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                   [Fritillaria agrestis]
                   402358
Seq. No.
Seq. ID
                  LIB3431-052-P1-N1-C4
                  BLASTX .
Method
                  q399333
NCBI GI
                   205
BLAST score
                   5.0e-16
E value
Match length
                   44
% identity
                  CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYLSERINE
NCBI Description
                   SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                  >gi_322740_pir__A43407 cysteine synthase (EC 4.2.99.8)
                  precursor - pepper >gi_17944_emb_CAA46086_ (X64874)
                   O-acetylserine (thiol)-lyase [Capsicum annuum]
                   402359
Séq. No.
Seq. ID
                   LIB3431-052-P1-N1-C5
                   BLASTX
Method
```

q4566614

BLAST score

```
BLAST score
                   183
                   2.0e-13
E value
Match length
                   42
                   81
% identity
NCBI Description
                   (AF112887) actin depolymerizing factor [Populus alba x
                   Populus tremula]
                   402360
Seq. No.
                  LIB3431-052-P1-N1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2501190
BLAST score
                   282
E value
                   6.0e-25
                   76
Match length
                   78
% identity
NCBI Description
                  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
                  >gi 2130147 pir S61420 thiamine biosynthetic enzyme thi1-2
                   - maize >gi 596080 (U17351) thiamine biosynthetic enzyme
                   [Zea mays]
Seq. No.
                  402361
                  LIB3431-052-P1-N1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5921663
BLAST score
                  206
                  3.0e-16
E value
Match length
                  41
% identity
                  93
NCBI Description
                   (AF162279) 10-formyltetrahydrofolate synthetase
                   [Arabidopsis thaliana]
Seq. No.
                  402362
Seq. ID
                  LIB3431-052-P1-N1-C9
Method
                  BLASTN
NCBI GI
                  g2739216,
BLAST score
                  76
E value
                  1.0e-34
Match length
                  84
% identity
                  98
NCBI Description
                  Hordeum vulgare L41 ribosomal protein
Seq. No.
                  402363
Seq. ID
                  LIB3431-052-P1-N1-D4
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                  213
E value
                  6.0e-17
Match length
                  68
% identity
                  68
NCBI Description
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa]
Seq. No.
                  402364
Seq. ID
                  LIB3431-052-P1-N1-D5
Method
                  BLASTX
NCBI GI
                  g517500
```

```
E value
                  8.0e-18
Match length
                  55
                  78
% identity
                  (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein [Zea mays] >gi_444338_prf__1906386A photosystem II
                  OE17 protein [Pisum sativum]
                  402365
Seq. No.
                  LIB3431-052-P1-N1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  426
                  7.0e-42
E value
Match length
                  77
% identity
                  100
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  402366
Seq. No.
                  LIB3431-052-P1-N1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4335763
BLAST score
                  167
                  1.0e-11
E value
Match length
                  75
% identity
                   (AC006284) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  402367
                  LIB3431-052-P1-N1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4566614
BLAST score
                  306
E value
                   9.0e-28
Match length
                  69
% identity
                  (AF112887) actin depolymerizing factor [Populus alba x
NCBI Description
                  Populus tremula]
Seq. No.
                  402368
Seq. ID
                  LIB3431-052-P1-N1-E1
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  295
E value
                  1.0e-165
Match length
                  295
                  100
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
                  402369
Seq. No.
Seq. ID
                  LIB3431-052-P1-N1-E12
Method
                  BLASTX
                  g3510256
NCBI GI
BLAST score
                  298
```

6.0e-27

E value

```
90
Match length
                  52
% identity
                 (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
                  402370
Seq. No.
Seq. ID
                  LIB3431-052-P1-N1-E2
Method
                  BLASTX
NCBI GI
                  g2947060
BLAST score
                  165
                  3.0e-11
E value
Match length
                  40
                  78
% identity
                  (AC002521) putative membrane protein [Arabidopsis thaliana]
NCBI Description
                  402371
Seq. No.
                  LIB3431-052-P1-N1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                  186
                  9.0e-14
E value
                  37
Match length
                  95
% identity
                  (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
                  402372
Seq. No.
Seq. ID
                  LIB3431-052-P1-N1-E4
Method
                  BLASTX
NCBI GI
                  g115787
BLAST score
                  396
E value
                  2.0e-38
Match length
                  77
                  97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  402373
Seq. No.
                  LIB3431-052-P1-N1-E5
Seq. ID
Method
                  BLASTX
                  g1519253
NCBI GI
BLAST score
                  277
E value
                  2.0e-24
Match length
                  58
                  93
% identity
                  (U65958) GF14-d protein [Oryza sativa]
NCBI Description
                  402374
Seq. No.
                  LIB3431-052-P1-N1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3126854
BLAST score
                  494
E value
                  8.0e-50
Match length
                  110
```

88

% identity

```
(AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  402375
Seq. ID
                  LIB3431-052-P1-N1-E7
Method
                  BLASTX
NCBI GI
                  g671740
BLAST score
                  346
E value
                  9.0e-33
Match length
                  76
                  84
% identity
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
                  402376
Seq. No.
Seq. ID
                  LIB3431-052-P1-N1-E9
Method
                  BLASTX
NCBI GI
                  q1173347
BLAST score
                  331
                  1.0e-30
E value
Match length
                  82
% identity
                  83
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  402377
Seq. ID
                  LIB3431-052-P1-N1-F10
Method
                  BLASTN
                  g3789951
NCBI GI
                  77
BLAST score
E value
                  3.0e - 35
Match length
                  245
% identity
NCBI Description
                  Oryza sativa chlorophyll a/b-binding protein presursor
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  402378
Seq. No.
                  LIB3431-052-P1-N1-F11
Seq. ID
Method
                  BLASTX
                  g21839
NCBI GI
BLAST score
                  343
E value
                  4.0e-32
Match length
                  72
% identity
                   (X57952) phosphoribulokinase [Triticum aestivum]
NCBI Description
                  402379
Seq. No.
                  LIB3431-052-P1-N1-F12
Seq. ID
Method
                  BLASTN
                  g21838
NCBI GI
BLAST score
                  36
                  1.0e-10
E value
```

139

Match length

Match length

```
% identity
                   88
NCBI Description
                  T.aestivum PRK gene for ribulose-5-phosphate kinase
Seq. No.
                   402380
Seq. ID
                  LIB3431-052-P1-N1-F8
Method
                  BLASTX
NCBI GI
                   g2129623
BLAST score
                   199
E value
                   1.0e-31
Match length
                   83
                   84
% identity
NCBI Description
                  immunophilin FKBP15-2 - Arabidopsis thaliana >gi 1272408
                   (U52047) immunophilin [Arabidopsis thaliana]
Seq. No.
                   402381
Seq. ID.
                  LIB3431-052-P1-N1-F9
Method
                  BLASTX
NCBI GI
                  g115802
BLAST score
                  251
E. value
                  2.0e-21
Match length
                  47
% identity
                  100
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
                  CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll
                  a/b-binding protein (cab-36) - common tobacco
                  >gi_19827_emb_CAA41188 (X58230) chlorophyll a/b binding
                  protein [Nicotiana tabacum]
Seq. No.
                  402382
Seq. ID
                  LIB3431-052-P1-N1-G1
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  620
E value
                  1.0e-64
Match length
                  121
% identity
NCBI Description
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  402383
Seq. ID
                  LIB3431-052-P1-N1-G10
Method
                  BLASTX
NCBI GI
                  g3914466
BLAST score
                  242
E value
                  1.0e-20
Match length
                  45
% identity
                  93
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                  (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
                  subunit precursor [Zea mays]
Seq. No.
                  402384
Seq. ID
                  LIB3431-052-P1-N1-G11
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  297
E value
                  9.0e-27
```

NCBI GI

q82080

```
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
                  402385
Seq. No.
Seq. ID
                  LIB3431-052-P1-N1-G3
Method
                  BLASTX
NCBI GI
                  q2501190
BLAST score
                  470
E value
                  5.0e-47
Match length
                  117
                  83
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
NCBI Description
                  >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2
                  - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  402386
Seq. ID
                  LIB3431-052-P1-N1-G8
Method
                  BLASTN
                  g21838
NCBI GI
BLAST score
                  70
E value
                  5.0e-31
Match length
                  207
% identity
                  85
                  T.aestivum PRK gene for ribulose-5-phosphate kinase
NCBI Description
                  402387
Seq. No.
                  LIB3431-052-P1-N1-G9
Seq. ID
Method
                  BLASTX
                  g693920
NCBI GI
BLAST score
                  403
E value
                  4.0e-39
Match length
                  77
% identity
NCBI Description
                   (U21113) chlorophyll a/b binding protein [Solanum
                  tuberosum]
                  402388
Seq. No.
                  LIB3431-052-P1-N1-H1
Seq. ID
Method
                  BLASTX
                  g115787
NCBI GI
BLAST score
                  495
E value
                  6.0e-50
Match length
                  98
                  97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                  402389
Seq. No.
                  LIB3431-052-P1-N1-H10
Seq. ID
                  BLASTX
Method
```

```
BLAST score
                   291
                   4.0e-26
E value
Match length
                   71
% identity
                   chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                   402390
Seq. ID
                   LIB3431-052-P1-N1-H11
Method
                   BLASTX
NCBI GI
                   q119194
BLAST score
                   270
                   9.0e-24
E value
Match length
                   62
% identity
                   85
                   ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU)
NCBI Description
                   >gi_81607_pir__S09152 translation elongation factor Tu
                   precursor, chloroplast - Arabidopsis thaliana
>gi_22565_emb_CAA36498_ (X52256) elongation factor Tu
                   precursor [Arabidopsis thaliana]
                   >gi_5738381_emb_CAB45802.2_ (AL080253) translation
                   elongation factor EF-Tu precursor, chloroplast [Arabidopsis
                   thaliana] >gi_226817_prf__1607332A elongation factor Tu
                   [Arabidopsis thaliana]
Seq. No.
                   402391
                   LIB3431-052-P1-N1-H2
Seq. ID
Method
                   BLASTX
                   g226263
NCBI GI
BLAST score
                   158
E value
                   1.0e-10
Match length
                   29
% identity
NCBI Description
                   chlorophyll a/b binding protein [Glycine max]
                   402392
Seq. No.
                   LIB3431-052-P1-N1-H3
Seq. ID
Method
                   BLASTX
                   g3789954
NCBI GI
BLAST score
                   237
E value
                   7.0e-20
Match length
                   44
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
Seq. No.
                   402393
                   LIB3431-052-P1-N1-H5
Seq. ID
Method
                   BLASTN
                   q14264
NCBI GI
BLAST score
                   60
E value
                   5.0e-25
Match length
                   100
% identity
                   90
```

NCBI Description T.aestivum gene for sedoheptulose-1,7-bisphoshatase

% identity

```
402394
Seq. No.
Seq. ID
                   LIB3431-052-P1-N1-H7
Method
                   BLASTX
NCBI GI
                   g131176
BLAST score
                   251
                   1.0e-21
E value
Match length
                   48
% identity
                   98
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR
                    (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)
                   >gi_72683_pir__F1BH4 photosystem I chain IV precursor -
                   barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A
                   10.8kD photosystem I protein [Hordeum vulgare var.
                   distichum
Seq. No.
                   402395
Seq. ID
                   LIB3431-052-P1-N1-H9
Method
                   BLASTX
NCBI GI
                   q3183079
BLAST score
                   209
                   1.0e-16
E value
Match length
                   54
% identity
                   76
                   MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
NCBI Description
                   >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate
                   dehydrogenase [Oryza sativa]
                   402396
Seq. No.
                   LIB3431-053-P1-K1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g871931
BLAST score
                   387
E value
                   2.0e-37
Match length
                   78
% identity
                   99
NCBI Description
                   (D30763) ferredoxin [Oryza sativa]
                                                                                135
Seq. No.
                   402397
                   LIB3431-053-P1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q729479
BLAST score
                   667
E value
                   1.0e-72
Match length
                   147
% identity
NCBI Description
                   FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi 551131
                   (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]
Seq. No.
                   402398
Seq. ID
                   LIB3431-053-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g131225
BLAST score
                   322
E value
                   3.0e-30
Match length
                   71
```

Match length

```
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                   402399
Seq. ID
                  LIB3431-053-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g4585882
BLAST score
                  638
E value
                  8.0e-67
Match length
                  143
                  79
% identity
NCBI Description
                  (AC005850) PSI type III chlorophyll a/b-binding protein
                   [Arabidopsis thaliana]
Seq. No.
                  402400
Seq. ID
                  LIB3431-053-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2894534
BLAST score
                  392
E value
                  4.0e-38
Match length
                  103
% identity
                  77
NCBI Description
                  (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                  402401
Seq. ID
                  LIB3431-053-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g4038699
BLAST score
                  198
E value
                  3.0e-23
Match length
                  65
% identity
NCBI Description
                  (AB020947) ribulose-1,5-bisphosphate carboxylase/oxygenase
                  small subunit [Aegilops speltoides]
Seq. No.
                  402402
Seq. ID
                  LIB3431-053-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g417154
BLAST score
                  429
E value
                  3.0e-42
Match length
                  135
% identity
                  63
NCBI Description
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
Seq. No.
                  402403
Seq. ID
                  LIB3431-053-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  399
                  5.0e-39
E value
```

BLAST score

```
% identity
                   96
NCBI Description
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
                   subunit [Oryza sativa]
Seq. No.
                   402404
Seq. ID
                   LIB3431-053-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   g6006848
BLAST score
                   570
E value
                   7.0e-59
Match length
                   132
% identity
                   79
NCBI Description
                   (AC009540) unknown protein, 5' partial [Arabidopsis
                   thaliana]
Seq. No.
                   402405
Seq. ID
                   LIB3431-053-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   370
E value
                   1.0e-35
Match length
                   94
                   82
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461 pir_ S03706 chlorophyll a/b-binding
                   protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   402406
Seq. No.
Seq. ID
                  LIB3431-053-P1-K1-B11
Method
                  BLASTX
NCBI GI
                   q2407281
BLAST score
                   638
E value
                   8.0e-67
Match length
                   124
                   94
% identity
NCBI Description
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
                   subunit [Oryza sativa]
Seq. No.
                  402407
Seq. ID
                  LIB3431-053-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g82080
BLAST score
                  346
E value
                  1.0e-32
Match length
                  98
% identity
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                  [Lycopersicon esculentum]
Seq. No.
                  402408
Seq. ID
                  LIB3431-053-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g2499819
```

```
3.0e-66
E value
Match length
                     121
                     99
% identity
                    ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR
NCBI Description
                    >gi_2130068_pir__S66516 aspartic proteinase 1 precursor -
rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease
[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic
                    protease [Oryza sativa]
                    402409
Seq. No.
Seq. ID
                    LIB3431-053-P1-K1-B3
Method
                    BLASTX
NCBI GI
                    q4982478
BLAST score
                    518
E value
                     9.0e-53
Match length
                    136
% identity
                     (AF069441) putative leucyl tRNA synthetase [Arabidopsis
NCBI Description
                    thaliana]
Seq. No.
                     402410
                    LIB3431-053-P1-K1-B4
Seq. ID
Method
                    BLASTX
NCBI GI
                    q320618
BLAST score
                     265
E value
                     3.0e-23
Match length
                     65
% identity
                    chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                    >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                    chlorophyll a/b-binding protein [Oryza sativa]
                    >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                     [Oryza sativa]
Seq. No.
                     402411
Seq. ID
                    LIB3431-053-P1-K1-B5
Method
                    BLASTX
NCBI GI
                    q1661160
BLAST score
                    246
                     2.0e-27
E value
Match length
                     91
% identity
NCBI Description
                     (U74295) chlorophyll a/b binding protein [Oryza sativa]
                     402412
Seq. No.
Seq. ID
                    LIB3431-053-P1-K1-B8
Method
                    BLASTX
NCBI GI
                     q400983
BLAST score
                    272
E value
                     7.0e-24
Match length
                     61
% identity
                    50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11)
NCBI Description
                    >gi_279648_pir__R5SP11 ribosomal protein L11 precursor -
                    {\tt spinach} > {\tt gi\_21\overline{31}3\_emb\_CAA39950\_(X56615)} \ {\tt ribosomal} \ {\tt protein}
```

L11 [Spinacia oleracea]

```
402413
Seq. No.
Seq. ID
                   LIB3431-053-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g1835731
BLAST score
                   319
E value
                   1.0e-29
Match length
                   66
                   95
% identity
NCBI Description
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                   402414
Seq. ID
                   LIB3431-053-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   q5734636
BLAST score
                   297
E value
                   8.0e-27
Match length
                   106
% identity
NCBI Description
                   (APO00391) Similar to putative lipase (AC006232) [Oryza
                   sativa]
                   402415
Seq. No.
Seq. ID
                   LIB3431-053-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g2130042<sub>.</sub>.
BLAST score
                   688
E value
                   1.0e-72
Match length
                   149
                   92
% identity
NCBI Description
                   Mg-chelatase chain Xantha-f - barley >gi_861199 (U26916)
                   protoporphyrin IX Mg-chelatase subunit precursor [Hordeum
                   vulgare]
                   402416
Seq. No.
Seq. ID
                   LIB3431-053-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q115772
BLAST score
                   675
E value
                   4.0e-71
Match length
                   136
% identity
                   94
                   CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108_
                   (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                   [Oryza sativa]
Seq. No.
                   402417
Seq. ID
                   LIB3431-053-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   194
                   6.0e-15
E value
Match length
                   52
                   73
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
```

E value

2.0e-45

protein [Oryza sativa]

```
Seq. No.
                   402418
Seq. ID
                   LIB3431-053-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   638
E value
                   1.0e-66
Match length
                   119
% identity
                   98
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4\overline{.1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   402419
Seq. ID
                   LIB3431-053-P1-K1-C4
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   36
E value
                   2.0e-10
Match length
                   36
% identity
                   100
NCBI Description
                   Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   402420
Seq. ID
                   LIB3431-053-P1-K1-C5
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   36
E value
                   2.0e-10
Match length
                   36
% identity
                   100
NCBI Description
                   Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   402421
Seq. ID
                   LIB3431-053-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g82734
BLAST score
                   812
E value
                   4.0e-87
Match length
                   164
% identity
NCBI Description
                   ubiquitin precursor - maize (fragment)
                   >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]
Seq. No.
                   402422
Seq. ID
                   LIB3431-053-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   455
```

Seq. No.

```
Match length
                    102
 % identity
                    84
 NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                    chlorophyll a/b-binding protein [Oryza sativa]
                    >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
 Seq. No.
                    402423
 Seq. ID
                   LIB3431-053-P1-K1-D10
 Method
                   BLASTX
 NCBI GI
                   g548605
 BLAST score
                   488
 E value
                   3.0e-49
 Match length
                   113
 % identity
                   87
 NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi_539055_pir__A48527 photosystem I protein psaK precursor
                   - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
 Seq. No.
                   402424
 Seq. ID
                   LIB3431-053-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   g3288821
BLAST score
                   422
E value
                   2.0e-41
Match length
                   106
% identity
                   75
NCBI Description
                   (AF063901) alanine:glyoxylate aminotransferase;
                   transaminase [Arabidopsis thaliana]
                   >gi_4733989_gb_AAD28669.1 AC007209_5 (AC007209)
                   alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
Seq. No.
                   402425
Seq. ID
                   LIB3431-053-P1-K1-D2
Method
                   BLASTN
NCBI GI
                   g5852170
BLAST score
                   86
E value
                   2.0e-40
Match length
                   130
% identity
                   46
NCBI Description
                  Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
                  clone:t17804
Seq. No.
                  402426
Seq. ID
                  LIB3431-053-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g4972052
BLAST score
                  372
E value
                  1.0e-35
Match length
                  134
% identity
NCBI Description
                  (AL078470) putative protein [Arabidopsis thaliana]
```

Method

BLASTN

```
Seq. ID
                    LIB3431-053-P1-K1-D4
Method
                    BLASTN
NCBI GI
                    g19094
BLAST score
                    33
E value
                    3.0e-09
Match length
                    57
% identity
                    89
NCBI Description
                    H.vulgare mRNA PsaN for photosystem I subunit N
Seq. No.
                    402428
Seq. ID
                    LIB3431-053-P1-K1-D5
Method
                    BLASTN
NCBI GI
                    g19094
BLAST score
                    44
E value
                    7.0e-16
Match length
                    64
% identity
                    92
NCBI Description
                    H.vulgare mRNA PsaN for photosystem I subunit N
Seq. No.
                    402429
Seq. ID
                    LIB3431-053-P1-K1-D6
Method
                    BLASTX
NCBI GI
                    g115787
BLAST score
                    616
E value
                    3.0e-64
Match length
                    140
% identity
                    88
NCBI Description
                    CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                    CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
Seq. No.
                    402430
Seq. ID
                    LIB3431-053-P1-K1-D8
Method
                    BLASTX
NCBI GI
                    g3789952
BLAST score
                    364
E value
                    6.0e-35
Match length
                    77
% identity
                    (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                    sativa]
Seq. No.
                    402431
Seq. ID
                   LIB3431-053-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   q5042413
BLAST score
                   278
E value
                   1.0e-24
Match length
                   90
% identity
NCBI Description
                   (AC006193) Hypothetical Protein [Arabidopsis thaliana]
Seq. No.
                   402432
Seq. ID
                   LIB3431-053-P1-K1-E1
```

BLAST score

```
NCBI GI
                   g3885891
 BLAST score
                   171
 E value
                   2.0e-91
Match length
                   209
 % identity
                   96
NCBI Description
                   Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                   mRNA, complete cds
Seq. No.
                   402433
Seq. ID
                   LIB3431-053-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g4544390
BLAST score
                   364
E value
                   1.0e-34
Match length
                   141
% identity
                   52
NCBI Description
                   (AC007047) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   402434
Seq. ID
                   LIB3431-053-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   1.0e-19
Match length
                   44
% identity
                   100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                   402435
Seq. ID
                  LIB3431-053-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  q218209
BLAST score
                  66
E value
                  2.0e-28
Match length
                  94
% identity
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS2106
Seq. No.
                  402436
Seq. ID
                  LIB3431-053-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2072727
BLAST score
                  736
E value
                  3.0e-78
Match length
                  143
% identity
                  99
NCBI Description
                  (Y12595) Fd-GOGAT protein [Oryza sativa]
Seq. No.
                  402437
Seq. ID
                  LIB3431-053-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  g3821780
```

NCBI GI

```
E value
                   7.0e-11
Match length
                   35
% identity
                   100
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
                   402438
Seq. No.
Seq. ID
                   LIB3431-053-P1-K1-E5
Method
                   BLASTN
NCBI GI
                   g3821780
BLAST score
                   35
E value
                   8.0e-11
Match length
                   35
% identity
                   100
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   402439
Seq. ID
                  LIB3431-053-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g131388
BLAST score
                   403
E value
                  3.0e-39
                  131
Match length
% identity
                   67
NCBI Description
                  OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
                  SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                  THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260
                  photosystem II oxygen-evolving complex protein 1 - common
                  wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
                  33kDa oxygen evolving protein of photosystem II [Triticum
                  aestivum]
Seq. No.
                  402440
Seq. ID
                  LIB3431-053-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g4417296
BLAST score
                  368
E value
                  3.0e-35
Match length
                  102
% identity
                  68
NCBI Description
                  (AC007019) unknown protein [Arabidopsis thaliana]
                  >gi 4587592 gb AAD25820.1 AC007232 10 (AC007232) unknown
                  protein [Arabidopsis thaliana]
                  402441
Seq. No.
Seq. ID
                  LIB3431-053-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q3885894
BLAST score
                  463
E value
                  2.0e-46
Match length
                  104
% identity
NCBI Description
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
Seq. No.
                  402442
                  LIB3431-053-P1-K1-F1
Seq. ID
Method
                  BLASTX
```

g2570511

```
BLAST score
                   628
                   1.0e-65
 E value
 Match length
                   121
 % identity
                   98
 NCBI Description
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
 Seq. No.
                   402443
 Seq. ID
                   LIB3431-053-P1-K1-F10
 Method
                   BLASTX
 NCBI GI
                   g2501189
 BLAST score
                   459
 E value
                   8.0e-46
 Match length
                   124
 % identity
                   74
 NCBI Description
                   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                   >gi 2130146 pir__S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
 Seq. No.
                   402444
 Seq. ID
                   LIB3431-053-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   533
E value
                   2.0e-54
Match length
                   120
% identity
                   86
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   402445
Seq. ID
                   LIB3431-053-P1-K1-F2
Method
                  BLASTX
NCBI GI
                   q320618
BLAST score
                   597
E value
                   6.0e-62
Match length
                  132
% identity
                  86
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  402446
Seq. ID
                  LIB3431-053-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q6063542
BLAST score
                  308
E value
                  8.0e-30
Match length
                  76
% identity
                  97
NCBI Description
                  (AP000615) EST C74302(E30840) corresponds to a region of
```

the predicted gene.; similar to glyceraldehyde-3-phosphate

dehydrogenase. (M64118) [Oryza sativa] Seq. No. 402447 Seq. ID LIB3431-053-P1-K1-F8 Method BLASTN NCBI GI g4835587 BLAST score 67 E value 1.0e-29 Match length 67 % identity 100 NCBI Description Oryza sativa ONIT4 mRNA for nitrilase-like protein, complete cds Seq. No. 402448 Seq. ID LIB3431-053-P1-K1-F9 Method BLASTX NCBI GI g733456 BLAST score 631 E value 6.0e-66 Match length 141 % identity 85 (U23189) chlorophyll a/b-binding apoprotein CP26 precursor NCBI Description [Zea mays] Seq. No. 402449 Seq. ID LIB3431-053-P1-K1-G1 Method BLASTX NCBI GI g3047064 BLAST score 406 E value 1.0e-39 Match length 143 % identity 57 NCBI Description (AF058825) contains similarity to peptidyl-prolyl cis-trans isomerase (Pfam: pro_isomerase.hmm, score: 23.86 and 28.41 [Arabidopsis thaliana] Seq. No. 402450 Seq. ID LIB3431-053-P1-K1-G10 Method BLASTX NCBI GI g671740 BLAST score 338 E value 2.0e-31 Match length 63 % identity NCBI Description (X84730) ribulose-bisphosphate carboxylase [synthetic construct] Seq. No. 402451 Seq. ID LIB3431-053-P1-K1-G11 Method BLASTX NCBI GI g132105 BLAST score 653 E value 2.0e-68 Match length 141 % identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir_ RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538 (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi 226375 prf 1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

```
Seq. No.
                 402452
Seq. ID
                 LIB3431-053-P1-K1-G2
Method
                 BLASTN
NCBI GI
                 g20262
BLAST score
                 340
E value
                 0.0e+00
Match length
                 340
% identity
                 100
NCBI Description O.sativa light-induced mRNA
Seq. No.
                 402453
Seq. ID
                 LIB3431-053-P1-K1-G3
Method
                 BLASTX
NCBI GI
                 g3510256
BLAST score
                 250
E value
                 3.0e-21
Match length
                 118
% identity
                 47
NCBI Description
                 (AC005310) unknown protein [Arabidopsis thaliana]
Seq. No.
                 402454
Seq. ID
                 LIB3431-053-P1-K1-G4
Method
                 BLASTX
NCBI GI
                 g132105
BLAST score
                 525
E value
                 1.0e-53
Match length
                 117
% identity
                 85
NCBI Description
                 RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                 (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                 precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                 (D00643) small subunit of ribulose-1,5-bisphosphate
                 carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                 ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
```

```
Seq. No.
                   402455
Seq. ID
                   LIB3431-053-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   313
E value
                   6.0e-29
Match length
                   80
% identity
```

80

NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9

carboxylase S [Oryza sativa]

ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) small chain

precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

```
Seq. No.
                    402456
Seq. ID
                    LIB3431-053-P1-K1-G7
Method
                    BLASTX
NCBI GI
                    g2735017
BLAST score
                    523
E value
                    3.0e-53
Match length
                    155
% identity
                    63
NCBI Description
                   (U82481) KI domain interacting kinase 1 [Zea mays]
Seq. No.
                   402457
Seq. ID
                   LIB3431-053-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g82080
BLAST score
                   535
E value
                   1.0e-54
Match length
                   148
% identity
                   69
NCBI Description
                   chlorophyll a/b-binding protein type III precursor - tomato
                   >gi_226872_prf__1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                   402458
Seq. ID
                   LIB3431-053-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   541
E value
                   2.0e-55
Match length
                   121
% identity
                   85
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxy\overline{1}ase (\overline{E}C 4.\overline{1.1.39}) small chain
```

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_(D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

1 11-1-1-1

Seq. No. 402459

Seq. ID LIB3431-053-P1-K1-H11

Method BLASTN
NCBI GI 94680178
BLAST score 84
E value 3.0e-39
Match length 129
% identity 90

NCBI Description Oryza sativa subsp. indica Retrosat 1 retrotransposon and Ty3-Gypsy type Retrosat 2 retrotransposon, complete

Seq. No.

402465

sequences; and unknown genes

```
Seq. No.
                    402460
 Seq. ID
                    LIB3431-053-P1-K1-H2
 Method
                   BLASTX
 NCBI GI
                    g733454
 BLAST score
                    357
 E value
                    6.0e-34
 Match length
                   101
 % identity
                   72
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
 NCBI Description
                    [Zea mays]
 Seq. No.
                   402461
 Seq. ID
                   LIB3431-053-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q4582459
BLAST score
                   329
E value
                   1.0e-30
Match length
                   98
% identity
                   63
                   (AC007071) putative RanBP7/importin protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   402462
Seq. ID
                   LIB3431-053-P1-K1-H6
Method
                   BLASTN:
NCBI GI
                   g2570496
BLAST score
                   118
E value
                   1.0e-59
Match length
                   126
% identity
                   98
NCBI Description
                   Oryza sativa H protein subunit of glycine decarboxylase
                   mRNA, complete cds
Seq. No.
                   402463
Seq. ID
                   LIB3431-053-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g5442410
BLAST score
                   380
E value
                   2.0e-36
Match length
                   133
% identity
                   58
NCBI Description
                  (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]
Seq. No.
                   402464
Seq. ID
                  LIB3431-053-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  661
E value
                  2.0e-69
Match length
                  129
% identity
                  94
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
```

Match length

```
Seq. ID
                   LIB3431-053-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q3789952
BLAST score
                   469
E value
                   4.0e-47
Match length
                   107
% identity
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                   sativa]
Seq. No.
                   402466
Seq. ID
                   LIB3431-053-P1-N1-A1
Method
                   BLASTN
NCBI GI
                   g218209
BLAST score
                   214
E value
                   1.0e-117
Match length
                   302
% identity
                   93
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
Seq. No.
                   402467
Seq. ID
                  LIB3431-053-P1-N1-A10
Method
                  BLASTX
NCBI GI
                  q729477
BLAST score
                   498
E value
                   3.0e-50
Match length
                   110
% identity
NCBI Description
                  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR)
                  >gi 320548 pir A44974 ferredoxin--NADP+ reductase (EC
                  1.18.1.2) precursor - common ice plant >gi_167256 (M25528)
                  ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
                   [Mesembryanthemum crystallinum] >gi_226768 prf 1604475A
                   ferredoxin NADP reductase [Mesembryanthemum crystallinum]
Seq. No.
                  402468
Seq. ID
                  LIB3431-053-P1-N1-A11
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  179
E value
                  4.0e-13
Match length
                  48
% identity
                  69
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  402469
Seq. ID
                  LIB3431-053-P1-N1-A12
Method
                  BLASTX
NCBI GI
                  g115813
BLAST score
                  211
E value
                  8.0e-25
```

```
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                   CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                   402470
Seq. ID
                   LIB3431-053-P1-N1-A2
Method
                   BLASTX
NCBI GI
                   q2696804
BLAST score
                   309
E value
                   1.0e-44
Match length
                   95
% identity
NCBI Description
                   (AB009665) water channel protein [Oryza sativa]
Seq. No.
                   402471
Seq. ID
                   LIB3431-053-P1-N1-A3
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   354
E value
                   1.0e-40
Match length
                   83
% identity
                   100
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   402472
Seq. ID
                   LIB3431-053-P1-N1-A6
Method
                   BLASTX
NCBI GI
                   q417154
BLAST score
                   302
                              4.
E value
                   7.0e-41
Match length
                   109
% identity
                   85
NCBI Description
                   HEAT SHOCK PROTEIN 82 >gi 100685 pir S25541 heat shock
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
Seq. No.
                   402473
Seq. ID
                   LIB3431-053-P1-N1-A7
Method
                   BLASTX
NCBI GI
                   q671740
BLAST score
                   202
E value
                   9.0e-16
Match length
                   38
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
```

construct]

```
402474
Seq. No.
Seq. ID
                    LIB3431-053-P1-N1-A9
Method
                    BLASTX
NCBI GI
                    g2407281
BLAST score
                    266
E value
                    2.0e-23
Match length
                    67
% identity
                    75
NCBI Description
                     (AF017363) ribulose 1,5-bisphosphate carboxylase small
                    subunit [Oryza sativa]
                     402475
Seq. No.
Seq. ID
                    LIB3431-053-P1-N1-B10
Method
                    BLASTX
NCBI GI
                    g3036942
BLAST score
                    181
E value
                    3.0e-13
Match length
                    37
% identity
                    89
NCBI Description
                     (AB012636) light harvesting chlorophyll a/b-binding protein
                     [Nicotiana sylvestris]
Seq. No.
                    402476
Seq. ID
                    LIB3431-053-P1-N1-B11
Method
                    BLASTX
NCBI GI
                    q347451
BLAST score
                    229
E value
                    9.0e-19
Match length
                    48
% identity
NCBI Description
                    (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                    sativa]
Seq. No.
                    402477
Seq. ID
                    LIB3431-053-P1-N1-B12
Method
                    BLASTX
NCBI GI
                    q115813
BLAST score
                    212
E value
                    8.0e-17
Match length
                    75
% identity
                    61
NCBI Description
                    CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                    CAB-8) >gi_19182_emb_CAA33330 (X15258) Type III
                    chlorophyll a/b-binding protein [Lycopersicon esculentum]
                    402478
Seq. No.
Seq. ID
                    LIB3431-053-P1-N1-B2
Method
                    BLASTX
NCBI GI
                    q2499819
BLAST score
                    215
E value
                    1.0e-30
Match length
                    73
% identity
                    86
NCBI Description
                    ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR
                    >gi_2130068_pir__S66516 aspartic proteinase 1 precursor -
rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease
[Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic
```

NCBI Description

protease [Oryza sativa] Seq. No. 402479 Seq. ID LIB3431-053-P1-N1-B3 Method BLASTX NCBI GI g4982478 BLAST score 168 E value 1.0e-11 Match length 47 % identity 68 (AF069441) putative leucyl tRNA synthetase [Arabidopsis NCBI Description Seq. No. 402480 Seq. ID LIB3431-053-P1-N1-B4 Method BLASTX NCBI GI q421916 BLAST score 237 E value 5.0e-20 Match length 49 % identity 90 NCBI Description chlorophyll a/b-binding protein - English ivy (fragment) >gi_12582_emb_CAA48410_ (X68333) light harvesting chlorophyll a /b binding protein [Hedera helix] Seq. No. 402481 Seq. ID LIB3431-053-P1-N1-B8 Method BLASTX NCBI GI q400983 BLAST score 250 E value 3.0e-21 Match length 70 % identity 69 NCBI Description 50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11) >gi_279648_pir__R5SP11 ribosomal protein L11 precursor spinach >gi_21313_emb_CAA39950 (X56615) ribosomal protein L11 [Spinacia oleracea] Seq. No. 402482 Seq. ID LIB3431-053-P1-N1-B9 Method BLASTX NCBI GI g1835731 BLAST score 230 E value 5.0e-19 Match length 55 % identity (U86018) photosystem II 10 kDa polypeptide [Oryza sativa] NCBI Description Seq. No. 402483 Seq. ID LIB3431-053-P1-N1-C10 Method BLASTX NCBI GI g687677 BLAST score 235 E value 1.0e-19 Match length 51 % identity 88

(U19925) unknown [Arabidopsis thaliana]

```
Seq. No.
                   402484
Seq. ID
                   LIB3431-053-P1-N1-C11
Method
                   BLASTX
NCBI GI
                   g2130042
BLAST score
                   317
E value
                   3.0e - 32
Match length
                   100
% identity
                   75
NCBI Description
                  Mg-chelatase chain Xantha-f - barley >gi 861199 (U26916)
                   protoporphyrin IX Mg-chelatase subunit precursor [Hordeum
                   vulgare]
Seq. No.
                   402485
Seq. ID
                   LIB3431-053-P1-N1-C12
Method
                   BLASTX
                   g2645999
NCBI GI
BLAST score
                   219
E value
                   8.0e-18
Match length
                   56
                   73
% identity
NCBI Description
                   (AF034631) chlorophyll a/b binding protein of LHCII type I
                  precursor [Panax ginseng]
Seq. No.
                   402486
Seq. ID
                  LIB3431-053-P1-N1-C2
Method
                  BLASTX
NCBI GI
                   g2072555
BLAST score
                   217
E value
                   2.0e-17
Match length
                   44
% identity
                   93
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  402487
Seq. ID
                  LIB3431-053-P1-N1-C3
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  245
                  1.0e-20
E value
Match length
                  49
% identity
                  96
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
Seq. No.
                  402488
Seq. ID
                  LIB3431-053-P1-N1-C5
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                  459
E value
                  1.0e-45
Match length
                  102
% identity
                  86
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
```

Method

BLASTX

```
402489
Seq. No.
                  LIB3431-053-P1-N1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                   g170354
                   422
BLAST score
                   2.0e-41
E value
Match length
                  85
% identity
                   21
                  (M74156) pentameric polyubiquitin [Nicotiana sylvestris]
NCBI Description
                   402490
Seq. No.
                   LIB3431-053-P1-N1-C8
Seq. ID
                   BLASTX
Method
                   g289920
NCBI GI
BLAST score
                   319
                   2.0e-29
E value
Match length
                   61
                   100
% identity
                   (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                   hirsutum]
                   402491
Seq. No.
                   LIB3431-053-P1-N1-D10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q304219
BLAST score
                   52 ·
E value
                   2.0e-20
Match length
                   80
                   91
% identity
NCBI Description
                  Hordeum vulgare chloroplast photosystem I PSK-I subunit
                   mRNA, complete cds
Seq. No.
                   402492
Seq. ID
                   LIB3431-053-P1-N1-D12
Method
                   BLASTX
NCBI GI
                   q2754849
BLAST score
                   192
E value
                   2.0e-29
Match length
                   74
% identity
NCBI Description
                   (AF039000) putative serine-glyoxylate aminotransferase
                   [Fritillaria agrestis]
                   402493
Seq. No.
Seq. ID
                   LIB3431-053-P1-N1-D8
Method
                   BLASTX
NCBI GI
                   q3789952
BLAST score
                   196
E value
                   7.0e-15
Match length
                   39
% identity
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                   sativa]
                   402494
Seq. No.
                   LIB3431-053-P1-N1-E1
Seq. ID
```

```
NCBI GI
                  q3885892
BLAST score
                  302
E value
                  2.0e-27
Match length
                  61
% identity
                  95
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
                  402495
Seq. No.
Seq. ID
                  LIB3431-053-P1-N1-E10
Method
                  BLASTX
NCBI GI
                  q5734636
BLAST score
                  187
                  6.0e-16
E value
Match length
                  87
% identity
                  49
                  (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                  sativa]
                  402496
Seq. No.
Seq. ID
                  LIB3431-053-P1-N1-E11
Method
                  BLASTX
NCBI GI
                  g4544390
BLAST score
                  188
E value
                  6.0e-14
Match length
                  62
                  50
% identity
NCBI Description (AC007047) hypothetical protein [Arabidopsis thaliana]
                  402497
Seq. No.
                  LIB3431-053-P1-N1-E2
Seq. ID
Method
                  BLASTN
                  g218209
NCBI GI
                  58
BLAST score
E value
                  1.0e-23
Match length
                  94
                  90
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
Seq. No.
                  402498
Seq. ID
                  LIB3431-053-P1-N1-E3
Method
                  BLASTN
NCBI GI
                  g2072726
BLAST score
                  460
                  0.0e + 00
E value
Match length
                  491
                  99
% identity
NCBI Description O.sativa mRNA for Fd-GOGAT, partial, clone OsGog2
                  402499
Seq. No.
                  LIB3431-053-P1-N1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q482311
BLAST score
                  420
                  4.0e-41
E value
```

84

Match length

```
% identity
                   photosystem II oxygen-evolving complex protein 1 - rice
 NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                   complex protein 1 [Oryza sativa]
                   402500
 Seq. No.
                   LIB3431-053-P1-N1-E7
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g4417296
BLAST score
                   163
E value
                   5.0e-22
                   78
Match length
                   59
 % identity
                   (AC007019) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >qi 4587592 gb AAD25820.1 AC007232 10 (AC007232) unknown
                   protein [Arabidopsis thaliana]
                   402501
 Seq. No.
                   LIB3431-053-P1-N1-E9
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g3885894
                   330
 BLAST score
E value
                   2.0e-38
                   113
Match length
                   77
 % identity
                   (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
 Seq. No.
                   402502
                   LIB3431-053-P1-N1-F1
Seq. ID
                   BLASTX
Method
 NCBI GI
                   q2570511
 BLAST score
                   163
                   3.0e-22
 E value
                   67
Match length
                   78
 % identity
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
 NCBI Description
                   402503
 Seq. No.
                   LIB3431-053-P1-N1-F10
 Seq. ID
 Method
                   BLASTX
 NCBI GI. .
                   g2501190
 BLAST score
                   167
                   6.0e-19
 E value
Match length
                   78
                   71
 % identity
                   THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
 NCBI Description
                   >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2

    maize >gi_596080 (U17351) thiamine biosynthetic enzyme

                   [Zea mays]
                   402504
 Seq. No.
 Seq. ID
                   LIB3431-053-P1-N1-F11
 Method
                   BLASTX
 NCBI GI
                   g115787
 BLAST score
                   471
                   4.0e-47
 E value
```

106

Match length

Seq. ID

```
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   402505
Seq. No.
Seq. ID
                   LIB3431-053-P1-N1-F2
Method
                   BLASTX
NCBI GI
                   q3036949
BLAST score
                   254
                   1.0e-21
E value
Match length
                   49
% identity
                   98
NCBI Description
                   (AB012638) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
                   402506
Seq. No.
Seq. ID
                   LIB3431-053-P1-N1-F3
Method
                   BLASTX
NCBI GI
                   g134034
BLAST score
                   250
                   3.0e-21
E value
Match length
                   87
% identity
                   56
NCBI Description
                   30S RIBOSOMAL PROTEIN S30, CHLOROPLAST PRECURSOR (CS-S5)
                   (CS5) (S22) (RIBOSOMAL PROTEIN 1) (PSRP-1)
                   >gi_279640_pir__R3SPS5 ribosomal protein_CS-S22 precursor,
                   chloroplast - spinach >gi 12316 emb CAA41960 (X59270)
                   chloroplast ribosomal protein S22 [Spinacia oleracea]
                   >qi 18031 emb CAA33403 (X15344) spinach S22 r-protein
                   [Spinacia oleracea]
                   402507
Seq. No.
Seq. ID
                   LIB3431-053-P1-N1-F4
Method
                   BLASTN
NCBI GI
                   g483443
BLAST score
                   79
                   3.0e-36
E value
Match length
                   154
                   90
% identity
NCBI Description
                   Z.mays IBP2 mRNA for initiator-binding protein
                   402508
Seq. No.
Seq. ID
                   LIB3431-053-P1-N1-F5
Method
                   BLASTX
NCBI GI
                   g671740
BLAST score
                   294
                   2.0e-26
E value
Match length
                   56
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                  402509
Seq. No.
```

LIB3431-053-P1-N1-F6

```
Method
                  BLASTX
NCBI GI
                   g6063542
BLAST score
                  198
E value
                   7.0e-16
Match length
                   45
% identity
                   98
NCBI Description
                   (APO00615) EST C74302(E30840) corresponds to a region of
                  the predicted gene.; similar to glyceraldehyde-3-phosphate
                  dehydrogenase. (M64118) [Oryza sativa]
                   402510
Seq. No.
Seq. ID
                  LIB3431-053-P1-N1-F8
Method
                  BLASTN
                  g4835587
NCBI GI
BLAST score
                  154
E value
                   6.0e-81
Match length
                  166
                   99
% identity
                  Oryza sativa ONIT4 mRNA for nitrilase-like protein,
NCBI Description
                  complète cds
Seq. No.
                   402511
Seq. ID
                  LIB3431-053-P1-N1-F9
Method
                  BLASTX
                              7.0
                  g733454
NCBI GI
BLAST score
                  240
E value
                  2.0e-37
Match length
                  90
% identity
                   92
NCBI Description
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
Seq. No.
                  402512
Seq. ID
                  LIB3431-053-P1-N1-G1
Method
                  BLASTX
NCBI GI
                  g3047064
BLAST score
                  374
E value
                  9.0e-36
                  90
Match length
% identity
NCBI Description
                   (AF058825) contains similarity to peptidyl-prolyl cis-trans
                  isomerase (Pfam: pro isomerase.hmm, score: 23.86 and 28.41
                  [Arabidopsis thaliana]
Seq. No.
                  402513
Seq. ID
                  LIB3431-053-P1-N1-G10
Method
                  BLASTX
NCBI GI
                  q132105
BLAST score
                  156
E value
                  1.0e-16
Match length
                  47
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208 dbj_BAA00538_
```

(D00643) small subunit of ribulose-1,5-bisphosphate

```
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]
```

```
Seq. No.
                   402514
Seq. ID
                   LIB3431-053-P1-N1-G11
- Method
                   BLASTX
NCBI GI
                   g671740
BLAST score
                   443
                   7.0e-44
E value
Match length
                   86
                   94
% identity
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct]
Seq. No.
                   402515
                   LIB3431-053-P1-N1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q5107149
BLAST score
                   309
E value
                   4.0e-28
Match length
                   84
% identity
                   75
                   (AF150080) small zinc finger-like protein [Oryza sativa]
NCBI Description
Seq. No.
                   402516
Seq. ID
                   LIB3431-053-P1-N1-G2
Method
                   BLASTN
NCBI GI
                   g20262
BLAST score
                   147
E value
                   9.0e-77
Match length
                   174
% identity
                   97
NCBI Description
                   O.sativa light-induced mRNA
Seq. No.
                   402517
Seq. ID
                   LIB3431-053-P1-N1-G3
Method
                   BLASTX
NCBI GI
                   g3510256
BLAST score
                   266
E value
                   4.0e-23
                   89
Match length
% identity
NCBI Description
                   (AC005310) unknown protein [Arabidopsis thaliana]
Seq. No.
                   402518
Seq. ID
                   LIB3431-053-P1-N1-G4
Method
                   BLASTX
NCBI GI
                   g347451
BLAST score
                   207
                   2.0e-16
E value
Match length
                  48
                   88
% identity
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
```

sativa]

Match length

```
Seq. No.
                   402519
Seq. ID
                  LIB3431-053-P1-N1-G5
Method
                   BLASTX
NCBI GI
                   g4530591
BLAST score
                   483
                   2.0e-48
E value
Match length
                   116
% identity
                   74
NCBI Description
                   (AF132475) heme oxygenase 1 [Arabidopsis thaliana]
                   >gi 4530593 gb AAD22108.1 (AF132476) heme oxygenase 1
                   [Arabidopsis thaliana] >gi 4877362 dbj BAA77758.1
                   (AB021857) plastid heme oxygenase [Arabidopsis thaliana]
                   >gi 4877397 dbj_BAA77759.1_ (AB021858) plastid heme
                   oxygenase [Arabidopsis thaliana] >gi 4883666 gb AAB95301.2
                   (AC003105) heme oxygenase 1 (HO1) [Arabidopsis thaliana]
Seq. No.
                   402520
Seq. ID
                  LIB3431-053-P1-N1-G9
Method
                  BLASTX
NCBI GI
                  q115813
BLAST score
                  257
E value
                  2.0e-35
Match length
                  95
% identity
                  83
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi 19182 emb CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                  402521
Seq. ID
                  LIB3431-053-P1-N1-H10
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  486
E value
                  7.0e-49
Match length
                  88
% identity
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                  402522
Seq. ID
                  LIB3431-053-P1-N1-H12
Method
                  BLASTX
NCBI GI
                  g2384956
BLAST score
                  275
E value
                  1.0e-25
Match length
                  149
% identity
                  43
NCBI Description
                  (AF022985) No definition line found [Caenorhabditis
                  elegans]
Seq. No.
                  402523
Seq. ID
                  LIB3431-053-P1-N1-H2
Method
                  BLASTX
NCBI GI
                  g733454
BLAST score
                  310
E value
                  6.0e-45
```

Seq. ID

Method

BLASTN

```
% identity
                  (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
Seq. No.
                  402524
                  LIB3431-053-P1-N1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131225
BLAST score
                  318
                  3.0e-37
E value
Match length
                  101
                  81
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >qi 100605 pir A39759 photosystem I 18K protein
                  precursor - barley >qi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  402525
Seq. No.
                  LIB3431-053-P1-N1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2499417
BLAST score
                  327 ...
                  2.0e-30
E value
Match length
                  78
                  79
% identity
                  GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR
NCBI Description
                  >gi 1085826 pir S49248 H-protein - Flaveria anomala
                  >gi_547558_emb_CAA85761_ (Z37524) H-protein [Flaveria
                  anomala]
                  402526
Seq. No.
Seq. ID
                  LIB3431-053-P1-N1-H7
Method
                  BLASTX
NCBI GI
                  q5442410
BLAST score
                  157
E value
                  1.0e-15
Match length
                  109
% identity
NCBI Description
                  (AF159254) ascorbate peroxidase [Zantedeschia aethiopica]
Seq. No.
                  402527
                  LIB3431-053-P1-N1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132081
BLAST score
                  170
                  2.0e-15
E value
Match length
                  53
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT) >gi 68093 pir RKRZS
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor - rice >gi_20341_emb_CAA30393_ (X07515) ribulose
                  bisphosphate carboxylase [Oryza sativa]
Seq. No.
                  402528
                  LIB3431-053-P1-N1-H9
```

```
NCBI GI
                  q3789951
BLAST score
                  102
                  6.0e-50
E value
Match length
                  212
% identity
                  87
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                  (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
                  402529
Seq. No.
                  LIB3431-054-P1-K1-A10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3913426
BLAST score
                  784
                  8.0e-84
E value
                  164
Match length
% identity
                  87
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                  (SAMDC) >qi 1532048 emb CAA69074 (Y07766)
                  S-adenosylmethionine decarboxylase [Oryza sativa]
                  402530
Seq. No.
                  LIB3431-054-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100880 -
BLAST score
                  282
E value
                  2.0e-25
Match length
                  86
                  71
% identity
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
NCBI Description
                   (phosphorylating) (EC 1.2.1.13) A, chloroplast - maize
Seq. No.
                  402531
                  LIB3431-054-P1-K1-A3
Seq. ID
Method
                  BLASTX
                  g1173347
NCBI GI
BLAST score
                  591
                  2.0e-61
E value
                  115
Match length
% identity
                  93
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description .
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7) P2ASE)
                  >gi 100803 pir S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi 14265 emb CAA46507
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
                  402532
Seq. No.
                  LIB3431-054-P1-K1-A4
Seq, ID
                  BLASTN
Method
NCBI GI
                  g3241924
BLAST score
                  45
                  5.0e-16
E value
Match length
                  185
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

MNC6, complete sequence

361 . .

Seq. ID

```
Seq. No.
                    402533
 Seq. ID
                    LIB3431-054-P1-K1-A8
 Method
                    BLASTX
 NCBI GI
                    g320618
 BLAST score
                    373
 E value
                    7.0e-36
 Match length
                    91
 % identity
                    78
 NCBI Description
                    chlorophyll a/b-binding protein I precursor - rice
                    >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                    chlorophyll a/b-binding protein [Oryza sativa]
                    >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
 Seq. No.
                   402534
 Seq. ID
                   LIB3431-054-P1-K1-B10
Method .
                   BLASTX
 NCBI GI
                   g4972093
BLAST score
                   466
E value
                   1.0e-46
Match length
                   125
% identity
                   70
NCBI Description
                   (AL078468) putative protein [Arabidopsis thaliana].
Seq. No.
                   402535
Seq. ID
                   LIB3431-054-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   1.0e-19
Match length
                   44
% identity
                   100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   402536
Seq. ID
                   LIB3431-054-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   717
E value
                   6.0e-76
Match length
                   152
% identity
                   89
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  402537
```

LIB3431-054-P1-K1-B2

Seq. No.

402542

```
Method
                   BLASTX
 NCBI GI
                   g2435519
 BLAST score
                   388
 E value
                   2.0e-37
 Match length
                   117
 % identity
                   64
 NCBI Description
                   (AF024504) similar to mouse MEM3 (GB:U47024 and S.
                   cerevisiae vacuolar sorting protein 35 (SW; P34110)
                   [Arabidopsis thaliana]
 Seq. No.
                   402538
 Seq. ID
                   LIB3431-054-P1-K1-B3
 Method
                   BLASTX
 NCBI GI
                   g461812
 BLAST score
                   245
 E value
                   1.0e-20
Match length
                   94
 % identity
                   45
                   CYTOCHROME P450 72A1 (CYPLXXII) (PROBABLE
NCBI Description
                   GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)
                   Cytochrome P-450 protein [Catharanthus roseus]
                   >gi_445604 prf 1909351A cytochrome P450 [Catharanthus
                   roseus
Seq. No.
                   402539
Seq. ID
                   LIB3431-054-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g3126854
BLAST score
                   629
E value
                   9.0e-66
Match length
                   126
% identity
                   94
NCBI Description
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   402540
Seq. ID
                   LIB3431-054-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g2894534
BLAST score
                   561
E value
                   8.0e-58
Match length
                   124
% identity
                   88
NCBI Description
                   (AJ224327) aquaporin [Oryza sativa]
Seq. No.
                  402541
Seq. ID
                  LIB3431-054-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g3024871
BLAST score
                  216
E value
                  3.0e-17
Match length
                  160
% identity
NCBI Description
                  HYPOTHETICAL 77.3 KD PROTEIN SLL0005
                  >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis
                  sp.]
```

.

```
Seq. ID
                  LIB3431-054-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g3913018
BLAST score
                  681
                  6.0e-72
E value
Match length
                  136
% identity
                  99
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi 218155 dbj_BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
Seq. No.
                  402543
                  LIB3431-054-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3789954
BLAST score
                  336
E value
                  2.0e-31
Match length
                  63
% identity
                  98
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
Seq. No.
                  402544
Seq. ID
                  LIB3431-054-P1-K1-C1
Method
                  BLASTX 4
NCBI GI
                  q167097
BLAST score
                  151
E value
                  1.0e-21
Match length
                  64
% identity
                   (M55449) ribulose 1,5-bisphosphate carboxylase activase
NCBI Description
                   [Hordeum vulgare]
Seq. No.
                  402545
                  LIB3431-054-P1-K1-C10
Seq. ID
Method
                  BLASTX
                  g1653935
NCBI GI
BLAST score
                  182
E value
                  3.0e-13
Match length
                  64
% identity
                  56
                  (D90917) hypothetical protein [Synechocystis sp.]
NCBI Description
Seq. No.
                  402546
Seq. ID
                  LIB3431-054-P1-K1-C11
                  BLASTX
Method
                  g2651310
NCBI GI
BLAST score
                  375
                  7.0e-36
E value
Match length
                  148
                  53
% identity
NCBI Description
                  (AC002336) putative PTR2-B peptide transporter [Arabidopsis
                  thaliana]
Seq. No.
                  402547
                  LIB3431-054-P1-K1-C12
Seq. ID
```

BLASTX

Method

E value

5.0e-61

```
NCBI GI
                   g3927827
BLAST score
                   195
                   7.0e-15
E value
Match length
                   115
% identity
                   42
NCBI Description
                   (AC005727) osmotin-like protein precursor [Arabidopsis
                   thaliana]
Seq. No.
                   402548
Seq. ID
                   LIB3431-054-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   q2306981
BLAST score
                   441
E value
                   9.0e-44
Match length
                   125
% identity
NCBI Description
                   (AF010321) photosystem I antenna protein [Oryza sativa]
Seq. No.
                   402549
Seq. ID
                   LIB3431-054-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g417260
BLAST score
                   421
E value
                   2.0e-41
Match length
                   128
% identity
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003_pir S33632
NCBI Description
                   lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                   light-regulated gene [Oryza sativa]
Seq. No.
                   402550
Seq. ID
                  LIB3431-054-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  g3885891
BLAST score
                  245
E value
                  1.0e-135
Match length
                  245
% identity
                  100
NCBI Description
                  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                  mRNA, complete cds
Seq. No.
                  402551
                  LIB3431-054-P1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2832672
BLAST score
                  160
E value
                  1.0e-10
Match length
                  33
% identity
                  97
NCBI Description
                  (AL021712) nifU-like protein [Arabidopsis thaliana]
Seq. No.
                  402552
Seq. ID
                  LIB3431-054-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  g1835730
BLAST score
                  120
```

```
Match length
                   176
% identity
                   92
NCBI Description
                   Oryza sativa photosystem II 10 kDa polypeptide mRNA,
                   complete cds
Seq. No.
                   402553
Seq. ID
                  LIB3431-054-P1-K1-C7
Method
                   BLASTX
:NCBI GI
                   g2924520
BLAST score
                   609
E value
                   3.0e-63
Match length
                   159
% identity
                   72
                   (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   402554
Seq. ID
                  LIB3431-054-P1-K1-C8
Method
                  BLASTX
NCBI GI
                   g3789954
BLAST score
                   628
E value
                   1.0e-65
Match length
                   159
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   402555
Seq. No.
Seq. ID
                  LIB3431-054-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                   237
E value
                  1.0e-19
Match length
                   44
% identity
                   100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                   402556
Seq. No.
Seq. ID
                  LIB3431-054-P1-K1-D1
Method
                  BLASTN
                  g2677829
NCBI GI
BLAST score
                  133
                  2.0e-68
E value
Match length
                  341
                  85
% identity
NCBI Description
                  Prunus armeniaca ribosomal protein L12 mRNA, complete cds
                   402557
Seq. No.
Seq. ID
                  LIB3431-054-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g1778095
BLAST score
                   452
                  4.0e-45
E value
Match length
                  122
```

71

% identity

```
NCBI Description (U64903) putative sugar transporter; member of major
                  facilitative superfamily; integral membrane protein [Beta
                  vulgaris]
                  402558
Seq. No.
                  LIB3431-054-P1-K1-D2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4138289
                  192
BLAST score
                  1.0e-104
E value
                  251
Match length
% identity
                  94
                  Oryza sativa mRNA for thioredoxin M
NCBI Description
Seq. No.
                  402559
Seq. ID
                  LIB3431-054-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q115796
BLAST score
                  571
                  1.0e-64
E value
Match length
                  127
% identity
                  98
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I
                  CAB) (LHCP) >gi 218174 dbj BAA00537 (D00642) type II
                  light-harvesting chlorophyll a/b-binding protein [Oryza
                  sativa]
Seq. No.
                  402560
Seq. ID
                  LIB3431-054-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q3075488
BLAST score
                  518
E value
                  1.0e-52
Match length
                  117
% identity
                  85 .
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  402561
Seq. ID
                  LIB3431-054-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q3789948
BLAST score
                  709
E value
                  5.0e-75
Match length
                  149
% identity
                  (AF094773) translation initiation factor 5A [Oryza sativa]
NCBI Description
Seq. No.
                  402562
                  LIB3431-054-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4239845
BLAST score
                  205
                  6.0e-16
E value
Match length
                  113
% identity
                  42
```

NCBI Description (AB015855) transcription factor TEIL [Nicotiana tabacum]

```
Seq. No.
                   402563
Seq. ID
                  LIB3431-054-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2191138
BLAST score
                  152
E value
                  8.0e-10
Match length
                  108
% identity
                   41
NCBI Description
                   (AF007269) A IG002N01.18 gene product [Arabidopsis
                  thaliana]
Seq. No.
                  402564
Seq. ID
                  LIB3431-054-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g3776005
BLAST score
                  746
E value
                  2.0e-79
Match length
                  163
% identity
                  89
NCBI Description
                  (AJ010466) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  402565
Seq. ID
                  LIB3431-054-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g4205079.
BLAST score
                  436
                  4.0e-43
E value
Match length
                  154
% identity
                  55
NCBI Description
                  (U70425) ankyrin repeat-containing protein 2 [Arabidopsis
                  thaliana]
Seq. No.
                  402566
Seq. ID
                  LIB3431-054-P1-K1-E3
Method
                  BLASTX
                  g320618
NCBI GI
BLAST score
                  380
E value
                  7.0e-37
Match length
                  96
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  402567
Seq. ID
                  LIB3431-054-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  q1928981
BLAST score
                  337
E value
                  1.0e-31
Match length
                  107
% identity
NCBI Description
                  (U92651) tonoplast intrinsic protein bobTIP26-1 [Brassica
```

oleracea var. botrytis]

Seq. No.

```
402568
Seq. No.
                  LIB3431-054-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  1.0e-19
Match length
                  44
% identity
                  100
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  402569
Seq. ID
                  LIB3431-054-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g3075488
BLAST score
                  749
                  1.0e-79
E value
Match length
                  143
% identity
                  100
                  (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  402570
Seq. ID
                  LIB3431-054-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g2760834
BLAST score
                  422
E value
                  2.0e-41
Match length
                  122
% identity
NCBI Description
                  (AC003105) putative nitrate transporter [Arabidopsis
                  thaliana]
                  402571
Seq. No.
Seq. ID
                 LIB3431-054-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
                  9.0e-20
E value
Match length
                  44
% identity
                  100
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  402572
Seq. ID
                  LIB3431-054-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  632
E value
                  4.0e-66
Match length
                  121
% identity
NCBI Description
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
```

```
LIB3431-054-P1-K1-F3
Seq. ID
                  BLASTX
Method
                  g115815
NCBI GI
BLAST score
                  454
                  1.0e-45
E value
Match length
                  84 -
                  99
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN M9 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-M9) (LHCP) >gi 100866 pir S13098 chlorophyll
                  a/b-binding protein precursor - maize
                  >qi 22355 emb CAA39376 (X55892) light-harvesting
                  chlorophyll a/b binding protein [Zea mays]
                  402574
Seq. No.
                  LIB3431-054-P1-K1-F4
Seq. ID
                  BLASTX
Method
                  g3345477
NCBI GI
BLAST score
                  404
                  2.0e-39
E value
Match length
                  127
% identity
                  64
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                  402575
Seq. No.
Seq. ID
                  LIB3431-054-P1-K1-F7
Method
                  BLASTX
                  g417260
NCBI GI
                   421
BLAST score
                   3.0e-41
E value
Match length
                  128
% identity
                   66
                  LIGHT REGULATED PROTEIN PRECURSOR >qi 422003 pir S33632
NCBI Description
                  lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                  light-regulated gene [Oryza sativa]
                   402576
Seq. No.
Seq. ID
                  LIB3431-054-P1-K1-F9
                  BLASTX
Method
                   g3885886
NCBI GI
BLAST score
                   710
E value
                   3.0e-75
                  138
Match length
                   100
% identity
                  (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
NCBI Description
                   402577
Seq. No.
Seq. ID
                  LIB3431-054-P1-K1-G10
Method
                   BLASTX
                   g1071913
NCBI GI
BLAST score
                   367
                   6.0e-35
E value
                   120
Match length
                   62
% identity
                  cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial
NCBI Description
                   - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine
```

synthase [Spinacia oleracea]

```
402578
Seq. No.
                   LIB3431-054-P1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3757521
BLAST score
                   567
                   2.0e-58
E value
                   169
Match length
                   58
% identity
NCBI Description (AC005167) unknown protein [Arabidopsis thaliana]
Seq. No.
                   402579
                   LIB3431-054-P1-K1-G3
Seq. ID
Method
                   BLASTX
                   g3789954
NCBI GI
BLAST score
                   550
                   1.0e-56
E value
Match length
                   122
                   93
% identity
                    (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
Seq. No.
                   402580
                   LIB3431-054-P1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1707657
BLAST score
                   538
                   5.0e-55
E value
Match length
                   167
% identity
                   62
                   (Z71640) DnaJ homologue [Pisum sativum]
NCBI Description
Seq. No.
                   402581
Seq. ID
                   LIB3431-054-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
                   1.0e-19
E value
Match length
                   44
% identity
                   100
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   402582
                   LIB3431-054-P1-K1-G7
Seq. ID
                   BLASTX
Method
                   g729478
NCBI GI
BLAST score
                   794
E value
                   5.0e-85
Match length
                   153
% identity
                   98
NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
                   >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1
                   (AP000616) ESTs AU078647(E15\overline{5}7),C724\overline{0}0(E\overline{1}557) correspond to
                   a region of the predicted gene.; similar to
```

ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

```
Seq. No.
                   402583
                   LIB3431-054-P1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3912968
BLAST score
                   172
                   3.0e-12
E value
Match length
                   123
% identity
                   30
                   ALPHA-ADAPTIN HOMOLOG >gi 1890329 emb CAA71991 (Y11104)
NCBI Description
                   alpha-adaptin [Drosophila melanogaster]
                   402584
Seq. No.
Seq. ID
                   LIB3431-054-P1-K1-H11
Method
                   BLASTX
                   g629670
NCBI GI
BLAST score
                   348
                   6.0e - 33
E value
Match length
                   94
% identity
                   68
                   hypothetical protein - tomato
NCBI Description
                   402585
Seq. No.
Seq. ID
                   LIB3431-054-P1-K1-H3
                   BLASTX
Method
                   q3885894
NCBI GI
                   398
BLAST score
                   7.0e-39
E value
Match length
                   90
% identity
                   (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
                   402586
Seq. No.
Seq. ID
                   LIB3431-054-P1-K1-H6
                   BLASTX
Method
                   g22380
NCBI GI
BLAST score
                   512
                   6.0e-52
E value
                   127
Match length
% identity
                    (X59714) CAAT-box DNA binding protein subunit B (NF-YB)
NCBI Description
                    [Zea mays]
                    402587
Seq. No.
Seq. ID
                   LIB3431-054-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   q320618
                    335
BLAST score
                    3.0e - 32
E value
                   88
Match length
                    83
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi 218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
```

[Oryza sativa]

E value

Match length

NCBI Description

% identity

```
402588
Seq. No.
                  LIB3431-054-P1-K1-H9
Seq. ID
                  BLASTX
Method
                  g132105
NCBI GI
                  635
BLAST score
                  1.0e-66
E value
                  116
Match length
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  402589
Seq. No.
                  LIB3431-054-P1-N1-A10
Seq. ID
                  BLASTX
Method
                  q3913426
NCBI GI
                  300
BLAST score
                  2.0e-33
E value
                  118
Match length
                  69
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                  (SAMDC) >gi_1532048 emb_CAA69074 (Y07766)
                  S-adenosylmethionine decarboxylase [Oryza sativa]
                  402590
Seq. No.
                  LIB3431-054-P1-N1-A3
Seq. ID
                  BLASTX
Method
                  g1173347
NCBI GI
                  276
BLAST score
                  1.0e-48
E value
                  116
Match length
% identity
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                  (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
                  402591
Seq. No.
                  LIB3431-054-P1-N1-A5
Seq. ID
                  BLASTX
Method
                  g6093830
NCBI GI
                  155
BLAST score
```

PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)

[CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor; putative photosytem II peptide [Spinacia oleracea]

4.0e-10

37

```
Seq. No.
                   402592
                  LIB3431-054-P1-N1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5091597
BLAST score
                  134
                   4.0e-69
E value
Match length
                  225
                  27
% identity
                  Oryza sativa chromosome 1 BAC 10A19I, complete sequence
NCBI Description
                   402593
Seq. No.
                  LIB3431-054-P1-N1-A8
Seq. ID
                  BLASTX
Method
                   g115787
NCBI GI
BLAST score
                   405
E value
                   1.0e-60
Match length
                   122
% identity
                   88
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir S03706 chlorophyll a/b-binding
                   protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   402594
Seq. No.
                   LIB3431-054-P1-N1-A9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q517500
BLAST score
                   374
                   6.0e-36
E value
                   90
Match length
% identity
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                   protein [Zea mays] >gi_444338_prf_ 1906386A photosystem II
                   OE17 protein [Pisum sativum]
                   402595
Seq. No.
Seq. ID
                   LIB3431-054-P1-N1-B10
Method
                   BLASTX
                   g4972093
NCBI GI
BLAST score
                   196
                   6.0e-27
E value
                   96
Match length
                   57
% identity
                   (AL078468) putative protein [Arabidopsis thaliana]
NCBI Description
                   402596
Seq. No.
                   LIB3431-054-P1-N1-B11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2072554
BLAST score
                   430
E value
                   0.0e + 00
Match length
                   484
                   98
% identity
                   Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
```

```
Seq. No.
                   402597
Seq. ID
                   LIB3431-054-P1-N1-B12
Method
                   BLASTX
NCBI GI
                   g347451
BLAST score
                   248
E value
                   4.0e-21
Match length
                   48
% identity
                   100
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                   sativa]
Seq. No.
                   402598
Seq. ID
                   LIB3431-054-P1-N1-B2
Method
                   BLASTX
NCBI GI
                   q2435519
BLAST score
                   183
E value
                   3.0e-13
Match length
                   62
% identity
                   58
NCBI Description
                   (AF024504) similar to mouse MEM3 (GB:U47024 and S.
                   cerevisiae vacuolar sorting protein 35 (SW; P34110)
                   [Arabidopsis thaliana]
Seq. No.
                   402599
Seq. ID
                   LIB3431-054-P1-N1-B3
Method
                   BLASTX
NCBI GI
                   q404688
BLAST score
                   242
E value
                   3.0e-20
Match length
                   69
% identity
                   55
NCBI Description
                  (L19074) cytochrome P450 [Catharanthus roseus]
Seq. No.
                   402600
Seq. ID
                  LIB3431-054-P1-N1-B4
Method
                   BLASTX
NCBI GI
                   q115802
BLAST score
                   205
E value.
                   4.0e-16
Match length
                   39
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
                  CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll
                  a/b-binding protein (cab-36) - common tobacco
                  >gi_19827_emb_CAA41188 (X58230) chlorophyll a/b binding
                  protein [Nicotiana tabacum]
Seq. No.
                  402601
Seq. ID
                  LIB3431-054-P1-N1-B5
Method
                  BLASTX
NCBI GI
                  q687677
BLAST score
                  221
E value
                  4.0e-18
Match length
                  51
% identity
                  82
NCBI Description
                  (U19925) unknown [Arabidopsis thaliana]
```

```
Seq. No.
                   402602
                   LIB3431-054-P1-N1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2696804
BLAST score
                   333
E value
                   3.0e-52
Match length
                   117
% identity
                   92
NCBI Description
                   (AB009665) water channel protein [Oryza sativa]
Seq. No.
                   402603
                   LIB3431-054-P1-N1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2407279
BLAST score
                   315
E value
                   3.0e-30
Match length
                   69
% identity
                   93
NCBI Description
                  (AF017362) aldolase [Oryza sativa]
Seq. No.
                   402604
Seq. ID
                   LIB3431-054-P1-N1-B9
Method
                   BLASTX
NCBI GI
                   g3789954
BLAST score
                   328
E value
                   2.0e-30
Match length
                   63
% identity
                   95
NCBI Description
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                   sativa]
Seq. No.
                   402605
Seq. ID
                   LIB3431-054-P1-N1-C1
Method
                   BLASTX
NCBI GI
                   g132166
BLAST score
                   156
E value
                   2.0e-10
Match length
                   31
% identity
                   84
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
                  CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE)
                  >gi_81660_pir_S04048 ribulose-bisphosphate carboxylase
                  activase precursor - Arabidopsis thaliana
                  >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 -
                  473) [Arabidopsis thaliana]
Seq. No.
                  402606
Seq. ID
                  LIB3431-054-P1-N1-C11
Method
                  BLASTX
NCBI GI
                  g2651310
BLAST score
                  163
E value
                  3.0e-11
Match length
                  69
% identity
                  45
NCBI Description
                  (AC002336) putative PTR2-B peptide transporter [Arabidopsis
                  thaliana]
```

```
Seq. No.
                   402607
Seq. ID
                   LIB3431-054-P1-N1-C2
Method
                   BLASTX
NCBI GI
                   g551047
BLAST score
                   268
E value
                   2.0e-23
Match length
                   52
% identity
                   96
                   (X79277) type II LHCI [Lolium temulentum]
NCBI Description
Seq. No.
                   402608
Seq. ID
                   LIB3431-054-P1-N1-C3
Method
                   BLASTX
NCBI GI
                   g417260
BLAST score
                   288
E value
                   1.0e-25
Match length
                   127
% identity
                   55
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir $33632
NCBI Description
                   lir1 protein - rice >gi 20263 emb CAA\overline{4}8706 (X688\overline{0}7)
                   light-regulated gene [Oryza sativa]
                   402609
Seq. No.
Seq. ID
                   LIB3431-054-P1-N1-C4
Method
                   BLASTN
NCBI GI
                   g3885891
BLAST score
                   241
E value
                   1.0e-133
Match length
                   245
                   100
% identity
NCBI Description
                   Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                   mRNA, complete cds
Seq. No.
                   402610
Seq. ID
                   LIB3431-054-P1-N1-C5
Method
                   BLASTX
NCBI GI
                   q2832672
BLAST score
                   587
E value
                   1.0e-60
                   135
Match length
% identity
                   81
NCBI Description
                  (AL021712) nifU-like protein [Arabidopsis thaliana]
Seq. No.
                   402611
Seq. ID
                   LIB3431-054-P1-N1-C6
Method
                   BLASTX
NCBI GI
                   g131400
BLAST score
                   284
E value
                   1.0e-34
Match length
                   130
                   63
% identity
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                   >gi 81471_pir__S00409 photosystem II 10K protein precursor
                   - spinach >gi 170127 (J03887) 10kd polypeptide precursor
                   [Spinacia oleracea]
```

```
Seq. No.
                    402612
 Seq. ID
                    LIB3431-054-P1-N1-C7
 Method
                    BLASTX
 NCBI GI
                    g3158476
 BLAST score
                    356
 E value
                   1.0e-33
 Match length
                   96
 % identity
                    72
NCBI Description
                   (AF067185) aquaporin 2 [Samanea saman]
 Seq. No.
                   402613
 Seq. ID
                   LIB3431-054-P1-N1-C8
                   BLASTX
Method
NCBI GI
                   g3789954
BLAST score
                   341
E value
                   8.0e-32
Match length
                   118
% identity
                   62
NCBI Description
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                   sativa]
Seq. No.
                   402614
Seq. ID
                   LIB3431-054-P1-N1-C9
Method
                   BLASTN
NCBI GI
                   g2072554
BLAST score
                   440
E value
                   0.0e + 00
Match length
                   483
% identity
                   98
NCBI Description
                   Oryza sativa metallothionein-like protein mRNA, complete
Seq. No.
                   402615
Seq. ID
                   LIB3431-054-P1-N1-D1
Method
                   BLASTX
NCBI GI
                   g4371282
BLAST score
                   541
E value
                   3.0e-55
Match length
                   119
% identity
NCBI Description
                   (AC006260) putative 60S ribosomal protein L12 [Arabidopsis
                   thaliana]
Seq. No.
                   402616
Seq. ID
                   LIB3431-054-P1-N1-D3
Method
                   BLASTX
NCBI GI
                   g3126854
BLAST score
                   296
E value
                   5.0e-53
Match length
                   108
% identity
                   99
NCBI Description
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   402617
Seq. ID
                   LIB3431-054-P1-N1-D4
Method
                   BLASTX
NCBI GI
                   g3075488
```

Method

BLASTX

```
BLAST score
                    525
 E value
                    2.0e-53
 Match length
                    111
 % identity
                    91
 NCBI Description
                    (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
 Seq. No.
                    402618
 Seq. ID
                    LIB3431-054-P1-N1-D5
 Method
                    BLASTX
 NCBI GI
                    g124226
 BLAST score
                    385
 E value
                    9.0e-59
 Match length
                    127
 % identity
                    92
 NCBI Description
                   INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D)
                    >gi_100278_pir__S21059 translation initiation factor
                    eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_
                   (X63542) eukaryotic initiation factor 5A (\overline{2}) [Nicotiana]
                   plumbaginifolial
 Seq. No.
                   402619
 Seq. ID
                   LIB3431-054-P1-N1-D8
Method
                   BLASTX
 NCBI GI
                   g2191138
 BLAST score
                   241
E value
                   1.0e-21
Match length
                   92
 % identity
                   64
NCBI Description
                   (AF007269) A IG002N01.18 gene product [Arabidopsis
                   thaliana]
Seq. No.
                   402620
                   LIB3431-054-P1-N1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q6093830
BLAST score
                   160
E value
                   7.0e-11
Match length
                   62
% identity
                   31
                   PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME)
NCBI Description
                   [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II
                   PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor;
                   putative photosytem II peptide [Spinacia oleracea]
Seq. No.
                   402621
Seq. ID
                   LIB3431-054-P1-N1-E2
Method
                   BLASTN
NCBI GI
                   g3819352
BLAST score
                   58
E value
                   9.0e-24
Match length
                  82
% identity
                  93
NCBI Description Hordeum vulgare genomic DNA fragment; clone MWG0813.rev
Seq. No.
                   402622
Seq. ID
                  LIB3431-054-P1-N1-E3
```

Seq. ID

```
NCBI GI
                    g115787
 BLAST score
                    356
 E value
                    3.0e-61
 Match length
                    123
 % identity
                    100
                    CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
 NCBI Description
                    CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                    protein 2R precursor - rice >gi_20182_emb_CAA32109
                    (X13909) chlorophyll a/b-binding preprotein (AA -2\overline{8} to 235)
                    [Oryza sativa]
 Seq. No.
                    402623
 Seq. ID
                    LIB3431-054-P1-N1-E4
 Method
                    BLASTX
 NCBI GI
                    q3695375
 BLAST score
                    288
 E value
                    7.0e-26
 Match length
                    67
 % identity
                    73
 NCBI Description
                   (AF096370) contains similarity to the major intrinsic
                   protein domain (Pfam: PF00230 MIP, E-value: 5.7e-111)
                   [Arabidopsis thaliana]
 Seq. No.
                   402624
 Seq. ID
                   LIB3431-054-P1-N1-E5
Method
                   BLASTX
 NCBI GI
                   q2072555
 BLAST score
                   237
E value
                   1.0e-19
Match length
                   44
 % identity
                   100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   402625
Seq. ID
                   LIB3431-054-P1-N1-E6
Method
                   BLASTX
NCBI GI
                   g1835731
BLAST score
                   424
E value
                   1.0e-55
Match length
                   126
% identity
NCBI Description
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                  402626
Seq. ID
                  LIB3431-054-P1-N1-E7
Method
                  BLASTX
NCBI GI
                  g4741954
BLAST score
                  296
E value
                  2.0e-49
Match length
                  111
% identity
NCBI Description
                  (AF134127) Lhcb4.2 protein [Arabidopsis thaliana]
Seq. No.
                  402627
```

LIB3431-054-P1-N1-F12

```
Method
                    BLASTX
 NCBI GI
                    g2072555
 BLAST score
                    222
 E value
                    6.0e-18
 Match length
                    41
 % identity
                    100
 NCBI Description
                    (AF001396) metallothionein-like protein [Oryza sativa]
                    >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                    protein [Oryza sativa]
 Seq. No.
                    402628
 Seq. ID
                    LIB3431-054-P1-N1-F2
 Method
                    BLASTX
 NCBI GI
                    g132105
 BLAST score
                    396
 E value
                    1.0e-38
 Match length
                    74
 % identity
                    96
 NCBI Description
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   402629
Seq. ID
                   LIB3431-054-P1-N1-F3
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   332
E value
                   6.0e-55
Match length
                   115
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                   protein 2R precursor - rice >gi 20182 emb CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                   402630
Seq. ID
                   LIB3431-054-P1-N1-F4
Method
                   BLASTX
NCBI GI
                   q606817
BLAST score
                   182
E value
                   3.0e-28
Match length
                   69
% identity
NCBI Description
                   (U08404) carbonic anhydrase [Oryza sativa]
                   >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic
                   anhydrase 3 [Oryza sativa]
Seq. No.
                   402631
Seq. ID
                  LIB3431-054-P1-N1-F6
Method
                  BLASTX
```

```
NCBI GI
                  g132105
BLAST score
                  747
                  2.0e-79
E value
Match length
                  158
% identity
                  89
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  402632
Seq. No.
                  LIB3431-054-P1-N1-F7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g20262
BLAST score
                  361
                  0.0e + 00
E value
Match length
                  361
                  100
% identity
                  O.sativa light-induced mRNA
NCBI Description
                  402633
Seq. No.
                  LIB3431-054-P1-N1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4982480
BLAST score
                  184
                   2.0e-13
E value
Match length
                  43
                  74
% identity
                   (AF069441) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   402634
                  LIB3431-054-P1-N1-F9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3885886
BLAST score
                   219
                   5.0e-33
E value
                   67
Match length
                   85
% identity
                   (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
NCBI Description
                   402635
Seq. No.
                   LIB3431-054-P1-N1-G1
Seq. ID
                   BLASTN
Method
                   g218209
NCBI GI
BLAST score
                   116
                   1.0e-58
E value
Match length
                   211
                   96
% identity
                   Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
```

pOSSS2106

BLAST score

```
402636
Seq. No.
                   LIB3431-054-P1-N1-G10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2118307
BLAST score
                   .166
                   4.0e-24
E value
Match length
                   91
% identity
                   cysteine synthase (EC 4.2.99.8) 3A - Arabidopsis thaliana
NCBI Description
                   >gi_804950_emb_CAA58893_ (X84097) cysteine synthase
                   [Arabidopsis thaliana] >gi_1096196_prf__2111276A Ser(Ac)
                   thiol lyase [Arabidopsis thaliana]
                   402637
Seq. No.
Seq. ID
                   LIB3431-054-P1-N1-G5
Method
                   BLASTX
NCBI GI
                   q2072555
BLAST score
                   230
E value
                   7.0e-19
Match length
                   44
% identity
                   98
                    (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   402638
Seq. No.
Seq. ID
                   LIB3431-054-P1-N1-G6
Method
                   BLASTX
NCBI GI
                   q6015059
BLAST score
                   320
E value
                   9.0e-51
Match length
                   104
                   97
% identity
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi 2996096
NCBI Description
                    (AF030517) translation elongation factor-1 alpha; EF-1
                   alpha [Oryza sativa]
Seq. No.
                   402639
                   LIB3431-054-P1-N1-G7
Seq. ID
Method
                   BLASTX
                   g729478
NCBI GI
BLAST score
                   429
E value
                   1.0e-73
Match length
                   152
                   93
% identity
                   FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR)
NCBI Description
                   >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+
reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1
                    (AP000616) ESTs AU078647(E15\overline{5}7),C724\overline{0}0(E\overline{1}557) correspond to
                   a region of the predicted gene.; similar to
                   ferredoxin-NADP+ reductase (D17790) [Oryza sativa]
                   402640
Seq. No.
                   LIB3431-054-P1-N1-H3
Seq. ID
Method
                   BLASTX
                   g3885894
NCBI GI
```

```
E value
                   9.0e-22
 Match length
                   64
 % identity
                   80
 NCBI Description
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
 Seq. No.
                   402641
 Seq. ID
                   LIB3431-054-P1-N1-H4
 Method
                   BLASTX
 NCBI GI
                   g115802
 BLAST score
                   191
 E value
                   1.0e-14
 Match length
                   37
 % identity
                   97
 NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
                   CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll
                   a/b-binding protein (cab-36) - common tobacco
                   >gi_19827 emb_CAA41188 (X58230) chlorophyll a/b binding
                   protein [Nicotiana tabacum]
 Seq. No.
                   402642
Seq. ID
                   LIB3431-054-P1-N1-H6
Method
                   BLASTX
NCBI GI
                   q115840
BLAST score
                   322
E value
                   1.0e-29
Match length
                   81
% identity
                   75
NCBI Description
                  CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y
                   PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN
                   SUBUNIT B)
Seq. No.
                   402643
Seq. ID
                  LIB3431-054-P1-N1-H7
Method
                  BLASTX
NCBI GI
                   q115787
BLAST score
                   410
E value
                  2.0e-70
Match length
                  144
% identity
                  96
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
Seq. No.
                  402644
Seq. ID
                  LIB3431-054-P1-N1-H8
Method
                  BLASTX
NCBI GI
                  q517500
BLAST score
                  389
E value
                  7.0e-49
Match length
                  126
% identity
                  83
NCBI Description
                  (M87435) precursor of the oxygen evolving complex 17 kDa
                  protein [Zea mays] >gi_444338_prf__1906386A photosystem II
```

OE17 protein [Pisum sativum]

```
Seq. No.
                    402645
 Seq. ID
                    LIB3431-055-P1-N1-A1
 Method
                    BLASTX
 NCBI GI
                    g1644427
 BLAST score
                    248
 E value
                    3.0e-21
 Match length
                    59
 % identity
                    78
 NCBI Description
                    (U74610) glyoxalase II [Arabidopsis thaliana]
 Seq. No.
                    402646
 Seq. ID
                    LIB3431-055-P1-N1-A11
 Method
                    BLASTX
 NCBI GI
                    g517500
 BLAST score
                    360
 E value
                    3.0e-34
Match length
                    87
 % identity
                    80
 NCBI Description
                    (M87435) precursor of the oxygen evolving complex 17 kDa
                    protein [Zea mays] >gi_444338_prf__1906386A photosystem II
                   OE17 protein [Pisum sativum]
Seq. No.
                    402647
Seq. ID
                   LIB3431-055-P1-N1-A2
Method
                   BLASTX
NCBI GI
                   g131225
BLAST score
                   216
E value
                   2.0e-17
Match length
                   56
% identity
                   73
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                   precursor - barley >g\overline{i}_116\overline{70}87 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
Seq. No.
                   402648
Seq. ID
                   LIB3431-055-P1-N1-A6
Method
                   BLASTX
NCBI GI
                   g693920
BLAST score
                   414
E value
                   2.0e-40
Match length
                   80
% identity
NCBI Description
                   (U21113) chlorophyll a/b binding protein [Solanum
                   tuberosum]
Seq. No.
                   402649
Seq. ID
                   LIB3431-055-P1-N1-A7
Method
                   BLASTX
NCBI GI
                   g21699
BLAST score
                   317
E value
                   3.0e-29
Match length
                   71
% identity
NCBI Description
                   (X66013) cathepsin B [Triticum aestivum]
Seq. No.
                   402650
```

```
Seq. ID
                    LIB3431-055-P1-N1-B1
 Method
                    BLASTX
 NCBI GI
                    g1168537
 BLAST score
                    254
 E value
                    6.0e-22
 Match length
                    46
 % identity
                    100
 NCBI Description
                    ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732
                    aspartic proteinase (EC 3.4.23.-) - rice
                    >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase
                    [Oryza sativa]
 Seq. No.
                    402651
 Seq. ID
                    LIB3431-055-P1-N1-B10
 Method
                    BLASTN
 NCBI GI
                    g2072554
 BLAST score
                    388
 E value
                    0.0e + 00
 Match length
                    388
 % identity
                    100
                   Oryza sativa metallothionein-like protein mRNA, complete
 NCBI Description
                    cds
 Seq. No.
                   402652
 Seq. ID
                   LIB3431-055-P1-N1-B11
Method
                   BLASTX
 NCBI GI
                   q1617197
 BLAST score
                   183
E value
                   9.0e-20
Match length
                   71
% identity
                   61
NCBI Description
                   (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                   402653
Seq. ID
                   LIB3431-055-P1-N1-B2
Method
                   BLASTX
NCBI GI
                   g3068705
BLAST score
                   203
E value
                   6.0e-16
Match length
                   62
% identity
                   56
NCBI Description
                   (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                   402654
Seq. ID
                  LIB3431-055-P1-N1-B3
Method
                   BLASTX
NCBI GI
                  g1173346
BLAST score
                  189
E value
                  1.0e-28
Match length
                  105
% identity
                  62
NCBI Description
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_515618_emb_CAA52439_ (X74418)
                  sedoheptulose-bisphosphatase [Chlamydomonas reinhardtii]
Seq. No.
```

E value

3.0e-22

```
Seq. ID
                    LIB3431-055-P1-N1-B5
  Method
                    BLASTX
  NCBI GI
                    g3738261
  BLAST score
                    340
 E value
                    4.0e-50
 Match length
                    122
  % identity
                    89
                    (AB018412) chloroplast phosphoglycerate kinase [Populus
 NCBI Description
 Seq. No.
                    402656
 Seq. ID
                    LIB3431-055-P1-N1-B8
 Method
                    BLASTX
 NCBI GI
                    g347451
 BLAST score
                    688
 E value
                    2.0e-72
 Match length
                   131
 % identity
                   96
 NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                   sativa]
 Seq. No.
                   402657
 Seq. ID
                   LIB3431-055-P1-N1-C1
 Method
                   BLASTX
 NCBI GI
                   g3126854
 BLAST score
                   303
 E value .
                   4.0e-47
 Match length
                   101
 % identity
                   91
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   402658
Seq. ID
                   LIB3431-055-P1-N1-C10
Method
                   BLASTX
NCBI GI
                   g3075488
BLAST score
                   200
E value
                   5.0e-30
Match length
                   69
% identity
                   93
NCBI Description (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                   402659
Seq. ID
                   LIB3431-055-P1-N1-C11
Method
                   BLASTX
NCBI GI
                   g3885886
BLAST score
                   439
E value
                   2.0e-43
Match length
                  79
% identity
NCBI Description (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
Seq. No.
                  402660
Seq. ID
                 LIB3431-055-P1-N1-C2
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                  163
```

NCBI GI

BLAST score

g3789952

```
Match length
                    67
  % identity
  NCBI Description
                    (AF022738) chlorophyll a-b binding protein [Oryza sativa]
  Seq. No.
                    402661
 Seq. ID
                    LIB3431-055-P1-N1-C6
 Method
                    BLASTX
 NCBI GI
                    q485518
 BLAST score
                    288
 E value
                    6.0e-26
 Match length
                    53
 % identity
                    100
 NCBI Description
                    ubiquitin / ribosomal protein CEP52 - rice
                    >gi_303857_dbj_BAA02154_ (D12629) ubiquitin/ribosomal
                    polyprotein [Oryza sativa]
 Seq. No.
                    402662
 Seq. ID
                    LIB3431-055-P1-N1-C7
 Method
                    BLASTN
 NCBI GI
                    g5714761
 BLAST score
                   50
 E value
                   7.0e-19
 Match length
                   78
 % identity
                   91
 NCBI Description
                   Oryza sativa subsp. indica serine/threonine protein
                   phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete
 Seq. No.
                   402663
 Seq. ID
                   LIB3431-055-P1-N1-C8
Method
                   BLASTX
NCBI GI
                   g4115925
BLAST score
                   166
E value
                   2.0e-15
Match length
                   67
% identity
                   64
NCBI Description
                   (AF118222) contains similarity to RNA recognition motifs
                   (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana]
                   >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein
                   [Arabidopsis thaliana] >gi_4959384_gb_AAD34325.1
                   (AF109721) RNA-binding protein [Arabidopsis thaliana]
Seq. No.
                   402664
Seq. ID
                  LIB3431-055-P1-N1-D11
Method
                  BLASTN
NCBI GI
                  g6016845
BLAST score
                  354
E value
                  0.0e+00
Match length
                  404
% identity
                  100
NCBI Description
                  Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                  402665
Seq. ID
                  LIB3431-055-P1-N1-D2
Method
                  BLASTX
```

E value

6.0e-45

```
E value
                     2.0e-29
  Match length
                     62
  % identity
                     97
 NCBI Description
                     (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                     sativa]
 Seq. No.
                     402666
 Seq. ID
                     LIB3431-055-P1-N1-D5
 Method
                     BLASTX
 NCBI GI
                     g671740
 BLAST score
                     541
 E value
                     3.0e-55
 Match length
                     99
 % identity
                     99
 NCBI Description
                     (X84730) ribulose-bisphosphate carboxylase [synthetic
                     construct]
 Seq. No.
                     402667
 Seq. ID
                    LIB3431-055-P1-N1-D7
 Method
                    BLASTX
 NCBI GI
                    g3861104
                               14.
 BLAST score
                    251
 E value
                    3.0e-21
 Match length
                    117
 % identity
                    46
 NCBI Description
                    (AJ235272) HEMOLYSIN (tlyA) [Rickettsia prowazekii]
 Seq. No.
                    402668
 Seq. ID
                    LIB3431-055-P1-N1-D8
 Method
                    BLASTX
NCBI GI
                    g115787
BLAST score
                    368
E value
                    2.0e-63
Match length
                    129
% identity
                    98
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
Seq. No.
                   402669
Seq. ID
                   LIB3431-055-P1-N1-E1
Method
                   BLASTX
NCBI GI
                   g5802955
BLAST score
                   235
E value
                   2.0e-19
Match length
                   58
% identity
NCBI Description
                   (AF178990) stress related protein [Vitis riparia]
Seq. No.
                   402670
Seq. ID
                   LIB3431-055-P1-N1-E12
Method
                   BLASTX
NCBI GI
                   g2130069
BLAST score
                   320
```

```
101
    Match length
    % identity
                       catalase (EC 1.11.1.6) catA - rice
NCBI Description
                       >gi 1261858 dbj BAA06232_ (D29966) catalase [Oryza sativa]
                       402671
    Seq. No.
                       LIB3431-055-P1-N1-E2
    Seq. ID
                       BLASTN
    Method
    NCBI GI
                       q3789951
    BLAST score
                       403
    E value
                       0.0e + 00
    Match length
                       480
    % identity
                       96
                       Oryza sativa chlorophyll a/b-binding protein presursor
    NCBI Description
                        (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                       complete cds
                       402672
    Seq. No.
                       LIB3431-055-P1-N1-E3
    Seq. ID
    Method
                       BLASTX
    NCBI GI
                       q4507769
                       257
    BLAST score
    E value
                       7.0e-37
                       98
    Match length
                       74
    % identity
                       ubiquitin-conjugating enzyme E2A (RAD6 homolog)
    NCBI Description
                       >gi_1351346_sp_P49459_UBCA_HUMAN_UBIQUITIN-CONJUGATING
                       ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN
                       CARRIER PROTEIN) (HR6A) >gi_108016_pir__A41222
                       ubiquitin-conjugating enzyme HHR6A - human >gi_184044
                        (M74524) HHR6A (Human homologue of yeast RAD 6); putative
                        [Homo sapiens]
                        402673
    Seq. No.
                       LIB3431-055-P1-N1-E9
    Seq. ID
    Method
                       BLASTX
    NCBI GI
                        g4335763
    BLAST score
                        333
                                                        *5
    E value
                        6.0e-31
    Match length
                        122
                        55
    % identity
    NCBI Description
                        (AC006284) unknown protein [Arabidopsis thaliana]
                        402674
    Seq. No.
                       LIB3431-055-P1-N1-F10
    Seq. ID
    Method
                        BLASTX
    NCBI GI
                        g4337175
    BLAST score
                        168
    E value
                        5.0e-25
    Match length
                        114
                        58
    % identity
                        (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
    NCBI Description
                       gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                        gb_AA720210 come from this gene. [Arabidopsis thaliana]
```

Seq. No.

Seq. ID

```
LIB3431-055-P1-N1-F2
Seq. ID
                  BLASTX
Method
                  g115787
NCBI GI
                  362
BLAST score
                  3.0e-50
E value
                  107
Match length
                  98
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  402676
                  LIB3431-055-P1-N1-F3
Seq. ID
                  BLASTX
Method
                  g2407279
NCBI GI
                  211
BLAST score
                  2.0e-26
E value
                  66
Match length
                  98
% identity
                  (AF017362) aldolase [Oryza sativa]
NCBI Description
                  402677
Seq. No.
                  LIB3431-055-P1-N1-F5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1321661
BLAST score
                  427
                  5.0e-42
E value
                  83
Match length
                  98
% identity
                  (D45423) ascorbate peroxidase [Oryza sativa]
NCBI Description
                  402678
Seq. No.
                  LIB3431-055-P1-N1-F6
Seq. ID
Method
                  BLASTX
                  g3036951
NCBI GI
BLAST score
                  343
                  2.0e-61
E value
                  122
Match length
                  98
% identity
                   (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                  402679
Seq. No.
                  LIB3431-055-P1-N1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2624325
BLAST score
                  227
                  1.0e-124
E value
Match length
                  239
% identity
                  Oryza sativa mRNA for glycine-rich RNA-binding protein
NCBI Description
                   (OsGRP1)
                   402680
Seq. No.
```

LIB3431-055-P1-N1-F9

Match length

```
Method
                    BLASTX
 NCBI GI
                    g4038663
 BLAST score
                    163
 E value
                    8.0e-24
 Match length
                    66
 % identity
                    69
 NCBI Description
                    (AB020929) ribulose-1,5-bisphosphate carboxylase/oxygenase
                    small subunit [Aegilops speltoides]
 Seq. No.
                    402681
 Seq. ID
                    LIB3431-055-P1-N1-G1
 Method
                    BLASTX
 NCBI GI
                    g3789954
 BLAST score
                    294
 E value
                    2.0e-26
 Match length
                    89
 % identity
                    56
 NCBI Description
                    (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                    sativa]
 Seq. No.
                    402682
 Seq. ID
                    LIB3431-055-P1-N1-G10
 Method
                    BLASTX
 NCBI GI
                    g3075488
 BLAST score
                    479
 E value
                    5.0e-48
Match length
                    93
 % identity
                    99
NCBI Description
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                    402683
Seq. ID
                   LIB3431-055-P1-N1-G11
Method
                   BLASTX
NCBI GI
                   g1617197
BLAST score
                   180
E value
                   3.0e-13
Match length
                   36
% identity
                   92
NCBI Description
                   (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                   402684
Seq. ID
                   LIB3431-055-P1-N1-G2
Method
                   BLASTN
NCBI GI
                   g20262
BLAST score
                   169
E value
                   7.0e-90
Match length
                   188
% identity
                   97
NCBI Description
                   O.sativa light-induced mRNA
Seq. No.
                   402685
Seq. ID
                   LIB3431-055-P1-N1-G4
Method
                   BLASTX
NCBI GI
                   g3075488
BLAST score
                   452
E value
                   7.0e-45
```

```
% identity
                    98
  NCBI Description
                    (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
  Seq. No.
                    402686
  Seq. ID
                    LIB3431-055-P1-N1-G5
 Method
                    BLASTX
 NCBI GI
                    g1617197
 BLAST score
                    261
 E value
                    2.0e-22
 Match length
                    71
 % identity
                    66
 NCBI Description
                   (Z72488) CP12 [Nicotiana tabacum]
 Seq. No.
                    402687
 Seq. ID
                   LIB3431-055-P1-N1-G6
 Method
                   BLASTX
 NCBI GI
                   q131225
 BLAST score
                    309
 E value
                    3.0e-28
 Match length
                   75
 % identity
                   79
 NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                   precursor - barley >gi_167087 (M61146) photosystem I
                   hydrophobic protein [Hordeum vulgare]
 Seq. No.
                   402688
 Seq. ID.
                   LIB3431-055-P1-N1-G8
Method
                   BLASTX
NCBI GI
                   g1076724
BLAST score
                   233
E value
                   1.0e-31
Match length
                   77
% identity
                   88
NCBI Description
                   LHCI-680, photosystem I antenna protein - barley
                   >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                   antenna protein [Hordeum vulgare]
Seq. No.
                   402689
Seq. ID
                   LIB3431-055-P1-N1-G9
Method
                   BLASTX
NCBI GI
                   g1617197
BLAST score
                   204
E value
                   7.0e-16
Match length
                   47
% identity
                   79
NCBI Description
                  (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                  402690
Seq. ID
                  LIB3431-055-P1-N1-H1
Method
                  BLASTN
NCBI GI
                  g3063523
BLAST score
                  117
E value
                  4.0e-59
Match length
                  281
% identity
                  86
NCBI Description Oryza sativa ribulose 1,5-bisphosphate carboxylase small
```

% identity

97

16

subunit mRNA, complete cds

```
402691
Seq. No.
 Seq. ID
                    LIB3431-055-P1-N1-H11
 Method
                   BLASTX
 NCBI GI
                    g3004565
 BLAST score
                    255
 E value
                    9.0e-22
 Match length
                    94
 % identity
                    55
                    (AC003673) putative protein kinase [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    402692
                   LIB3431-055-P1-N1-H2
 Seq. ID
 Method
                    BLASTN
                    g2773153
 NCBI GI
 BLAST score
                    371
                    0.0e + 00
 E value
                    375
 Match length
                    100
 % identity
 NCBI Description
                   Oryza sativa abscisic acid- and stress-inducible protein
                    (Asr1) mRNA, complete cds
                    402693
 Seq. No.
 Seq. ID
                    LIB3431-055-P1-N1-H3
 Method
                    BLASTX
 NCBI GI
                    g548605
 BLAST score
                    420
                    4.0e-56
 E value
                    131
 Match length
                    91
 % identity
 NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                    (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                    >gi 539055_pir__A48527 photosystem I protein psaK precursor
                    - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                    [Hordeum vulgare]
 Seq. No.
                    402694
                    LIB3431-055-P1-N1-H4
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q115813
 BLAST score
                    432
 E value
                    1.0e-42
 Match length
                    104
                    81
 % identity
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
 NCBI Description
                    CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                    chlorophyll a/b-binding protein [Lycopersicon esculentum]
 Seq. No.
                    402695
                    LIB3431-055-P1-N1-H5
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g132105
 BLAST score
                    521
 E value
                    6.0e-53
 Match length
                    99
```

Seq. ID

```
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   402696
Seq. ID
                  LIB3431-055-P1-N1-H6
Method
                  BLASTX
                  q671740
NCBI GI
BLAST score
                   458
                   1.0e-45
E value
Match length
                  86
                   99
% identity
NCBI Description
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
                   construct],
Seq. No.
                   402697
Seq. ID
                  LIB3431-055-P1-N1-H7
Method
                  BLASTX
NCBI GI
                  q4325041
BLAST score
                   632
E value
                   6.0e-66
Match length
                  140
% identity
                  (AF117339) FtsH-like protein Pftf precursor [Nicotiana
NCBI Description
                  tabacum]
Seq. No.
                   402698
Seq. ID
                  LIB3431-055-P1-N1-H8
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  251
E value
                   1.0e-29
Match length
                  69
                  100
% identity .
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   402699
                  LIB3431-055-P1-N1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                   495
E value
                   7.0e-50
                  125
Match length
                   78
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                   402700
Seq. No.
```

LIB3431-055-P2-K1-A9

BLAST score

```
Method
                    BLASTX
 NCBI GI
                    g3650033
 BLAST score
                    293
 E value
                    2.0e-42
 Match length
                    153
 % identity
 NCBI Description
                    (AC005396) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    402701
 Seq. ID
                    LIB3431-055-P2-K1-B1
 Method
                    BLASTN
 NCBI GI
                    g218142
 BLAST score
                    77
 E value
                    2.0e-35
 Match length
                    225
 % identity
                    85
 NCBI Description
                   Rice mRNA for aspartic proteinase, complete cds
 Seq. No.
                    402702
 Seq. ID
                   LIB3431-055-P2-K1-B10
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   233
E value
                   6.0e-20
Match length
                   44
 % identity
                   98
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   402703
Seq. ID
                   LIB3431-055-P2-K1-B5
Method
                   BLASTX
NCBI GI
                   g3328122
BLAST score
                   150
E value
                   1.0e-09
Match length
                   41
% identity
                   78
                   (AF073473) phosphoglycerate kinase precursor [Solanum
NCBI Description
                   tuberosum]
Seq. No.
                   402704
Seq. ID
                   LIB3431-055-P2-K1-B8
Method
                   BLASTX
NCBI GI
                   g2407281
BLAST score
                   668
E value
                   2.0e-70
Match length
                  135
% identity
NCBI Description
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
                  subunit [Oryza sativa]
Seq. No.
                  402705
Seq. ID
                  LIB3431-055-P2-K1-B9
Method
                  BLASTX
NCBI GI
                  g3914005
```

Match length

```
E value
                    7.0e-34
 Match length
                    90
  % identity
                    90
 NCBI Description
                    MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586
                    (U85494) LON1 protease [Zea mays]
 Seq. No.
                    402706
 Seq. ID
                    LIB3431-055-P2-K1-C1
 Method
                    BLASTX
 NCBI GI
                    g3126854
 BLAST score
                    443
 E value
                    5.0e-44
 Match length
                    119
 % identity
                    84
 NCBI Description
                    (AF061577) chlorophyll a/b binding protein [Oryza sativa]
 Seq. No.
                    402707
 Seq. ID
                    LIB3431-055-P2-K1-C11
 Method
                    BLASTN
 NCBI GI
                    g3885885
 BLAST score
                    32
 E value
                    3.0e-09
 Match length
                   32
 % identity
                   100
                   Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA,
 NCBI Description
                   complete cds
 Seq. No.
                   402708
 Seq. ID
                   LIB3431-055-P2-K1-C6
Method
                   BLASTN
NCBI GI
                   q303856
BLAST score
                   139
E value
                   4.0e-72
Match length
                   227
% identity
                   93
NCBI Description
                   Rice mRNA for ubiquitin protein fused to a ribosomal
                   protein, complete cds
Seq. No.
                   402709
Seq. ID
                   LIB3431-055-P2-K1-C7
Method
                   BLASTX
NCBI GI
                   g517500
BLAST score
                   160
E value
                   1.0e-10
Match length
                   61
% identity
NCBI Description
                   (M87435) precursor of the oxygen evolving complex 17 kDa \,
                  protein [Zea mays] >gi_444338_prf__1906386A photosystem II
                  OE17 protein [Pisum sativum]
Seq. No.
                  402710
Seq. ID
                  LIB3431-055-P2-K1-D11
Method
                  BLASTN
NCBI GI
                  g6016845
BLAST score
                  66
E value
                  1.0e-28
```

Seq. No.

```
% identity
                    90
 NCBI Description
                   Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
 Seq. No.
                   402711
 Seq. ID
                   LIB3431-055-P2-K1-E11
Method
                   BLASTX
NCBI GI
                   g2129512
 BLAST score
                   207
E value
                   7.0e-17
Match length
                   56
 % identity
                   75
NCBI Description
                   glycerate dehydrogenase (EC 1.1.1.29) splice form HPR2 -
                   cucurbit >gi_1304044_dbj_BAA08411_ (D49433) hydroxypyruvate
                   reductase [Cucurbita sp.]
Seq. No.
                   402712
Seq. ID
                   LIB3431-055-P2-K1-E4
Method
                   BLASTX
NCBI GI
                   g6041808
BLAST score
                   258
E value
                   5.0e-27
Match length
                   92
% identity
                   66
NCBI Description
                   (AC009755) unknown protein [Arabidopsis thaliana]
Seq. No.
                   402713
Seq. ID
                   LIB3431-055-P2-K1-F3
                   BLASTN
Method
NCBI GI
                   g2407278
BLAST score
                   56
E value
                   9.0e-23
Match length
                   208
% identity
                   82
NCBI Description
                   Oryza sativa aldolase mRNA, complete cds
Seq. No.
                   402714
Seq. ID
                   LIB3431-055-P2-K1-F6
Method
                   BLASTX
NCBI GI
                   g1661160
BLAST score
                   441
E value
                   1.0e-43
Match length
                   104
% identity
                   80
NCBI Description
                   (U74295) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   402715
Seq. ID
                  LIB3431-055-P2-K1-F7
Method
                  BLASTN
NCBI GI
                  g2407282
BLAST score
                  57
E value
                  6.0e-24
Match length
                  73
% identity
                  95
NCBI Description
                  Oryza sativa ribulose 1,5-bisphosphate carboxylase small
                  subunit mRNA, complete cds
```

```
LIB3431-055-P2-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2407281
BLAST score
                  645
                  1.0e-67
E value
                  122
Match length
                   97
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
Seq. No.
                   402717
                  LIB3431-055-P2-K1-G10
Seq. ID
Method
                  BLASTN
                  g3075487
NCBI GI
BLAST score
                  99
E value
                  1.0e-48
Match length
                  123
                  95
% identity
                  Oryza sativa chlorophyll a/b-binding protein (RCABP69)
NCBI Description
                  mRNA, complete cds
                  402718
Seq. No.
                  LIB3431-055-P2-K1-G2
Seq. ID
Method
                  BLASTN
                  g20262
NCBI GI
BLAST score
                  227
E value
                  1.0e-125
Match length
                  231
                  100
% identity
NCBI Description O.sativa light-induced mRNA
Seq. No.
                  402719
Seq. ID
                  LIB3431-055-P2-K1-H11
Method
                  BLASTX
                  g3004565
NCBI GI
BLAST score
                   340
E value
                   4.0e-32
                  97
Match length
% identity
                   (AC003673) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   402720
Seq. No.
                  LIB3431-055-P2-K1-H12
Seq. ID
Method
                  BLASTX
                  g4678920
NCBI GI
BLAST score
                  227
E value
                   1.0e-18
Match length
                  102
                   48
% identity
                   (AL049711) putative heat shock transcription factor
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   402721
                  LIB3431-055-P2-K1-H2
Seq. ID
Method
                  BLASTN
                  g2773153
NCBI GI
```

BLAST score

```
E value
                    2.0e-91
 Match length
                    186
  % identity
                    98
 NCBI Description
                    Oryza sativa abscisic acid- and stress-inducible protein
                    (Asr1) mRNA, complete cds
 Seq. No.
                    402722
 Seq. ID
                    LIB3431-055-P2-K1-H6
 Method
                    BLASTX
 NCBI GI
                    g2407281
 BLAST score
                    575
 E value
                    2.0e-59
 Match length
                    113
 % identity
                    96
 NCBI Description
                    (AF017363) ribulose 1,5-bisphosphate carboxylase small
                    subunit [Oryza sativa]
 Seq. No.
                    402723
 Seq. ID
                    LIB3431-055-P2-K1-H7
 Method
                    BLASTX
 NCBI GI
                    g3808101
 BLAST score
                    211
 E value
                    2.0e-26
                    95
 Match length
 % identity
                    74
 NCBI Description
                   (AJ012165) chloroplast protease [Capsicum annuum]
 Seq. No.
                    402724
 Seq. ID
                   LIB3431-055-P2-K1-H8
Method
                   BLASTN
NCBI GI
                   g2570512
BLAST score
                   51
E value
                   2.0e-20
Match length
                   55
% identity
                   98
                   Oryza sativa chlorophyll a-b binding protein mRNA, complete
NCBI Description
Seq. No.
                   402725
Seq. ID
                   LIB3431-056-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g5690431
BLAST score
                   241
E value
                   2.0e-20
Match length
                   97
% identity
                   48
NCBI Description
                   (AF165883) prefoldin subunit 2 [Homo sapiens]
Seq. No.
                   402726
Seq. ID
                   LIB3431-056-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   609
E value
                   2.0e-63
Match length
                   131
% identity
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
```

.7

% identity

53.

```
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir_RKRZS9
ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
(D00643) small subunit of ribulose-1,5-bisphosphate
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf_1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

402727
LIB3431_056_PL_K1_314
```

```
Seq. No.
 Seq. ID
                    LIB3431-056-P1-K1-A11
 Method
                    BLASTX
 NCBI GI
                    g1519251
 BLAST score
                    673
 E value
                    7.0e-71
 Match length
                   150
 % identity
                    91
 NCBI Description
                   (U65957) GF14-c protein [Oryza sativa]
 Seq. No.
                   402728
 Seq. ID
                   LIB3431-056-P1-K1-A2
 Method
                   BLASTX
 NCBI GI
                   g3126854
 BLAST score
                   488
 E value
                   3.0e-49
Match length
                   114
 % identity
                   85
NCBI Description
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                   402729
Seq. ID
                   LIB3431-056-P1-K1-A3
Method
                   BLASTN
NCBI GI
                   g4959460
BLAST score
                   36
E value
                   1.0e-10
Match length
                   36
% identity
                   100
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
Seq. No.
                   402730
Seq. ID
                   LIB3431-056-P1-K1-A4
Method .
                  BLASTN
NCBI GI
                  g4959460
BLAST score
                  35
E value
                  6.0e-10
Match length
                  35
% identity
                  100
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
Seq. No.
                  402731
Seq. ID
                  LIB3431-056-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g5734634
BLAST score
                  318
E value
                  3.0e-29
Match length
                  107
```

```
(AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                  sativa]
Seq. No.
                  402732
                  LIB3431-056-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3288821
                  259
BLAST score
E value
                  2.0e-47
Match length
                  110
                  87
% identity
                  (AF063901) alanine:glyoxylate aminotransferase;
NCBI Description
                  transaminase [Arabidopsis thaliana]
                  >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209)
                  alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
                  402733
Seq. No.
                  LIB3431-056-P1-K1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1245938
BLAST score
                  35
                  5.0e-10
E value
                  35
Match length
                  100
% identity
                  rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
NCBI Description
                  heart atrium, mRNA, 2998 nt]
Seq. No.
                  402734
                  LIB3431-056-P1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g132096
BLAST score
                  500
                  8.0e-60
E value
Match length
                  125
                  94
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN A PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT A) >gi_68095_pir__RKRZS6
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS2106) - rice >gi 218210 dbj BAA00539_
                  (D00644) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa]
Seq. No.
                  402735
                  LIB3431-056-P1-K1-B10
Seq. ID
                  BLASTX
Method
                  g4678311
NCBI GI
BLAST score
                  272
                  6.0e-24
E value
Match length
                  77
% identity
NCBI Description
                  (AL049655) aquaporin/MIP-like protein [Arabidopsis
                  thaliana]
                  402736
Seq. No.
                  LIB3431-056-P1-K1-B11
Seq. ID
                  BLASTX
Method
```

g1076724

NCBI GI

```
BLAST score
                  451
E value
                  4.0e-66
Match length
                  141
% identity
                  87
NCBI Description
                  LHCI-680, photosystem I antenna protein - barley
                  >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                  402737
                  LIB3431-056-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3789952
BLAST score
                  652
                  2.0e-68
E value
Match length
                  132
% identity
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
Seq. No.
                  402738
                  LIB3431-056-P1-K1-B2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q433216
BLAST score
                  115
E value
                  6.0e-58
Match length
                  118
% identity
                  99
                  Rice mRNA for ascorbate peroxidase (gene name SS622),
NCBI Description
                  partial cds
Seq. No.
                  402739
                  LIB3431-056-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173347
BLAST score
                  326
E value
                  2.0e-39
Match length
                  103
% identity
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi 14265 emb CAA46507
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
                  402740
Seq. No.
Seq. ID
                  LIB3431-056-P1-K1-B6
Method
                  BLASTX
                  g2407281
NCBI GI
BLAST score
                  673
                  6.0e-71
E value
Match length
                  133
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
```

Seq. No.

```
LIB3431-056-P1-K1-B7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2072555
BLAST score
                   193
                   1.0e-14
E value
                   35
Match length
                   100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   402742
Seq. No.
                   LIB3431-056-P1-K1-B8
Seq. ID
Method
                   BLASTX
                   q4585882
NCBI GI
BLAST score
                   469
                   7.0e-51
E value
                   145
Match length
% identity
                   66
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   402743
Seq. No.
                   LIB3431-056-P1-K1-B9
Seq. ID
                                                        \mathcal{A}^{p_{p_{p}}}
                   BLASTX
Method
NCBI GI
                   g2264373
BLAST score
                   355
E value
                   9.0e-34
                   103
Match length
% identity
                   (AC002354) putative NAM/no apical meristem protein
NCBI Description
                   [Arabidopsis thaliana]
                   402744
Seq. No.
                   LIB3431-056-P1-K1-C1
Seq. ID
                   BLASTX
Method
                   g4079798
NCBI GI
BLAST score
                   231
                   6.0e-30
E value
                   93
Match length
                   78
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                   sativa]
                   402745
Seq. No.
                   LIB3431-056-P1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3885896
BLAST score
                   524
                   2.0e-53
E value
                   100
Match length
                   100
% identity
                   (AF093636) plastocyanin precursor [Oryza sativa]
NCBI Description
Seq. No.
                   402746
                   LIB3431-056-P1-K1-C12
Seq. ID
Method
                   BLASTX
```

```
NCBI GI
                   g132105
BLAST score
                   537
                   6.0e-55
E value
Match length
                   111
                   91
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4\overline{.1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   402747
                  LIB3431-056-P1-K1-C2
Seq. ID
                   BLASTX
Method
                   g2073375
NCBI GI
BLAST score
                   459
E value
                   2.0e-54
                   110
Match length
                   90
% identity
                   (D85317) farnesyl pyrophosphate synthase [Oryza sativa]
NCBI Description
                   >gi_4063829_dbj_BAA36276_ (AB021747) farnesyl diphosphate
                   synthase [Oryza sativa]
                   402748
Seq. No.
                   LIB3431-056-P1-K1-C3
Seq. ID
Method
                   BLASTX
                   g417260
NCBI GI
BLAST score
                  -421
                   3.0e-41
E value
                   128
Match length
                   66
% identity
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                   lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                   light-regulated gene [Oryza sativa]
                   402749
Seq. No.
                   LIB3431-056-P1-K1-C4
Seq. ID
                   BLASTX
Method
                   g2407281
NCBI GI
                   650
BLAST score
                   3.0e-68
E value
Match length
                   125
                   94
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq. No.
                   402750
                   LIB3431-056-P1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2191151
                   170
BLAST score
                   4.0e-17
E value
```

Match length

```
% identity
                  60
                  (AF007269) contains similarity to membrane associated
NCBI Description
                  salt-inducible protein [Arabidopsis thaliana]
                  402751
Seq. No.
                  LIB3431-056-P1-K1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g548605
                  541
BLAST score
                  2.0e-55
E value
                  118
Match length
                  91
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                  - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
                  402752
Seq. No.
                  LIB3431-056-P1-K1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                 g871931
BLAST score
                  416
                  1.0e-40
E value
                  108
Match length
% identity
                  78
                  (D30763) ferredoxin [Oryza sativa]
NCBI Description
Seq. No.
                  402753
                  LIB3431-056-P1-K1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2688828
                  169
BLAST score
                  7.0e-12
E value
                  82
Match length
                  43
% identity
                   (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus
NCBI Description
                  armeniaca]
                  402754
Seq. No.
                  LIB3431-056-P1-K1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2072555
BLAST score
                  237
                  9.0e-20
E value
                  44
Match length
                  100
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  402755
Seq. No.
                  LIB3431-056-P1-K1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q671740
                  606
BLAST score
```

5.0e-63

E value

```
111
Match length
                  100
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  402756
Seq. No.
                  LIB3431-056-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076660
                  219
BLAST score
E value
                  9.0e-20
Match length
                  126
% identity
                   45
                  D13F(MYBST1) protein - potato >gi_786426_bbs_159122
NCBI Description
                   (S74753) MybSt1=Myb-related transcriptional activator
                   {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
                  leaf, Peptide, 342 aa] [Solanum tuberosum]
                  402757
Seq. No.
                  LIB3431-056-P1-K1-D4
Seq. ID
                  BLASTN
Method
NCBI GI
                  g6015437
                  36
BLAST score
                  9.0e-11
E value
Match length
                  36
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  402758
Seq. No.
                  LIB3431-056-P1-K1-D5
Seq. ID
Method
                  BLASTN
                  g218209
NCBI GI
                  135
BLAST score
                   9.0e-70
E value
                  246
Match length
% identity
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
                  402759
Seq. No.
Seq. ID
                  LIB3431-056-P1-K1-D6
Method
                  BLASTX
                  g3738261
NCBI GI
                  209
BLAST score
                  9.0e-17
E value
                  48
Match length
                   92
% identity
                   (AB018412) chloroplast phosphoglycerate kinase [Populus
NCBI Description
                  nigra]
                   402760
Seq. No.
                  LIB3431-056-P1-K1-D7
Seq. ID
Method
                  BLASTX
                  g320618
NCBI GI
                   648
BLAST score
```

6.0e-68

E value

```
140
Match length
                   89
% identity
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   402761
Seq. ID
                   LIB3431-056-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   q3885892
BLAST score
                   557
E value
                   3.0e-57
Match length
                   104
% identity
                   100
                   (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
Seq. No.
                   402762
                   LIB3431-056-P1-K1-D9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3885891
BLAST score
                   114
E value
                   2.0e-57
Match length
                   188
% identity
                   Oryza sativa photosystem-1 F subunit precursor (PSI-F)
NCBI Description
                   mRNA, complete cds
                   402763
Seq. No.
Seq. ID
                   LIB3431-056-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   q3789954
BLAST score
                   515
E value
                   2.0e-52
Match length
                   96
% identity
                   100
NCBI Description
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza-
                   sativa]
Seq. No.
                   402764
Seq. ID
                   LIB3431-056-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g1458245
BLAST score
                   261
E value
                   1.0e-22
Match length
                   130
% identity
NCBI Description
                   (U64834) coded for by C. elegans cDNA cm17a1; coded for by
                   C. elegans cDNA cm7g1; coded for by C. elegans cDNA
                   CEMSE26F; similar to methyltransferases [Caenorhabditis
                   elegans]
Seq. No.
                   402765
Seq. ID
                   LIB3431-056-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g1076724
```

NCBI GI

```
BLAST score
                   581
E value
                   4.0e-60
Match length
                   121
% identity
                   86
NCBI Description
                   LHCI-680, photosystem I antenna protein - barley
                   >gi_666054_emb_CAA59049 (X84308) LHCI-680, photosystem I
                   antenna protein [Hordeum vulgare]
Seq. No.
                   402766
Seq. ID
                   LIB3431-056-P1-K1-E12
Method
                   BLASTX
NCBI GI ·
                   g1084461
BLAST score
                   212
E value
                   5.0e-17
Match length
                   79
% identity
                   56
NCBI Description
                  RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]
Seq. No.
                   402767
Seq. ID
                  LIB3431-056-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g82080
BLAST score
                  336
E value
                  1.0e-32
Match length
                  113
% identity
                   68
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                  402768
Seq. ID
                  LIB3431-056-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  38
E value
                  5.0e-12
Match length
                  38
% identity
                  100
NCBI Description
                  Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  402769
Seq. ID
                  LIB3431-056-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g5733872
BLAST score
                  457
E value
                  2.0e-45
Match length
                  119
% identity
NCBI Description
                  (AC007932) Similar to gi 4982048 ribosomal protein L18 from
                  Thermotoga maritima genome gb AE001798. ESTs gb Z35613,
                  gb_T75951, gb_T22182, gb_T45962, gb_H76281 and gb AI100025
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  402770
Seq. ID
                  LIB3431-056-P1-K1-E9
Method
                  BLASTX
```

g3789952

```
235
BLAST score
                   2.0e-19
E value
                   44
Match length
                   100
% identity
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                   sativa]
                   402771
Seq. No.
                                            . .
                   LIB3431-056-P1-K1-F1
Seq. ID
                   BLASTX
Method
                   q115787
NCBI GI
                   636
BLAST score
                   2.0e-74
E value
                   142
Match length
                   95
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   402772
Seq. No.
                   LIB3431-056-P1-K1-F10
Seq. ID
                   BLASTX
Method
                   q1173347
NCBI GI
                   605
BLAST score
                   4.0e-63
E value
Match length
                   117
                   95
% identity
                   SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                   >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                   3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                   aestivum]
                   402773
Seq. No.
                   LIB3431-056-P1-K1-F12
Seq. ID
Method
                   BLASTX
                   q3913808
NCBI GI
                   477
BLAST score
                   6.0e-48
E value
                   102
Match length
                   88
% identity
                   FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME
NCBI Description
                   SYNTHETASE) >gi_2429618_dbj_BAA22284_ (AB007120)
                   ferrochelatase [Oryza sativa]
                   402774
Seq. No.
                   LIB3431-056-P1-K1-F2
Seq. ID
Method
                   BLASTX
                   g585350
NCBI GI
                   384
BLAST score
                   3.0e-37
E value
                   109
Match length
                   68
% identity
NCBI Description CASEIN KINASE II, ALPHA CHAIN 2 (CK II)
```

```
>gi_419753_pir__S31099 casein kinase II (EC 2.7.1.-)
alpha-type chain (clone ATCKA2) - Arabidopsis thaliana
>qi 391605 dbj BAA01091 (D10247) casein kinase II
catalytic subunit [Arabidopsis thaliana]
402775
LIB3431-056-P1-K1-F3
```

Seq. ID Method BLASTX NCBI GI g115787 BLAST score 529 E value 4.0e-54 Match length 121 % identity

Seq. No.

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I

CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_

(X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)

[Oryza sativa]

Seq. No. 402776

Seq. ID LIB3431-056-P1-K1-F5

Method BLASTX g2506826 NCBI GI BLAST score 328 E value 2.0e-30 90

Match length % identity 74

NONSPECIFIC LIPID-TRANSFER PROTEIN 1 PRECURSOR (LTP 1) NCBI Description

> (PAPI) >gi_1619604_emb_CAA69949.1_ (Y08691) lipid transfer protein [Oryza satīva] >gi 1667590 (U77295) lipid transfer

protein [Oryza sativa]

402777 Seq. No.

Seq. ID LIB3431-056-P1-K1-F6

Method BLASTX NCBI GI g5689238 BLAST score 341 E value 2.0e-32 Match length 73

% identity 86

(AB024292) histidine-containing phosphotransfer protein NCBI Description

[Zea mays]

402778 Seq. No.

LIB3431-056-P1-K1-F7 Seq. ID

Method BLASTN NCBI GI g2062705 BLAST score 37 E value 3.0e-11

Match length 37 % identity 100

Human butyrophilin (BTF5) mRNA, complete cds NCBI Description

402779 Seq. No.

LIB3431-056-P1-K1-F9 Seq. ID

Method BLASTX NCBI GI g4836892

```
BLAST score
                   430
E value
                   2.0e-42
Match length
                   138
                   58
% identity
                   (ACO07369) Putative RNA helicase [Arabidopsis thaliana]
NCBI Description
                   402780
Seq. No.
                   LIB3431-056-P1-K1-G1
Seq. ID
Method
                   BLASTX.
                   g3335349
NCBI GI
BLAST score
                   416
                   1.0e-40
E value
Match length
                   155
% identity
                   (ACO04512) Similar to gb U46691 putative chromatin
NCBI Description
                   structure regulator (SUPT6H) from Homo sapiens. ESTs
                   gb T42908, gb AA586170 and gb_AA395125 come from this gene.
                   [Arabidopsis thaliana]
                   402781
Seq. No.
                   LIB3431-056-P1-K1-G10
Seq. ID .
Method
                   BLASTX
                   g5326825
NCBI GI
BLAST score
                   164
E value
                   3.0e-11
                   90
Match length
% identity
                   32
                   (AF044953) NADH:ubiquinone oxidoreductase PGIV subunit
NCBI Description
                   [Homo sapiens]
                   402782
Seq. No.
Seq. ID
                   LIB3431-056-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   512
                   4.0e-52
E value
Match length
                   114
% identity
                   85
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza satīva]
                   402783
Seq. No.
                   LIB3431-056-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   1.0e-19
Match length
                   44
                   100
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
```

Seq. No.

Seq. ID Method

```
LIB3431-056-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q320618
BLAST score
                  532
E value
                  2.0e-54
Match length
                  117
% identity
                  86
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                  402785
Seq. ID
                  LIB3431-056-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q320618
BLAST score
                  292
E value
                  2.0e-26
Match length
                  73
                  74
% identity
NCBI Description
                  chlorophyll a/b-binding protein I precursor - rice
                  >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                  chlorophyll a/b-binding protein [Oryza sativa]
                  >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                  [Oryza sativa]
Seq. No.
                  402786
Seq. ID
                  LIB3431-056-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  q548605
BLAST score
                  588
E value
                  7.0e-61
Match length
                  130
% identity
                  90
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                  (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                  >gi 539055 pir A48527 photosystem I protein psaK precursor
                  - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                  [Hordeum vulgare]
Seq. No.
                  402787
Seq. ID
                  LIB3431-056-P1-K1-G6
Method
                  BLASTX
                  g417154
NCBI GI
BLAST score
                  526
E value
                  7.0e-54
Match length
                  105
                  97
% identity
NCBI Description
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                  (HSP82) [Oryza sativa]
                  402788
Seq. No.
```

LIB3431-056-P1-K1-G7

BLASTN

```
q1261857
NCBI GI
BLAST score
                  54
                  2.0e-21
E value
Match length
                  54
                  100
% identity
                  Rice CatA gene for catalase, complete cds
NCBI Description
                  402789
Seq. No.
                  LIB3431-056-P1-K1-G8
Seq. ID
                  BLASTX
Method
                  q4678338
NCBI GI
                  202
BLAST score
                  1.0e-15
E value
                  48
Match length
                  73
% identity
                  (AL049658) putative protein [Arabidopsis thaliana]
NCBI Description
                  402790
Seq. No.
Seq. ID
                  LIB3431-056-P1-K1-H1
Method
                  BLASTN
                  g3345476
NCBI GI
                  132
BLAST score
                  7.0e-68
E value
                  241
Match length
                  96
% identity
                  Oryza sativa gene for carbonic anhydrase, complete cds
NCBI Description
                  402791
Seq. No.
                  LIB3431-056-P1-K1-H10
Seq. ID
                  BLASTN
Method
                  g2570512
NCBI GI
BLAST score
                  112
                  3.0e-56
E value
                  212
Match length
                  100
% identity
                  Oryza sativa chlorophyll a-b binding protein mRNA, complete
NCBI Description
                  cds
                   402792
Seq. No.
                  LIB3431-056-P1-K1-H12
Seq. ID
                                                              14.5
                  BLASTN
Method
NCBI GI
                  g20191
                  279
BLAST score
                  1.0e-156
E value
Match length
                  279
                   100
% identity
                  O.sativa mRNA for catalase
NCBI Description
                   402793
Seq. No.
Seq. ID
                  LIB3431-056-P1-K1-H2
                  BLASTX
Method
                   g133867
NCBI GI
                   558
BLAST score
                   2.0e-57
E value
                   124
Match length
                   85
% identity
                  40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal
NCBI Description
```

```
ribosomal protein S11 [Zea mays]
Seq. No.
                   402794
Seq. ID
                   LIB3431-056-P1-K1-H3
Method
                   BLASTN
NCBI GI
                   q6015437
BLAST score
                   38
E value
                   5.0e-12
Match length
                   38
% identity
                   100
                   Homo sapiens PEX1 mRNA, complete cds
NCBI Description
                   402795
Seq. No.
                   LIB3431-056-P1-K1-H4
Seq. ID
Method
                   BLASTX
                   g2624326
NCBI GI
BLAST score
                   294
E value
                   8.0e-27
Match length
                   61
% identity
                   93
NCBI Description
                   (AJ002893) OsGRP1 [Oryza sativa]
                   402796
Seq. No.
Seq. ID
                   LIB3431-056-P1-K1-H5
Method
                   BLASTX
                   q1173347
NCBI GI
BLAST score
                   663
E value
                   9.0e-70
Match length
                   129
% identity
                   95
                   SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                   >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                   3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                   aestivum]
Seq. No.
                   402797
                   LIB3431-056-P1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3128206
BLAST score
                   143
E value
                   2.0e-09
Match length
                   47
% identity
NCBI Description
                   (AC004077) unknown protein [Arabidopsis thaliana]
                   402798
Seq. No.
Seq. ID
                   LIB3431-056-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   547
E value
                   4.0e-56
Match length
                   119
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
```

protein S11 - maize >gi 22470_emb_CAA39438_ (X55967)

```
(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]
```

```
Seq. No.
                  402799
                  LIB3431-056-P1-N1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  443
                  7.0e-44
E value
                  80
Match length
% identity
                  100
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  402800
Seq. No.
                  LIB3431-056-P1-N1-A11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2331130
BLAST score
                  100
                  8.0e-49
E value
Match length
                  148
% identity
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
                  cds
                  402801
Seq. No.
                  LIB3431-056-P1-N1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  203
E value
                  7.0e-16
Match length
                  71
% identity
                  58
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  402802
                  LIB3431-056-P1-N1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  349
E value
                  9.0e-33
                  66
Match length
% identity
                  100
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
```

BLASTX

LIB3431-056-P1-N1-A6

Seq. No.

Seq. ID Method

Method

BLASTN

```
g2754849
NCBI GI
BLAST score .
                  284
E value 🥯
                  3.0e-25
Match length
                  63
% identity
                  87
                   (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                  [Fritillaria agrestis]
                  402804
Seq. No.
                  LIB3431-056-P1-N1-B1
Seq. ID
                  BLASTX
Method
                  g671740
NCBI GI
BLAST score
                  234
                  2.0e-19
E value
                  47
Match length
                  96
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
                  402805
Seq. No.
                  LIB3431-056-P1-N1-B10
Seq. ID
                  BLASTX
Method
                  g886100
NCBI GI
BLAST score
                  265
                  6.0e-23
E value
                  63
Match length
                  76
% identity
                  (U27347) putative water channel protein; plasmalemma
NCBI Description
                  intrinsic protein; similar to Arabidopsis Pip2a gene
                  product, PIR Accession Number S44084 [Glycine max]
                  402806
Seq. No.
Seq. ID
                  LIB3431-056-P1-N1-B11
Method
                  BLASTX
                  g1076724
NCBI GI
BLAST score
                  477
                  8.0e-48
E value
Match length
                  90
% identity
                  96
NCBI Description
                  LHCI-680, photosystem I antenna protein - barley
                  >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
                  402807
Seq. No.
                  LIB3431-056-P1-N1-B12
Seq. ID
                  BLASTX
Method
                  g3789952
NCBI GI
                  269
BLAST score
                  2.0e-23
E value
Match length
                  51
                  100
% identity
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                  sativa]
                  402808
Seq. No.
                  LIB3431-056-P1-N1-B3
Seq. ID
```

```
q304219
NCBI GI
                  51
BLAST score
E value
                  1.0e-19
Match length
                  71
% identity
                  93
                  Hordeum vulgare chloroplast photosystem I PSK-I subunit
NCBI Description
                  mRNA, complete cds
Seq. No.
                  402809
                  LIB3431-056-P1-N1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173347
BLAST score
                  405
E value
                  2.0e-39
Match length
                  86
                  97
% identity
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
                  402810
Seq. No.
Seq. ID
                  LIB3431-056-P1-N1-B6
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  301
                  3.0e-27
E value
Match length
                  57
                  100
% identity
NCBI Description
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
                  construct]
                  402811
Seq. No.
Seq. ID
                  LIB3431-056-P1-N1-B7
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  269
E value
                  1.0e-150
Match length
                  269
% identity
                  100
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
                  cds
                  402812
Seq. No.
                  LIB3431-056-P1-N1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115813
BLAST score
                  165
E value
                  2.0e-11
Match length
                  38
% identity
                  79
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
```

CAB-8) >gi 19182 emb CAA33330 (X15258) Type III

chlorophyll a/b-binding protein [Lycopersicon esculentum]

```
402813
Seq. No.
Seq. ID
                  LIB3431-056-P1-N1-C1
Method
                  BLASTX
                  q4079798
NCBI GI
BLAST score
                  414
                  2.0e-40
E value
Match length
                  81
% identity
NCBI Description
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                  402814
Seq. No.
                  LIB3431-056-P1-N1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3885896
BLAST score
                  524
                  2.0e-53
E value
Match length
                  100
                  100
% identity
                   (AF093636) plastocyanin precursor [Oryza sativa]
NCBI Description
                  402815
Seq. No.
                  LIB3431-056-P1-N1-C12"
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218209
BLAST score
                  37
E value
                  3.0e-11
                  53
Match length
                  92
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
                  402816
Seq. No.
                  LIB3431-056-P1-N1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2073375
BLAST score
                  576
                  2.0e-59
E value
Match length
                  107
                  100
% identity
                   (D85317) farnesyl pyrophosphate synthase [Oryza sativa]
NCBI Description
                  >gi_4063829_dbj_BAA36276_ (AB021747) farnesyl diphosphate
                  synthase [Oryza sativa]
                  402817
Seq. No.
                  LIB3431-056-P1-N1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417260
BLAST score
                  321
                  1.0e-29
E value
                  106
Match length
                  61
% identity
NCBI Description LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
                  lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
```

light-regulated gene [Oryza sativa]

```
402818
 Seq. No.
 Seq. ID
                    LIB3431-056-P1-N1-C4
 Method
                    BLASTX
 NCBI GI
                    g671740
 BLAST score
                    361
 E value
                    3.0e-34
 Match length
                    70
 % identity
                    97
                    (X84730) ribulose-bisphosphate carboxylase [synthetic
 NCBI Description
                    construct]
                    402819
 Seq. No.
 Seq. ID
                    LIB3431-056-P1-N1-C6
 Method
                    BLASTX
 NCBI GI
                    q548605
 BLAST score
                    599
 E value
                    5.0e-62
 Match length.
                    131
 % identity
                    91
                    PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 NCBI Description
                    (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                    >gi_539055_pir__A48527 photosystem I protein psaK precursor
                    - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                    [Hordeum vulgare]
 Seq. No.
                    402820
 Seq. ID
                    LIB3431-056-P1-N1-C7
 Method
                    BLASTX
 NCBI GI
                    q871931
 BLAST score
                    161
 E value
                    5.0e-11
 Match length
                    44
 % identity
                    75
. NCBI Description
                    (D30763) ferredoxin [Oryza sativa]
 Seq. No.
                    402821
 Seq. ID
                    LIB3431-056-P1-N1-D1
 Method
                    BLASTX
 NCBI GI
                    g2072555
 BLAST score
                    228
 E value
                    1.0e-18
 Match length
                    42
                    100
 % identity
 NCBI Description
                    (AF001396) metallothionein-like protein [Oryza sativa]
                    >gi_6103441 gb_AAF03603.1 (AF147786) metallothionein-like
                    protein [Oryza sativa]
 Seq. No.
                    402822
 Seq. ID
                    LIB3431-056-P1-N1-D12
 Method
                    BLASTX
 NCBI GI
                    a671740
 BLAST score
                    433
 E value
                    1.0e-42
 Match length
                    78
                    100
 % identity
 NCBI Description
                    (X84730) ribulose-bisphosphate carboxylase [synthetic
```

construct]

```
402823
Seq. No.
                  LIB3431-056-P1-N1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1076660
BLAST score
                  222
                  6.0e-18
E value
                  89
Match length
                  57
% identity
                  D13F(MYBST1) protein - potato >gi_786426_bbs_159122
NCBI Description
                  (S74753) MybSt1=Myb-related transcriptional activator
                  {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
                  leaf, Peptide, 342 aa] [Solanum tuberosum]
                  402824
Seq. No.
                  LIB3431-056-P1-N1-D5
Seq. ID
Method
                  BLASTN
                  g218209
NCBI GI
                  39
BLAST score
                  2.0e-12
E value
                  55
Match length
                  93
% identity
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
                  402825
Seq. No.
Seq. ID
                  LIB3431-056-P1-N1-D7
Method
                  BLASTX
                  g115787
NCBI GI
                  409
BLAST score
                  6.0e-40
E value
                  77
Match length
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                  (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
                  402826
Seq. No.
                  LIB3431-056-P1-N1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3885892
                  544
BLAST score
                  9.0e-56
E value
                  102
Match length
% identity
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
                  402827
Seq. No.
                  LIB3431-056-P1-N1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3885892
BLAST score
                  286
                  2.0e-25
E value
```

Match length

```
% identity
                  100
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
                  402828
Seq. No.
                  LIB3431-056-P1-N1-E1
Seq. ID
Method
                  BLASTX
                  g3789954
NCBI GI
BLAST score
                  611
E value
                  2.0e-63
Match length
                  113
                  100
% identity
                  (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
Seq. No.
                  402829
                  LIB3431-056-P1-N1-E11
Seq. ID
                  BLASTX
Method
                  g1076724
NCBI GI
                  374
BLAST score
                  8.0e-36
E value
Match length
                  72
                  94
% identity
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                  >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                  402830
                  LIB3431-056-P1-N1-E12
Seq. ID
                  BLASTX
Method
                  g1084461
NCBI GI
                  287
BLAST score
                  1.0e-25
E value
                  98
Match length
                  60
% identity
                  RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]
NCBI Description
                  402831
Seq. No.
Seq. ID
                  LIB3431-056-P1-N1-E2
Method
                  BLASTX -
                  g115813
NCBI GI
                  234
BLAST score
                  2.0e-19
E value
                  56
Match length
% identity
                  80
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi 19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  402832
Seq. No.
                  LIB3431-056-P1-N1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5733872
                  182
BLAST score
                  2.0e-13
E value
                  57
Match length
                  60
% identity
                   (AC007932) Similar to gi 4982048 ribosomal protein L18 from
NCBI Description
```

4.

Thermotoga maritima genome gb AE001798. ESTs gb_Z35613, gb T75951, gb T22182, gb T459 $\overline{6}$ 2, gb H76281 and g \overline{b} AI100025 come from this gene. [Arabidopsis thaliana]

402833 Seq. No.

LIB3431-056-P1-N1-E8 Seq. ID

Method BLASTX NCBI .GI q6093830 BLAST score 218 E value 2.0e-17 97 Match length % identity

PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) NCBI Description [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II

PROTEIN PSBY-2] >qi 3337435 (AF060198) PsbY precursor;

putative photosytem II peptide [Spinacia oleracea]

402834 Seq. No.

LIB3431-056-P1-N1-E9 Seq. ID

Method BLASTN NCBI GI q3789951 -BLAST score 127 E value 6.0e-65 Match length 372 91 % identity

Oryza sativa chlorophyll a/b-binding protein presursor NCBI Description

(Cab27) mRNA, nuclear gene encoding chloroplast protein,

complete cds

402835 Seq. No.

Seq. ID LIB3431-056-P1-N1-F1

Method BLASTX NCBI GI q115772 BLAST score 273 5.0e-24 E value Match length 57

% identity - 91

CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I NCBI Description

CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108_

(X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)

[Oryza sativa]

402836 Seq. No.

LIB3431-056-P1-N1-F10 Seq. ID

Method BLASTX NCBI GI q1173347 BLAST score 401 E value 6.0e-39 85 Match length

% identity

SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR NCBI Description (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)

>gi 100803 pir S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum

aestivum]

```
402837
Seq. No.
Seq. ID
                  LIB3431-056-P1-N1-F11
Method
                  BLASTX
NCBI GI
                  g2244734
BLAST score
                  166
E value
                  2.0e-11
Match length
                  32
% identity
                  97
NCBI Description
                   (D88414) actin [Gossypium hirsutum]
                  402838
Seq. No.
                  LIB3431-056-P1-N1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q585350
BLAST score
                  496
E value
                  5.0e-50
Match length
                  110
                  83
% identity
                  CASEIN KINASE II, ALPHA CHAIN 2 (CK II)
NCBI Description
                  >gi_419753_pir__S31099 casein kinase II (EC 2.7.1.-)
                  alpha-type chain (clone ATCKA2) - Arabidopsis thaliana
                  >gi_391605_dbj_BAA01091_ (D10247) casein kinase II
                  catalytic subunit [Arabidopsis thaliana]
Seq. No.
                  402839
Seq. ID
                  LIB3431-056-P1-N1-F3
Method
                  BLASTX
NCBI GI
                  q3036951
BLAST score
                  427
E value
                   6.0e-42
Match length
                  80
                  100
% identity
NCBI Description
                   (AB012639) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
Seq. No.
                  402840
Seq. ID
                  LIB3431-056-P1-N1-F5
Method
                  BLASTN
                  g1619603
NCBI GI
BLAST score
                  370
E value
                  0.0e + 00
Match length
                  414
                  97
% identity
                  O.sativa mRNA for lipid transfer protein
NCBI Description
                  >gi_1667589_gb_U77295_OSU77295 Oryza sativa lipid transfer .
                  protein (LTP) mRNA, complete cds
Seq. No.
                  402841
Seq. ID
                  LIB3431-056-P1-N1-F9
Method
                  BLASTX
NCBI GI
                  g2673917
BLAST score
                  305
E value
                  1.0e-27
Match length
                  80
% identity
                   66
                   (AC002561) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
```

thaliana] 402842 Seq. No. LIB3431-056-P1-N1-G1 Seq. ID BLASTX Method NCBI GI g3335349 BLAST score 170 E value 5.0e-12 Match length 108 38 % identity (AC004512) Similar to gb U46691 putative chromatin NCBI Description structure regulator (SUPT6H) from Homo sapiens. ESTs qb T42908, gb AA586170 and gb AA395125 come from this gene. [Arabidopsis thaliana] 402843 Seq. No. LIB3431-056-P1-N1-G10 Seq. ID Method BLASTX NCBI GI q5326825 BLAST score 153 8.0e-10 E value Match length 87 % identity 31 (AF044953) NADH: ubiquinone oxidoreductase PGIV subunit NCBI Description [Homo sapiens] 402844 Seq. No. LIB3431-056-P1-N1-G11 Seq. ID Method BLASTX NCBI GI g136640 BLAST score 514 3.0e-52 E value 102 Match length % identity UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN NCBI Description LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 170785 (M62720) ubiquitin carrier protein [Triticum aestivum] 402845 Seq. No. LIB3431-056-P1-N1-G12 Seq. ID Method BLASTN g20177 NCBI GI BLAST score 204 1.0e-111 E value 219 Match length % identity NCBI Description Rice cab1R gene for light harvesting chlorophyll a/b-binding protein

Seq. No. 402846

Seq. ID LIB3431-056-P1-N1-G2

Method BLASTX
NCBI GI g2072555
BLAST score 228
E value 1.0e-18
Match length 42
% identity 100

والرحوف

```
(AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   402847
                   LIB3431-056-P1-N1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   676
E value
                   4.0e-71
Match length
                   130
% identity
                   100
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   402848
Seq. No.
Seq. ID
                   LIB3431-056-P1-N1-G4
Method
                   BLASTX
NCBI GI
                   q3036951
BLAST score
                   650
E value
                   4.0e-68
Match length
                   124
% identity
                   (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
                   402849
Seq. No.
Seq. ID
                   LIB3431-056-P1-N1-G5
Method
                   BLASTX
NCBI GI
                   a548605
BLAST score
                   301
                   2.0e-27
E value
Match length
                   64
% identity
                   92
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi_539055_pir__A48527 photosystem I protein psaK precursor
                   - barley >gi_304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
Seq. No.
                   402850
                   LIB3431-056-P1-N1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q417154
BLAST score
                   392
E value
                   7.0e-38
                   93
Match length
                   85
% identity
                   HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                   protein 82 - rice (strain Taichung Native One)
                   >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
```

Seq. No.

```
LIB3431-056-P1-N1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   a4006881 -
BLAST score
                   585
                   2.0e-60
E value
                   139
Match length
                   79
% identity
                   (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   402852
                   LIB3431-056-P1-N1-H1
Seq. ID
Method
                   BLASTN
                   g3345476
NCBI GI
BLAST score
                   342
E value
                   0.0e + 00
Match length
                   386
                   97
% identity
                   Oryza sativa gene for carbonic anhydrase, complete cds
NCBI Description
                   402853
Seq. No.
                   LIB3431-056-P1-N1-H2
Seq. ID
Method
                   BLASTN
                   g22469
NCBI GI
BLAST score
                   34
E value
                   1.0e-09
                   38
Match length
'% identity
                   97
                   Maize mRNA for cytoplasmic ribosomal protein S11
NCBI Description
                   402854
Seq. No.
                   LIB3431-056-P1-N1-H5
Seq. ID
Method
                   BLASTN
                   g14264
NCBI GI
BLAST score
                   67
E value
                   3.0e-29
                   115
Match length
                   90
% identity
                   T.aestivum gene for sedoheptulose-1,7-bisphoshatase
NCBI Description
                   402855
Seq. No.
                   LIB3431-056-P1-N1-H9
Seq. ID
                   BLASTX
Method
                   g671740
NCBI GI
                   546
BLAST score
                   6.0e-56
E value
                   99
Match length
% identity
                   100
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
Seq. No.
                   402856
                   LIB3431-058-P1-K1-A1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3355468
                   355
BLAST score
                   1.0e-33
E value
```

Match length

```
% identity
                   (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                  402857
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q2244749
BLAST score
                  383
                  7.0e-37
E value
Match length
                  112
% identity
                  66
                   (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
NCBI Description
                  402858
Seq. No.
                  LIB3431-058-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                  214
E value
                  4.0e-17
Match length
                  41
                  95
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
Seq. No.
                  402859
                  LIB3431-058-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1514643
BLAST score
                  180
E value
                  4.0e-26
Match length
                  102
% identity
                  63
                   (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
NCBI Description
                  402860
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-A3
Method
                  BLASTN
                  g1159878
NCBI GI
BLAST score
                  52
E value
                  3.0e-20
Match length
                  64
                  95
% identity
                  A.fatua mRNA for DNA-binding protein (clone ABF2)
NCBI Description
                  402861
Seq. No.
                  LIB3431-058-P1-K1-A4
Seq. ID
Method
                  BLASTX
                  g2072555
NCBI GI
BLAST score
                  165
E value
                  3.0e-11
Match length
                  32
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
```

Seq. No.

.

```
LIB3431-058-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2462760
BLAST score
                  143
                  8.0e-09
E value
                  75
Match length
% identity
                   (AC002292) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  402863
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q3402713
BLAST score
                  379
E value
                  2.0e-36
Match length
                  123
                  60
% identity
                   (AC004261) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  402864
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  494
E value
                   6.0e-50
Match length
                  109
% identity
                  83
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  402865
                  LIB3431-058-P1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3046693
BLAST score
                  573
                  3.0e-59
E value
Match length
                  136
                  74
% identity
                   (AL022140) receptor like protein (fragment) [Arabidopsis
NCBI Description
                  thaliana]
                  402866
Seq. No.
                  LIB3431-058-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3550983
                  358
BLAST score
                  5.0e-34
E value
                  98
Match length
% identity
                   68
                   (AB010690) mutM homologue-2 [Arabidopsis thaliana]
NCBI Description
```

```
>gi 5903054 gb AAD55613.1 AC008016 23 (AC008016) Identical
                  to gb AB010690 mutM homologue-2 (formamidopyrimidine-DNA
                  glycosylase 1) from Arabidopsis thaliana. EST gb Z18192
                  comes from this gene
Seq. No.
                  402867
Seq. ID
                  LIB3431-058-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q3885886
BLAST score
                  748
E value
                  1.0e-79
Match length
                  144
% identity
                  100
NCBI Description
                  (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
                  402868
Seq. No.
                  LIB3431-058-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2582381
BLAST score
                  458
E value
                  4.0e-46
Match length
                  87
% identity
NCBI Description
                   (AF021220) cation-chloride co-transporter [Nicotiana
                  tabacum]
                  402869
Seq. No.
                  LIB3431-058-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                  485
                  5.0e-49
E value
Match length
                  92
% identity
                  99
NCBI Description
                  (AF022738) chlorophyll a-b binding protein [Oryza sativa]
                  402870
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q3850566
BLAST score
                  236
E value
                  1.0e-22
Match length
                  156
% identity
                  40
                  (AC005278) F15K9.3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  402871
                  LIB3431-058-P1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g5730046
BLAST score
                  35
E value
                  3.0e-10
Match length
                  35
% identity
NCBI Description Homo sapiens solute carrier family 17 (sodium phosphate),
```

>gi_3820622 (AF099971) putative formamidopyrimidine-DNA

qlycosylase 2 [Arabidopsis thaliana]

```
cds
                   402872
Seq. No.
                   LIB3431-058-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q430947
BLAST score
                   360
E value
                   3.0e-34
Match length
                   102
% identity
                   71
                   (U01103) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   402873
Seq. No.
                   LIB3431-058-P1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   468
E value
                   4.0e-52
Match length
                   101
                   100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   402874
Seq. No.
                  LIB3431-058-P1-K1-B7
Seq. ID
Method
                   BLASTX
                   g21839
NCBI GI
BLAST score
                   734
E value
                   5.0e-78
                   148
Match length
                   93
% identity
NCBI Description
                   (X57952) phosphoribulokinase [Triticum aestivum]
                   402875
Seq. No.
                   LIB3431-058-P1-K1-B8
Seq. ID
                   BLASTX
Method
```

member 3 (SLC17A3) mRNA >gi_2062691_gb_U90545 Human sodium phosphate transporter (NPT4) mRNA, complete

```
Method BLASTX
NCBI GI g82080
BLAST score 152
E value 4.0e-10
Match length 68
```

NCBI Description chlorophyll a/b-binding protein type III precursor - tomato >gi 226872 prf 1609235A chlorophyll a/b binding protein

[Lycopersicon esculentum]

Seq. No. 402876

% identity

Seq. ID LIB3431-058-P1-K1-B9

```
BLASTX
Method
                   q671740
NCBI GI
                   588
BLAST score
E value
                   5.0e-61
                   108
Match length
                   100
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   402877
Seq. No.
                   LIB3431-058-P1-K1-C1
Seq. ID
                   BLASTX
Method
                   g2191138
NCBI GI
BLAST score
                   310
                   3.0e-28
E value
Match length
                   136
                   53
% identity
                   (AF007269) A IG002N01.18 gene product [Arabidopsis
NCBI Description
                   thaliana]
                   402878
Seq. No.
                   LIB3431-058-P1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1001355
BLAST score
                   228
                   7.0e-19
E value
Match length
                   119
% identity
                   42
                   (D64006) auxin-induced protein [Synechocystis sp.]
NCBI Description
                   402879
Seq. No.
Seq. ID
                   LIB3431-058-P1-K1-C12
Method
                   BLASTN
NCBI GI
                   g606816
BLAST score
                   229
                   1.0e-126
E value
Match length
                   229
% identity
                   100
                   Oryza sativa chloroplast carbonic anhydrase mRNA, complete
NCBI Description
                   cds
                   402880
Seq. No.
                   LIB3431-058-P1-K1-C2
Seq. ID
Method
                   BLASTX
                   g1698548
NCBI GI
BLAST score
                   664
                   8.0e-70
E value
                   155
Match length
                   78
% identity
                   (U58971) calmodulin-binding protein [Nicotiana tabacum]
NCBI Description
Seq. No.
                   402881
                   LIB3431-058-P1-K1-C3
Seq. ID
                   BLASTN
Method
                   g2570512
NCBI GI
                   283
BLAST score
```

1.0e-158

_ .

E value

```
367
Match length
                   94
% identity
NCBI Description
                   Oryza sativa chlorophyll a-b binding protein mRNA, complete
                   402882
Seq. No.
                   LIB3431-058-P1-K1-C4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3789951
BLAST score
                   66
E value
                   1.0e-28
Match length
                   162
% identity
                   85
                   Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
                   402883
Seq. No.
                   LIB3431-058-P1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4678949
                                                  Sec. 16.3
                   517
BLAST score
                   1.0e-52
E value
                   123
Match length
                   79
% identity
                   (AL049711) dihydrolipoamide S-acetyltransferase precursor
NCBI Description
                   [Arabidopsis thaliana]
                   402884
Seq. No.
                   LIB3431-058-P1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4531444
                   482
BLAST score
                   2.0e-48
E value
                   142
Match length
                   66
% identity
                   (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                   402885
Seq. No.
                   LIB3431-058-P1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1421730
BLAST score
                   753
                   3.0e-80
E value
                   146
Match length
% identity
NCBI Description
                   (U43082) RF2 [Zea mays]
                   402886
Seq. No.
                   LIB3431-058-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1698548
                   302
BLAST score
E value
                   2.0e-32
                   131
Match length
% identity
                   (U58971) calmodulin-binding protein [Nicotiana tabacum]
NCBI Description
```

. .

```
402887
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g5816996
BLAST score
                  325
E value
                  4.0e-30
Match length
                  88
% identity
NCBI Description
                  (AL110123) ribosomal protein L32-like protein [Arabidopsis
                  thaliana]
                  402888
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q4587563
BLAST score
                  301
E value
                  2.0e-27
Match length
                  81
% identity
                  77
                  (AC006550) Similar to gb_U51990 pre-mRNA-splicing factor
NCBI Description
                  hPrp18 from Homo sapiens. ESTs gb_T46391 and gb_AA721815
                  come from this gene. [Arabidopsis thaliana]
                  402889
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-D10
Method
                  BLASTN
                  q6015437
NCBI GI
                  38
BLAST score
                  7.0e-12
E value
Match length
                  50
                  67
% identity
NCBI Description
                  Homo sapiens PEX1 mRNA, complete cds -
Seq. No.
                  402890
Seq. ID
                  LIB3431-058-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g115796
BLAST score
                  482
                  4.0e-55
E value
Match length
                  112
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB) (LHCP) >gi_218174_dbj_BAA00537_ (D00642) type II
                  light-harvesting chlorophyll a/b-binding protein [Oryza
                  sativa]
Seq. No.
                  402891
Seq. ID
                  LIB3431-058-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q6016151
BLAST score
                  492
E value
                  9.0e-50
Match length
                  128
                  77
% identity
                  IMMUNOGLOBULIN BINDING PROTEIN HOMOLOG 3 PRECURSOR (HEAT
NCBI Description
                  SHOCK PROTEIN 70 HOMOLOG 3) >gi_1575130 (U58209) lumenal
```

binding protein cBiPe3 [Zea mays] Seq. No. 402892 Seq. ID LIB3431-058-P1-K1-D2 Method BLASTX

NCBI GI g15961
BLAST score 259
E value 3.0e-22
Match length 92
% identity 48

NCBI Description (Z12621) precursor alliinase [Allium cepa]

Seq. No. 402893

Seq. ID LIB3431-058-P1-K1-D3

Method BLASTN
NCBI GI g4097337
BLAST score 304
E value 1.0e-170
Match length 368
% identity 99

NCBI Description Oryza sativa metallothionein-like protein mRNA, complete

cds

Seq. No. 402894

Seq. ID LIB3431-058-P1-K1-D4

Method BLASTX
NCBI GI g1707998
BLAST score 510
E value 6.0e-52
Match length 117
% identity 85

NCBI Description SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR

(SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE)

(SHMT) >gi 481944 pir S40218 glycine

hydroxymethyltransferase (EC 2.1.2.1) - potato >gi 438247 emb CAA81082 (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No. 402895

Seq. ID LIB3431-058-P1-K1-D6

Method BLASTX
NCBI GI g1835731
BLAST score 564
E value 3.0e-58
Match length 110
% identity 99

NCBI Description (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No. 402896

Seq. ID LIB3431-058-P1-K1-D7

Method BLASTX
NCBI GI g2130043
BLAST score 600
E value 3.0e-62
Match length 145
% identity 82

NCBI Description Mg-chelatase chain Xantha-h - barley (fragment) >gi 847873

(U26545) Mg-chelatase subunit [Hordeum vulgare] 402897 Seq. No. LIB3431-058-P1-K1-D8 Seq. ID Method BLASTX NCBI GI q115787 679 BLAST score 1.0e-71 E value 152 Match length % identity CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I NCBI Description CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi 20182 emb_CAA32109 (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235) [Oryza sativa] 402898 Seq. No. LIB3431-058-P1-K1-E10 Seq. ID Method BLASTX NCBI GI q482311 551 BLAST score E value 8.0e-57 109 Match length % identity photosystem II oxygen-evolving complex protein 1 - rice NCBI Description (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa] 402899 Seq. No. LIB3431-058-P1-K1-E12 Seq. ID Method BLASTN NCBI GI g20243 BLAST score 145 1.0e-75 E value 169 Match length 95 % identity O.sativa GP28 gene (partial) NCBI Description 402900 Seq. No. LIB3431-058-P1-K1-E2 Seq. ID Method BLASTX NCBI GI g543711 BLAST score 191 2.0e-18 E value 86 Match length 70 % identity 14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 NCBI Description protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140) brain specific protein [Oryza satīva] 402901 Seq. No. LIB3431-058-P1-K1-E4 Seq. ID Method BLASTX

q132105

479 3.0e-48

109

NCBI GI BLAST score

E value Match length

```
% identity
                  85
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  402902
                  LIB3431-058-P1-K1-E5
Seq. ID
                  BLASTX
Method
                  q132105
NCBI GI
                  372
BLAST score
                  8.0e-36
E value
                  90
Match length
                  82
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  402903
Seq. No.
                  LIB3431-058-P1-K1-E7
Seq. ID
                  BLASTX
Method
                  g2570511
NCBI GI
                  244
BLAST score
                  7.0e-21
E value
                  86
Match length
                  57
% identity
                  (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                  402904
Seq. No.
                  LIB3431-058-P1-K1-E8
Seq. ID
                  BLASTX
Method
                  g132105
NCBI GI
BLAST score
                  396
                  2.0e-59
E value
                  133
Match length
                  86
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
```

carboxylase S [Oryza sativa]

```
402905
Seq. No.
                  LIB3431-058-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2245020
                  212
BLAST score
                  7.0e-17
E value
                  137
Match length
% identity
                  40
                  (Z97341) growth regulator like protein [Arabidopsis
NCBI Description
                  thaliana]
                  402906
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q3885894
BLAST score
                  447
                  2.0e-44
E value
                  101
Match length
                  87
% identity
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
Seq. No.
                  402907
                  LIB3431-058-P1-K1-F2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2501189
BLAST score
                  313
E value
                  3.0e-43
                  107
Match length
                  88
% identity
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi 596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
                  402908
Seq. No.
                  LIB3431-058-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2924520
BLAST score
                  486
                   6.0e-49
E value
Match length
                  151
% identity
                   (AL022023) plasma membrane intrinsic protein (SIMIP)
NCBI Description
                   [Arabidopsis thaliana]
                  402909
Seq. No.
Seq. ID
                  LIB3431-058-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                   713
                   1.0e-75
E value
Match length
                  133
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   402910
Seq. No.
                  LIB3431-058-P1-K1-F9
Seq. ID
```

BLAST score

```
BLASTN
Method
NCBI GI
                   q3821780
                   34
BLAST score
E value
                   2.0e-09
                   34
Match length
                   100
% identity
                  Xenopus laevis cDNA clone 27A6-1
NCBI Description
                   402911
Seq. No.
                   LIB3431-058-P1-K1-G1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q20262
                   300
BLAST score
                   1.0e-168
E value
Match length
                   328
                   98
% identity
NCBI Description O.sativa light-induced mRNA
                   402912
Seq. No.
                   LIB3431-058-P1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4581207
BLAST score
                   570
E value
                   6.0e-61
Match length
                   145
% identity
                   81
                   (Y17914) cyclic nucleotide and calmodulin-regulated ion
NCBI Description
                   channel [Arabidopsis thaliana]
                   402913
Seq. No.
Seq. ID
                   LIB3431-058-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   q417260
BLAST score
                   416
E value
                   1.0e-40
Match length
                   127
% identity
                   66
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003_pir__$33632
NCBI Description
                   lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807)
                   light-regulated gene [Oryza sativa]
                   402914
Seq. No.
Seq. ID
                   LIB3431-058-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g4538934
BLAST score
                   275
E value
                   4.0e-24
Match length
                   102
                   53
% identity
                   (AL049483) putative leucine-rich-repeat protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   402915
                   LIB3431-058-P1-K1-G4
Seq. ID
Method
                   BLASTN
                   g3885891
NCBI GI
```

```
E value
                  9.0e-60
Match length
                  163
                  99
% identity
NCBI Description
                  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                  mRNA, complete cds
                  402916
Seq. No.
                  LIB3431-058-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407279
BLAST score
                  277
E value
                  6.0e-25
Match length
                  78
                  71
% identity
                  (AF017362) aldolase [Oryza sativa]
NCBI Description
                  402917
Seq. No.
                  LIB3431-058-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g136636
BLAST score
                  197
                  9.0e-20
E value
                  54
Match length
                  88
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1)
                  >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 -
                  Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin
                  Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_
                  Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana
                  >gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis
                  thaliana] >gi 431260 (L19351) ubiquitin conjugating enzyme
                  [Arabidopsis Thaliana]
                  402918
Seq. No.
                  LIB3431-058-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3004565
BLAST score
                  230
E value
                  6.0e-25
Match length
                  143
% identity
NCBI Description
                  (AC003673) putative protein kinase [Arabidopsis thaliana]
                  402919
Seq. No.
                  LIB3431-058-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  550
E value
                  2.0e-56
Match length
                  113
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{E}C 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
```

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

```
402920
Seq. No.
                   LIB3431-058-P1-K1-H12
Seq. ID
                   BLASTX
Method
                   g5916444
NCBI GI
BLAST score
                   240
                   4.0e-20
E value
                   120
Match length
                   40
% identity
NCBI Description
```

402921

(AC007633) putative protein [Arabidopsis thaliana]

LIB3431-058-P1-K1-H2 Seq. ID Method BLASTX g3789954 NCBI GI 607 BLAST score 3.0e-63 E value Match length 120 % identity

Seq. No.

(AF094776) chlorophyll a/b-binding protein precursor [Oryza NCBI Description

sativa] .

402922 Seq. No. LIB3431-058-P1-K1-H6 Seq. ID

Method BLASTX q4585882 NCBI GI 446 BLAST score 2.0e-44 E value 117 Match length % identity

(AC005850) PSI type III chlorophyll a/b-binding protein NCBI Description

[Arabidopsis thaliana]

402923 Seq. No.

LIB3431-058-P1-K1-H8 Seq. ID

Method BLASTX NCBI GI g132105 BLAST score 455 2.0e-45 E value 106 Match length 84 % identity

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR NCBI Description

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_

(D00643) small subunit of ribulose-1,5-bisphosphate

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate

carboxylase S [Oryza sativa]

402924 Seq. No.

LIB3431-058-P1-K1-H9 Seq. ID

```
BLASTX
Method
                  q3913018
NCBI GI
                  585
BLAST score
E value
                  1.0e-60
                  118
Match length
                   100
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
                   402925
Seq. No.
                  LIB3431-058-P1-N1-A1
Seq. ID
Method
                  BLASTX
                  g3355468
NCBI GI
BLAST score
                   324
E value
                  2.0e-38
                  106
Match length
                  85
% identity
                   (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                   thaliana]
                   402926
Seq. No.
                  LIB3431-058-P1-N1-A10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2274988
BLAST score
                   281 .
E value
                   8.0e-25
Match length
                  96
                   55
% identity
                   (AJ000226) partial sequence, homology to serine
NCBI Description
                  hydroxymethyltransferases [Hordeum vulgare]
                   402927
Seq. No.
                  LIB3431-058-P1-N1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g517500
BLAST score
                  311
E value
                   1.0e-28
                   77
Match length
% identity
                   81
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                   protein [Zea mays] >gi_444338_prf__1906386A photosystem II
                  OE17 protein [Pisum sativum]
Seq. No.
                   402928
                  LIB3431-058-P1-N1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3345477
BLAST score
                   216
E value
                   2.0e-17
                   40
Match length
                   100
% identity
                   (AB016283) carbonic anhydrase [Oryza sativa]
NCBI Description
                   402929
Seq. No.
                  LIB3431-058-P1-N1-A2
Seq. ID
Method
                  BLASTX
```

```
q1514643
NCBI GI
                  168
BLAST score
                  3.0e-26
E value
Match length
                  144
                  45
% identity
                  (Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
NCBI Description
                  402930
Seq. No.
                  LIB3431-058-P1-N1-A3
Seq. ID
                  BLASTN
Method
NCBI GI
                  q1159878
                  50
BLAST score
                   7.0e-19
E value
                  82
Match length
                  90
% identity
NCBI Description A.fatua mRNA for DNA-binding protein (clone ABF2)
                   402931
Seq. No.
                  LIB3431-058-P1-N1-A4
Seq. ID
                  BLASTN
Method
NCBI GI
                   g2072554
                   313
BLAST score
                   1.0e-175
E value
                   313
Match length
                   100
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   402932
Seq. No.
                   LIB3431-058-P1-N1-A5
Seq. ID
                   BLASTN
Method
                   g2570510
NCBI GI
                   131
BLAST score
                   2.0e-67
E value
                   267
Match length
% identity
                   Oryza sativa chlorophyll a-b binding protein mRNA, complete
NCBI Description
                   cds
                   402933
Seq. No.
                   LIB3431-058-P1-N1-A7
Seq. ID
                   BLASTX
Method
                   g671740
NCBI GI
                   431
BLAST score
                   2.0e-42
E value
                   80
Match length
                   96
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic ...
NCBI Description
                   construct]
                   402934
Seq. No.
                   LIB3431-058-P1-N1-B10
Seq. ID
Method
                   BLASTX
                   q3885886
NCBI GI
BLAST score
                   244
                   1.0e-22
E value
```

Match length

E value

4.0e-38

```
% identity
                  (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
NCBI Description
                  402935
Seq. No.
                  LIB3431-058-P1-N1-B11
Seq. ID
                  BLASTX
Method
                  q2582381
NCBI GI
                  144
BLAST score
E value
                  1.0e-08
                  31
Match length
% identity
                   (AF021220) cation-chloride co-transporter [Nicotiana
NCBI Description
                  tabacum]
                  402936
Seq. No.
                  LIB3431-058-P1-N1-B12
Seq. ID
Method
                  BLASTX
                  g115793
NCBI GI
BLAST score
                  396
E value
                  2.0e-38
Match length
                  7.8
                  95
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR
NCBI Description
                   (CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein
                  type III precursor - barley >gi_19023_emb_CAA44881
                   (X63197) type III LHCII CAB precursor protein [Hordeum
                  vulgare]
                  402937
Seq. No.
                  LIB3431-058-P1-N1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3924605
BLAST score
                  227
                  8.0e-19
E value
                  53
Match length
                  72
% identity
                   (AF069442) putative inhibitor of apoptosis [Arabidopsis
NCBI Description
                  thaliana]
                  402938
Seq. No.
Seq. ID
                  LIB3431-058-P1-N1-B5
Method
                  BLASTX
                  g115813 -
NCBI GI
BLAST score
                  201
                  2.0e-15
E value
                  46
Match length
                  83
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                   402939
Seq. No.
Seq. ID
                  LIB3431-058-P1-N1-B6
Method
                  BLASTX
                  g4038663
NCBI GI
BLAST score
                  282
```

A 100

Seq. No.

```
95
Match length
                  77
% identity
                  (AB020929) ribulose-1,5-bisphosphate carboxylase/oxygenase
NCBI Description
                  small subunit [Aegilops speltoides]
                  402940
Seq. No.
                  LIB3431-058-P1-N1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q21838
BLAST score
                  67
E value
                  3.0e-29
Match length
                  207
% identity
                  84
                  T.aestivum PRK gene for ribulose-5-phosphate kinase
NCBI Description
Seq. No.
                  402941
                  LIB3431-058-P1-N1-B8
Seq. ID
Method
                  BLASTX
                  g115813
NCBI GI
BLAST score
                  265
                  6.0e-23
E value
Match length
                  97
                  61
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
NCBI Description
                  CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                  chlorophyll a/b-binding protein [Lycopersicon esculentum]
                  402942
Seq. No.
                  LIB3431-058-P1-N1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  396
E value
                  2.0e-38
Match length
                  73
                  99
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf_ 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  402943
Seq. ID
                  LIB3431-058-P1-N1-C1
Method
                  BLASTX
NCBI GI
                  g2191138
BLAST score
                  390
E value
                  1.0e-37
Match length
                  91
% identity
                  (AF007269) A IG002N01.18 gene product [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. No.

```
Seq. ID
                     LIB3431-058-P1-N1-C12
 Method
                     BLASTN
 NCBI GI
                     g3345476
 BLAST score
                     86
 E value
                     1.0e-40
 Match length
                     220
 % identity
                     83
 NCBI Description Oryza sativa gene for carbonic anhydrase, complete cds
 Seq. No.
                     402945
 Seq. ID
                    LIB3431-058-P1-N1-C2
 Method
                    BLASTX
 NCBI GI
                    g483410
 BLAST score
                    216
 E value
                    1.0e-21
 Match length
                    76
 % identity
                    79
 NCBI Description (L01496) calmodulin-binding protein [Zea mays]
 Seq. No.
                    402946
 Seq. ID
                    LIB3431-058-P1-N1-C3
 Method
                    BLASTX
 NCBI GI
                    g115802
 BLAST score
                    249
 E value
                    3.0e-21
Match length
                    48
 % identity
                    98
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
                    CAB-36) (LHCP) >gi_100311_pir__ S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco
                    >gi_19827_emb_CAA41188_ (X58230) chlorophyll a/b binding
                    protein [Nicotiana tabacum]
Seq. No.
                    402947
Seq. ID
                   LIB3431-058-P1-N1-C4
Method
                   BLASTN
NCBI GI
                   g3789951
BLAST score
                   153
                                                                   v.
E value
                   2.0e-80
Match length
                   233
% identity
                   Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
Seq. No.
                   402948
Seq. ID
                   LIB3431-058-P1-N1-C5
Method
                   BLASTX
NCBI GI
                   g4678949
BLAST score
                   428
E value
                   5.0e-42
Match length
                   104
% identity
                   77
NCBI Description
                   (AL049711) dihydrolipoamide S-acetyltransferase precursor
                   [Arabidopsis thaliana]
```

```
17.
Seq. ID
                  LIB3431-058-P1-N1-C9
Method
                  BLASTX
NCBI GI
                  q5816996
BLAST score
                  514
E value
                  4.0e-52
Match length
                  116
% identity
NCBI Description
                  (AL110123) ribosomal protein L32-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  402950
                  LIB3431-058-P1-N1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1617197
BLAST score
                  264
E value
                  7.0e-23
Match length
                  71
                  68
% identity
                  (Z72488) CP12 [Nicotiana tabacum]
NCBI Description
                  402951
Seq. No.
                  LIB3431-058-P1-N1-D11
Seq. ID
Method
                  BLASTX
                  g3126854
NCBI GI
                  249
BLAST score
E value
                  9.0e-38
                  85
Match length
% identity
NCBI Description (AF061577) chlorophyll a/b binding protein [Oryza sativa]
Seq. No.
                  402952
                  LIB3431-058-P1-N1-D12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2267005
BLAST score
                  269
E value
                  1.0e-149
Match length
                  341
% identity
                  98
                  Oryza sativa endosperm lumenal binding protein (BiP) mRNA,
NCBI Description
                  complete cds
                  402953
Seq. No.
                  LIB3431-058-P1-N1-D2
Seq. ID
Method
                  BLASTX
                  g166341
NCBI GI
                  266
BLAST score
E value
                  5.0e-23
Match length
                  88
% identity
                  56
                  (M98267) alliinase [Allium cepa] >gi 1044969 (L48614)
NCBI Description
                  allinase [Allium cepa]
Seq. No.
                  402954
                  LIB3431-058-P1-N1-D3
Seq. ID
Method
                  BLASTN
                  g4097337
NCBI GI
```

BLAST score .

BLAST score

```
0.0e+00
E value
Match length
                   495
% identity
                   100
                   Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   cds
                   402955
Seq. No.
Seq. ID
                   LIB3431-058-P1-N1-D4
Method
                   BLASTN
NCBI GI
                   g438246
BLAST score
                   57
E value
                   5.0e-23
                   77
Match length
% identity
                   94
                   S.tuberosum mRNA for glycine hydroxymethyltransferase
NCBI Description
                   402956
Seq. No.
Seq. ID
                   LIB3431-058-P1-N1-D6
Method
                   BLASTX
NCBI GI
                   q131400
BLAST score
                   276
                   2.0e-35
E value
Match length
                   113
% identity
NCBI Description
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                   >gi_81471_pir__S00409 photosystem II 10K protein precursor
- spinach >gi_170127 (J03887) 10kd polypeptide precursor
                    [Spinacia oleracea]
                   402957
Seq. No.
Seq. ID
                   LIB3431-058-P1-N1-D7
Method
                   BLASTX
NCBI GI
                   q3334149
BLAST score
                   206
                   4.0e-22
E value
Match length
                   64
% identity
                   91
                   MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR
NCBI Description
                    (MG-PROTOPORPHYRIN IX CHELATASE) >gi 2323329 (AF014053) Mg
                   protoporphyrin chelatase subunit [Nicotiana tabacum]
Seq. No.
                  402958
Seq. ID
                   LIB3431-058-P1-N1-D8
Method
                   BLASTX
NCBI GI
                   q693920
BLAST score
                   416
E value
                   1.0e-40
Match length
                   80
% identity
                    (U21113) chlorophyll a/b binding protein [Solanum
NCBI Description
                   tuberosum]
Seq. No.
                   402959
                   LIB3431-058-P1-N1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q400989
```

```
1.0e-55
E value
Match length
                   137
% identity
                   73
                   50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24)
NCBI Description
                   >gi_322771_pir__A45113 ribosomal protein L24 precursor -
common tobacco >gi_170273 (M87838) ribosomal protein L24
                   [Nicotiana tabacum] >gi_170324 (M87839) ribosomal protein
                   L24 [Nicotiana tabacum]
                   402960
Seq. No.
                   LIB3431-058-P1-N1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q482311
BLAST score
                   502
E value
                   1.0e-50
Match length
                   99
                   99
% identity
                   photosystem II oxygen-evolving complex protein 1 - rice
NCBI Description
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                   complex protein 1 [Oryza sativa]
                   402961
Seq. No.
Seq. ID
                   LIB3431-058-P1-N1-E12
Method
                   BLASTN
                   q20243
NCBI GI
BLAST score
                   145
E value
                   1.0e-75
                   169
Match length
                   95
% identity
NCBI Description
                  O.sativa GP28 gene (partial)
Seq. No.
                   402962
                   LIB3431-058-P1-N1-E2
Seq. ID
Method
                   BLASTN
                   g303858
NCBI GI
BLAST score
                  . 68
E value
                   9.0e-30
Match length
                   147
                   87
% identity
                   Rice mRNA for brain specific protein (S94 gene), complete
NCBI Description
                   402963
Seq. No.
                   LIB3431-058-P1-N1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   289
E value
                   4.0e-49
Match length
                   97
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
```

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

Seq. ID

```
sativa] >gi_226375_prf__1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]
```

```
402964
Seq. No.
Seq. ID
                   LIB3431-058-P1-N1-E5
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   325
                   2.0e-47
E value
Match length
                   94
% identity
                   99
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                   ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   402965
Seq. ID
                   LIB3431-058-P1-N1-E7
Method
                   BLASTX
NCBI GI
                   g115794
BLAST score
                   439
E value
                   1.0e-66
Match length
                   134
                   92
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 13 PRECURSOR (LHCII TYPE
                   III CAB-13) >gi_72748_pir__CDTO33 chlorophyll a/b-binding protein type III precursor (cab-13) - tomato
                   >gi 19277 emb CAA42818 (X60275) LHCII type III
                   [Lycopersicon esculentum]
Seq. No.
                   402966
Seq. ID
                   LIB3431-058-P1-N1-F11
Method
                   BLASTX
NCBI GI
                   q2245106
BLAST score
                   328
E yalue
                   2.0e-30
Match length
                   80.
% identity
                   70
                  (Z97343) thioesterase like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   402967
Seq. ID
                   LIB3431-058-P1-N1-F12
Method
                   BLASTX
NCBI GI
                   g3885894
BLAST score
                   517
E value
                   2.0e-52
Match length
                   115
% identity
                   (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
Seq. No.
                   402968
```

LIB3431-058-P1-N1-F2

BLAST score

```
Method
                   BLASTX
NCBI GI
                   q2501190
BLAST score
                   325
E value
                   6.0e-30
Match length
                   85
% identity
                   THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR
NCBI Description
                   >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme
                   [Zea mays]
Seq. No.
                   402969
Seq. ID
                   LIB3431-058-P1-N1-F3
Method
                   BLASTX
NCBI GI
                   q115871
BLAST score
                   236
E value
                   2.0e-31
Match length
                   103
                   60
% identity
NCBI Description
                   [Segment 2 of 2] SERINE CARBOXYPEPTIDASE II CHAINS A AND B
                   (CARBOXYPEPTIDASE D) (CPDW-II) (CP-WII)
                   >gi_82623_pir__B29639 serine-type carboxypeptidase (EC
                   3.4.16.1) II B chain - wheat >gi_1421108_pdb_1BCR_B Chain
                   B, Complex Of The Wheat Serine Carboxypeptidase, Cpdw-Ii,
                   With The Microbial Peptide Aldehyde Inhibitor, Antipain,
                   And Arginine At Room Temperature >gi_1421113_pdb_1BCS_B
                   Chain B, Complex Of The Wheat Serine Carboxypeptidase,
                   Cpdw-Ii, With The Microbial Peptide Aldehyde Inhibitor,
                   Chymostatin, And Arginine At 100 Degrees Kelvin
                   >gi 226041 prf 1408164B CPase II B [Triticum aestivum]
                   402970
Seq. No.
Seq. ID
                   LIB3431-058-P1-N1-F4
Method
                   BLASTX
NCBI GI
                   q3158476
BLAST score
                   217
E value
                   8.0e-31
Match length
                   89
                   78
% identity
                   (AF067185) aquaporin 2 [Samanea saman]
NCBI Description
Seq. No.
                   402971
Seq. ID
                   LIB3431-058-P1-N1-F5
Method
                   BLASTX
NCBI GI
                   q4960154
BLAST score
                   318
E value
                   4.0e-29
Match length
                   73
% identity
                   85
                   (AF153283) putative progesterone-binding protein homolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   402972
Seq. ID
                   LIB3431-058-P1-N1-F6
Method
                   BLASTN
NCBI GI
                   q505134
```

```
E value
                   1.0e-114
Match length
                   305
                   93
% identity
                   Rice mRNA for ferredoxin, complete cds
NCBI Description
                   402973
Seq. No.
Seq. ID
                   LIB3431-058-P1-N1-F8
Method
                   BLASTX
NCBI GI -
                   g3126854
BLAST score
                   411
E value
                   4.0e-54
                   113
Match length
                   96
% identity
                  (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   402974
Seq. No.
                   LIB3431-058-P1-N1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g417260
                   255
BLAST score
E value
                   1.0e-24
Match length
                   79
% identity
                   69
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                   lir1 protein - rice >gi_20263_emb_CAA\overline{4}8706_ (X68\overline{80}7)
                   light-regulated gene [Oryza sativa]
Seq. No.
                   402975
                   LIB3431-058-P1-N1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g517500
BLAST score
                   301
E value
                   2.0e-27
Match length
                   89
% identity
                   70
NCBI Description
                   (M87435) precursor of the oxygen evolving complex 17 kDa
                   protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                   OE17 protein [Pisum sativum]
                   402976
Seq. No.
Seq. ID
                   LIB3431-058-P1-N1-G12
Method
                   BLASTX
NCBI GI
                   g417260
BLAST score
                   411
                   5.0e-40
E value
Match length
                   128
% identity
                   66
                   LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                   lir1 protein - rice >gi 20263 emb CAA\overline{4}8706 (X68\overline{80}7)
                   light-regulated gene [Oryza sativa]
Seq. No.
                   402977
                   LIB3431-058-P1-N1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3885892
BLAST score
                   513
E value
                   4.0e-52
```

Seq. No.

```
96
Match length
                   100
% identity
                   (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
                   402978
Seq. No.
                   LIB3431-058-P1-N1-G8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q548603
BLAST score
                   543
E value
                   1.0e-55
                   108
Match length
                   95
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                   >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                   barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
                   402979
Seq. No.
Seq. ID
                   LIB3431-058-P1-N1-G9
Method
                   BLASTX
NCBI GI
                   g3004565
BLAST score
                   188
E value
                   2.0e-18
Match length
                   94
% identity
NCBI Description
                   (AC003673) putative protein kinase [Arabidopsis thaliana]
                   402980
Seq. No.
                   LIB3431-058-P1-N1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   234
E value
                   4.0e-21
Match length
                   70
                   81
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   402981
Seq. No.
Seq. ID
                   LIB3431-058-P1-N1-H2
Method
                   BLASTX
NCBI GI
                   q3789954
BLAST score
                   339
E value
                   1.0e-54
Match length .
                   110
% identity
NCBI Description
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                   sativa]
```

NCBI GI

```
LIB3431-058-P1-N1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                    482
                    2.0e-48
E value
                    99
Match length
% identity
                    89
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                    402983
Seq. ID
                   LIB3431-058-P1-N1-H9
Method
                   BLASTX
NCBI GI
                    q2407279
BLAST score
                    206
E value
                    4.0e-16
Match length
                    43
% identity
NCBI Description
                    (AF017362) aldolase [Oryza sativa]
Seq. No.
                    402984
Seq. ID
                   LIB3431-059-P1-K1-A10
Method
                   BLASTX
NCBI GI
                    q115787
BLAST score
                    571
E value
                    4.0e-59
Match length
                    111
% identity
                    98
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
Seq. No.
                    402985
Seq. ID
                   LIB3431-059-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   q6006871
BLAST score
                   333
E value
                    4.0e-31
Match length
                   126
% identity
                   52
NCBI Description
                    (AC009540) hypothetical protein [Arabidopsis thaliana]
                   >gi 6091753 gb AAF03463.1 AC009327 2 (AC009327)
                   hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   402986
Seq. ID
                   LIB3431-059-P1-K1-A12
Method
                   BLASTX
```

q3789952

```
BLAST score
                    568
                    1.0e-58
E value
Match length
                    114
% identity
                    98
                    (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                    sativa]
Seq. No.
                    402987
Seq. ID
                    LIB3431-059-P1-K1-A2
Method
                    BLASTX
NCBI GI
                    g1001355
BLAST score
                    144
E value
                    6.0e-09
Match length
                    60
% identity
NCBI Description
                    (D64006) auxin-induced protein [Synechocystis sp.]
                    402988
Seq. No.
                    LIB3431-059-P1-K1-A3
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3126854
BLAST score
                    578
E value
                    7.0e-60
Match length
                    109
% identity
                    99
                    (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                    402989
Seq. No.
                    LIB3431-059-P1-K1-A4
Seq. ID
Method
                    BLASTX
NCBI GI
                    q548774
BLAST score
                    464
                    2.0e-46
E value
                    109
Match length
                    83
% identity
                   60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
NCBI Description
                    ribosomal protein L7A [Oryza sativa]
                    402990
Seq. No.
                   LIB3431-059-P1-K1-A6
Seq. ID
Method
                    BLASTX
                    g4469021
NCBI GI
BLAST score
                    312
                    2.0e-28
E value
Match length
                    85
% identity
                    71
                    (AL035602) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    402991
                   LIB3431-059-P1-K1-A9
Seq. ID
Method
                    BLASTX
NCBI GI
                    g320618
BLAST score
                    643
                    2.0e-67
E value
Match length
                    142
```

% identity

```
chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   402992
Seq. No.
Seq. ID
                   LIB3431-059-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g3860277
BLAST score
                   423
                   1.0e-41
E value
                   96
Match length
% identity
NCBI Description
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
                   thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                   402993
Seq. ID
                   LIB3431-059-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   q2736155
BLAST score
                   476
E value
                   9.0e-48
Match length
                   122
% identity
                   (AF022082) sulfolipid biosynthesis protein [Arabidopsis
NCBI Description
                   thaliana] >gi_3688184_emb_CAA21212_ (AL031804) sulfolipid
                   biosynthesis protein SQD1 [Arabidopsis thaliana]
Seq. No.
                   402994
Seq. ID
                   LIB3431-059-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   8.0e-20
Match length
                   44
% identity
                   100
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   402995
Seq. No.
                   LIB3431-059-P1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1352461
BLAST score
                   178
E value
                   4.0e-15
Match length
                   93
% identity
                   49
NCBI Description
                   IN2-2 PROTEIN
Seq. No.
                   402996
                   LIB3431-059-P1-K1-B2
Seq. ID
Method
                   BLASTX
```

g6041833

200

NCBI GI

BLAST score

% identity

```
E value
                  2.0e-15
Match length
                  123
% identity
                  38
                   (AC009853) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  402997
                  LIB3431-059-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q131192
                                                                      BLAST score
                  297
E value
                  6.0e-27
Match length
                  97
% identity
                  65
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
                   (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_100606_pir__S20937
                  photosystem I chain V precursor - barley
                  >qi 19091 emb CAA42727 (X60158) photosystem I polypeptide
                  PSI-G precursor [Hordeum vulgare]
Seq. No.
                  402998
                  LIB3431-059-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3618310
BLAST score
                  334
                  3.0e - 31
E value
Match length
                  97
% identity.
                   67
                   (AB001883) zinc finger protein [Oryza sativa]
NCBI Description
Seq. No.
                  402999
Seq. ID
                  LIB3431-059-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q1881585
BLAST score
                  231
E value
                  4.0e-19
Match length
                  117
% identity
                  45
NCBI Description
                   (U72489) remorin [Solanum tuberosum]
                  -403000
Seq. No.
                  LIB3431-059-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2293480
BLAST score
                  168
E value
                  2.0e-12
Match length
                  48
% identity
NCBI Description
                  (AF011331) glycine-rich protein [Oryza sativa]
                  403001
Seq. No.
Seq. ID
                  LIB3431-059-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q3885894
BLAST score
                  402
E value
                  3.0e-39
Match length
                  91
```

Seq. ID Method

```
NCBI Description
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
                  403002
Seq. No.
Seq. ID
                  LIB3431-059-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q1351270
BLAST score
                  562
                  7.0e-58
E value
Match length
                  123
                  89
% identity
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
                  >gi_478410_pir__JQ2255 triose-phosphate isomerase (EC
                  5.3.1.1) - rice >gi 169821 (M87064) triosephosphate
                  isomerase [Oryza sativa]
                  403003
Seq. No.
                  LIB3431-059-P1-K1-B9
Seq. ID
Method
                  BLASTX
                  g4732091
NCBI GI
BLAST score
                  254
E value
                  7.0e-22
Match length
                  69
                  67
% identity
                  (AF126742) bundle sheath defective protein 2 [Zea mays]
NCBI Description
Seq. No.
                  403004
Seq. ID
                  LIB3431-059-P1-K1-C1
Method
                  BLASTN
NCBI GI
                  q3617841
BLAST score
                  190
E value
                  1.0e-103
Match length
                  190
                  100
% identity
                  Oryza sativa clone F14605 calmodulin (CaM1) mRNA, complete
NCBI Description
Seq. No.
                  403005
                  LIB3431-059-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  614
                  6.0e-64
E value
Match length
                  132
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                 _sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  403006
Seq. No.
```

LIB3431-059-P1-K1-C11

BLASTN

```
g4218534
NCBI GI
                   34
BLAST score
                   2.0e-09
E value
Match length
                   46
% identity
                   93
NCBI Description
                  Triticum sp. mRNA for GRAB1 protein
                  403007
Seq. No.
Seq. ID
                  LIB3431-059-P1-K1-C12
Method
                  BLASTN
NCBI GI
                   q3885891
BLAST score
                   141
                   1.0e-73
E value
                   141
Match length
% identity
                   100
                  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
NCBI Description
                  mRNA, complete cds
                   403008
Seq. No...
                   LIB3431-059-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g5734720
BLAST score
                   231
E value
                   4.0e-19
Match length
                  138
                   43
% identity
                   (AC008075) Contains PF 01426 BAH (bromo-adjacent homology)
NCBI Description
                   domain. ESTs gb_N96349, gb_T42710, gb_H77084, gb_AA395147
                   and gb AA605500 come from this gene. [Arabidopsis thaliana]
                   403009
Seq. No.
                   LIB3431-059-P1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1848214
BLAST score
                   197
E value
                   4.0e-15
Match length
                   49
% identity
                   73
                   (Y11210) uracil phosphoribosyltransferase [Nicotiana
NCBI Description
                   tabacum]
                   403010
Seq. No.
                   LIB3431-059-P1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2570511
BLAST score
                   625
E value
                   2.0e-65
Match length
                   123
% identity
                   95
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                   403011
Seq. No.
Seq. ID
                   LÍB3431-059-P1-K1-C8
Method
                   BLASTX
                   g3885894
NCBI GI
                   436
BLAST score
```

3.0e-43

E value

```
97
Match length
% identity
                   88
NCBI Description
                   (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
Seq. No.
                   403012
                  LIB3431-059-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3138799
BLAST score
                   603
E value
                   1.0e-62
Match length
                  125
% identity
                   92
                   (AB014058) beta 6 subunit of 20S proteasome [Oryza sativa]
NCBI Description
Seq. No.
                   403013
Seq. ID
                   LIB3431-059-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   8.0e-20
Match length
                   44
% identity
                   100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                   403014
                  LIB3431-059-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g671740
BLAST score
                   695
                   2.0e-73
E value
                   128
Match length
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
Seq. No.
                   403015
Seq. ID
                  LIB3431-059-P1-K1-D12
Method
                  BLASTX
NCBI GI
                   q3915826
BLAST score
                   309
E value
                   2.0e-28
Match length
                   67
% identity
                   93
NCBI Description
                  60S RIBOSOMAL PROTEIN L5
Seq. No.
                   403016
Seq. ID
                  LIB3431-059-P1-K1-D3
Method
                  BLASTX
                   g548605
NCBI GI
BLAST score
                   386
E value
                   3.0e-37
Match length
                  80
                   95
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
```

(LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)

```
[Hordeum vulgare]
                    403017
Seq. No.
                   LIB3431-059-P1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2407281
BLAST score
                    567
E value
                    2.0e-58
                   109
Match length
                    98
% identity
                    (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
                    403018
Seq. No.
                   LIB3431-059-P1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                    g132105
BLAST score
                    576
E value
                    1.0e-59
Match length
                    124
% identity
                    87
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                    403019
Seq. No.
                   LIB3431-059-P1-K1-D7
Seq. ID
Method
                   BLASTX
                    g3894170
NCBI GI
BLAST score
                    174
                    2.0e-12
E value
Match length
                    41
% identity
NCBI Description
                    (AC005312) putative glutathione s-transferase [Arabidopsis
                    thaliana]
                    403020
Seq. No.
                   LIB3431-059-P1-K1-D8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                    609
E value
                    2.0e-63
Match length
                   131
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
```

>gi_539055_pir_ A48527 photosystem I protein psaK precursor - barley >gi 304220 (L12707) photosystem I PSI-K subunit

```
carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]
```

```
Seq. No.
                  403021
                  LIB3431-059-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3914466
BLAST score
                  307
                  5.0e-28
E value
Match length
                  63
                  92
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                   (PSI-N) >gi 2981214 (AF052429) photosystem I complex PsaN
                  subunit precursor [Zea mays]
                  403022
Seq. No.
                  LIB3431-059-P1-K1-E1
Seq. ID
Method
                  BLASTX
                  q3738329
NCBI GI
BLAST score
                  237
                  9.0e-20
E value
Match length
                  61
% identity
                  (AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
                  403023
Seq. No.
                  LIB3431-059-P1-K1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g169133
BLAST score
                  60
E value
                  4.0e-25
Match length
                  156
                  85
% identity
                  Zea mays precursor of the oxygen evolving complex 17 kDa
NCBI Description
                  protein mRNA, complete cds
Seq. No.
                  403024
                  LIB3431-059-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2407281
BLAST score
                  642
E value
                  2.0e-67
Match length
                  121
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
Seq. No.
                  403025
                  LIB3431-059-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q548603
BLAST score
                  271
E value
                  5.0e-28
Match length
                  115
```

65

% identity

BLAST score

```
NCBI Description
                    PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                     (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                    >gi 478404 pir JQ2247 photosystem I chain D precursor -
                    barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
                    403026
Seq. No.
Seq. ID
                    LIB3431-059-P1-K1-E4
Method
                    BLASTX
NCBI GI
                    q2198851
BLAST score
                    794
                    5.0e-85
E value
Match length
                    155
% identity
                    97
NCBI Description
                     (AF007785) cystathionine gamma-synthase [Zea mays]
                    403027
Seq. No.
                    LIB3431-059-P1-K1-E5
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1235664
BLAST score
                    631
E value
                     6.0e-66
Match length
                    131
% identity
                    59
NCBI Description
                     (U37936) novel calmodulin-like protein [Oryza sativa]
                    >gi 3171148 (AF064456) calmodulin-like protein [Oryza
                    satīva subsp. indica]
                    403028
Seq. No.
                    LIB3431-059-P1-K1-E6
Seq. ID
Method
                    BLASTX
NCBI GI
                    q133999
BLAST score
                    378
E value
                    2.0e-36
Match length
                    79
                    97
% identity
NCBI Description
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi 70904 pir R3RZ7
                    ribosomal protein S7 - rice chloroplast
>gi_12037_emb_CAA33942_ (X15901) ribosomal protein S7
[Oryza sativa] >gi_12065_emb_CAA33919_ (X15901) ribosomal protein S7 [Oryza sativa] >gi_226657_prf__1603356CH
                    ribosomal protein S7 [Oryza sativa]
Seq. No.
                    403029
Seq. ID
                    LIB3431-059-P1-K1-E7
Method
                    BLASTX
NCBI GI
                    q1835731
BLAST score
                    520
E value
                     4.0e-53
Match length
                    99
% identity
                    (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                    403030
Seq. ID
                    LIB3431-059-P1-K1-E9
Method
                    BLASTX
NCBI GI
                    q733454
```

Seq. ID

....

```
8.0e-53
E value
                  121
Match length
                  82
% identity
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
                  403031
Seq. No.
                  LIB3431-059-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173347
BLAST score
                  593
                  2.0e-61
E value
Match length
                  130
% identity
                  91
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi 100803_pir__S23452_sedoheptulose-bisphosphatase (EC
                  3.1.3.37) precursor - wheat >gi 14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                  aestivum]
Seq. No.
                  403032
                  LIB3431-059-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3288821
BLAST score
                  484
E value
                  9.0e-49
Match length
                  132
% identity
NCBI Description
                   (AF063901) alanine:glyoxylate aminotransferase;
                  transaminase [Arabidopsis thaliana]
                  >gi 4733989 gb_AAD28669.1_AC007209_5 (AC007209)
                  alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
Seq. No.
                  403033
Seq. ID
                  LIB3431-059-P1-K1-F11
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  35
E value
                  4.0e-10
Match length
                  35
% identity
                  100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  403034
Seq. ID
                  LIB3431-059-P1-K1-F12
Method
                  BLASTN
NCBI GI
                  g1245938
BLAST score
                  35
E value
                  4.0e-10
Match length
                  35
% identity
                  rabClC-2 beta=chloride channel ClC-2G isoform [rabbits,
NCBI Description
                  heart atrium, mRNA, 2998 nt]
Seq. No.
                  403035
```

S...

LIB3431-059-P1-K1-F3

Match length

```
Method
                    BLASTX
NCBI GI
                    g1800227
BLAST score
                    246
                    6.0e-21
E value
                    67 .
Match length
                    60
% identity
                    (U76004) Bowman-Birk proteinase inhibitor [Oryza sativa]
NCBI Description
Seq. No.
                    403036
                    LIB3431-059-P1-K1-F4
Seq. ID
                    BLASTX
Method
NCBI GI
                    q115787
BLAST score
                    519
E value
                    7.0e-53
                    120
Match length
% identity
                    87
                    CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
Seq. No.
                    403037
Seq. ID
                    LIB3431-059-P1-K1-F5
Method
                    BLASTX
NCBI GI
                    q132105
BLAST score
                    395
E value
                    2.0e-38
Match length
                    73
% identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
Seq. No.
                    403038
Seq. ID
                    LIB3431-059-P1-K1-F6
Method
                    BLASTN
NCBI GI
                    q3819345
BLAST score
                    60
                    7.0e-25
E value
Match length
                    168
% identity
                   Hordeum vulgare genomic DNA fragment; clone MWG0803
NCBI Description
                    403039
Seq. No.
Seq. ID
                    LIB3431-059-P1-K1-G2
Method
                    BLASTX
NCBI GI
                    q132105
BLAST score
                    429
                    2.0e-42
E value
```

BLAST score

E value

308

9.0e-29

```
% identity
                  82
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094 pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  403040
Seq. No.
Seq. ID
                  LIB3431-059-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g3450889
BLAST score
                  207
                  2.0e-16
E value
Match length
                  96
% identity
                  69
NCBI Description (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
Seq. No.
                  403041
                  LIB3431-059-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3264767
BLAST score
                  183
E value
                  2.0e-13
Match length
                  59
% identity
NCBI Description (AF071893) AP2 domain containing protein [Prunus armeniaca]
                  403042
Seq. No.
Seq. ID
                  LIB3431-059-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q100796
BLAST score
                  650
E value
                  3.0e-68
Match length
                  132
% identity
                  92
NCBI Description phosphoribulokinase (EC 2.7.1.19) - wheat
Seq. No.
                  403043
Seq. ID
                  LIB3431-059-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q3345477 -
BLAST score
                  179
E value
                  2.0e-13
Match length
                  63
% identity
NCBI Description
                  (AB016283) carbonic anhydrase [Oryza sativa]
                  403044
Seq. No.
Seq. ID
                  LIB3431-059-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g21693
```

% identity

```
67
Match length
% identity
                   82
NCBI Description (X66012) cathepsin B [Triticum aestivum]
                   403045
Seq. No.
                   LIB3431-059-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4567283
BLAST score
                   270
                   8.0e-24
E value
                   125
Match length
                   46
% identity
                   (AC006841) unknown protein [Arabidopsis thaliana]
NCBI Description
                   403046
Seq. No.
                   LIB3431-059-P1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2582822
BLAST score
                   213
                   6.0e-17
E value
Match length
                   53
% identity
                   74
                    (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress
NCBI Description
                   Protein of 32kDa) [Solanum tuberosum]
Seq. No.
                   403047
                   LIB3431-059-P1-K1-H4
Seq. ID
Method (
                   BLASTX
NCBI GI
                   g115772
BLAST score
                   298
E value
                   1.0e-34
Match length
                   96
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
                   CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108_
                    (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                    [Oryza sativa]
Seq. No.
                   403048
Seq. ID
                   LIB3431-059-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g871931
BLAST score
                   281
E value
                   4.0e-25
Match length
                   77
% identity
NCBI Description (D30763) ferredoxin [Oryza sativa]
                   403049
Seq. No.
Seq. ID
                   LIB3431-059-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   q131773
BLAST score
                   583
E value
                   2.0e-60
Match length
                   122
```

```
40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
NCBI Description
                   >gi 82724 pir B30097 ribosomal protein S14 (clone MCH2) -
                   maize
                   403050
Seq. No.
Seq. ID
                   LIB3431-059-P1-K1-H8
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   .38
E value
                   9.0e-12
Match length
                   49
                   66
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                   403051
Seq. ID
                   LIB3431-059-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   g3894197
BLAST score
                   346
E value
                   1.0e-32
Match length
                   139
                   49
% identity
NCBI Description
                   (AC005662) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   403052
Seq. ID
                   LIB3431-059-P1-N1-A1
Method-
                   BLASTX
                  g115813
257
NCBI GI
BLAST score
E value
                   3.0e-22
Match length
                   61
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                   CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                   chlorophyll a/b-binding protein [Lycopersicon esculentum]
Seq. No.
                   403053
Seq. ID
                   LIB3431-059-P1-N1-A10
Method
                   BLASTX
NCBI GI
                   q421916
BLAST score
                   190
E value
                   2.0e-14
Match length
                   36
                   97
% identity
                   chlorophyll a/b-binding protein - English ivy (fragment)
>gi_12582_emb_CAA48410_ (X68333) light harvesting
NCBI Description
                   chlorophyll a /b binding protein [Hedera helix]
Seq. No.
                   403054
Seq. ID
                   LIB3431-059-P1-N1-A12
Method
                   BLASTN
NCBI GI
                   q3789951
BLAST score
                   160
E value
                   1.0e-84
Match length
                   362
                   99
% identity
NCBI Description Oryza sativa chlorophyll a/b-binding protein presursor
```

```
(Cab27) mRNA, nuclear gene encoding chloroplast protein,
                    complete cds
                    403055
Seq. No.
Seq. ID
                   LIB3431-059-P1-N1-A2
Method
                   BLASTX
NCBI GI
                   g1001355
BLAST score
                   192
E value
                    1.0e-14
Match length
                    57
% identity
NCBI Description
                    (D64006) auxin-induced protein [Synechocystis sp.]
                    403056
Seq. No.
Seq. ID
                   LIB3431-059-P1-N1-A3
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   211
E value
                    1.0e-19
Match length
                    66
                   79
% identity
                    (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                    403057
Seq. No.
                   LIB3431-059-P1-N1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   a548774
BLAST score
                    267
E value
                    2.0e-23
Match length
                    69
% identity
                   80
                   60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631)
NCBI Description
                   ribosomal protein L7A [Oryza sativa]
Seq. No.
                    403058
Seq. ID
                   LIB3431-059-P1-N1-A6
Method
                   BLASTX
NCBI GI
                   q4469021
BLAST score
                   287
E value
                    1.0e-25
Match length
                   71
% identity
NCBI Description
                    (AL035602) hypothetical protein [Arabidopsis thaliana]
                   403059
Seq. No.
Seq. ID
                   LIB3431-059-P1-N1-A9
Method
                   BLASTX
NCBI GI
                   q289920
BLAST score
                   329
E value
                   1.0e-30
Match length
                   63
% identity
                   100
NCBI Description
                    (L07119) chlorophyll A/B binding protein [Gossypium
                   hirsutum]
                    403060
Seq. No.
```

```
Seq. ID
                   LIB3431-059-P1-N1-B1
Method
                   BLASTX
NCBI GI
                   q3860277
BLAST score
                   167
E value
                   1.0e-11
Match length
                   32
                   100
% identity
NCBI Description
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
                   thaliana] >gi 4314394 gb AAD15604_ (AC006232) putative
                   ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                   403061
Seq. ID
                   LIB3431-059-P1-N1-B11
Method
                   BLASTN
NCBI GI
                   a2072554
BLAST score
                   321
                   0.0e + 00
E value
                   321
Match length
                   100
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
Seq. No.
                   403062
Seq. ID
                   LIB3431-059-P1-N1-B2
Method
                   BLASTX
NCBI GI
                   g6041833
BLAST score
                   151
E value
                   9.0e-10
                  85
Match length
% identity
                   42
                   (AC009853) unknown protein [Arabidopsis thaliana]
NCBI Description
                   403063
Seq. No.
                   LIB3431-059-P1-N1-B3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g19090
BLAST score
                   45
E value
                   5.0e-16
                  65
Match length
                   92
% identity
NCBI Description
                  H.vulgare PsaG mRNA
                   403064
Seq. No.
                  LIB3431-059-P1-N1-B4
Seq. ID
Method
                  BLASTX
                   g3618310
NCBI GI
BLAST score
                   317
E value
                   3.0e-29
Match length
                   61
% identity
                   100
                   (AB001883) zinc finger protein [Oryza sativa]
NCBI Description
                   403065
Seq. No.
                  LIB3431-059-P1-N1-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2624325
```

224

BLAST score

E value

3.0e-23

```
1.0e-123
E value
                   248
Match length
% identity
                   98
                   Oryza sativa mRNA for glycine-rich RNA-binding protein
NCBI Description
                    (OsGRP1)
                   403066
Seq. No.
Seq. ID
                   LIB3431-059-P1-N1-B7
Method
                   BLASTX
NCBI GI
                   g3885894
                   193
BLAST score
                   1.0e-14
E value
                   53
Match length
% identity
                   75
                   (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
Seq. No.
                   403067
Seq. ID
                   LIB3431-059-P1-N1-B8
Method
                   BLASTX
NCBI GI
                   g1351270
BLAST score
                   195
E value
                   6.0e-15
Match length
                   48
% identity
NCBI Description
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM)
                   >gi_478410_pir__JQ2255 triose-phosphate isomerase (EC 5.3.1.1) - rice >gi_169821 (M87064) triosephosphate
                   isomerase [Oryza sativa]
                   403068
Seq. No.
Seq. ID
                   LIB3431-059-P1-N1-C1
Method
                   BLASTN
NCBI GI
                   q3617841
BLAST score
                   186
E value
                   1.0e-100
Match length
                   190
% identity
                   99
                   Oryza sativa clone F14605 calmodulin (CaM1) mRNA, complete
NCBI Description
Seq. No.
                   403069
                   LIB3431-059-P1-N1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g347451
BLAST score
                   197
E value
                   3.0e-15
Match length
                   37
% identity
                    (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   403070
                   LIB3431-059-P1-N1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3885892
BLAST score
                   266
```

Seq. ID

```
53
Match length
                  100
% identity
NCBI Description
                   (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.
                   403071
                  LIB3431-059-P1-N1-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4079797
BLAST score
                  39
E value
                  2.0e-12
Match length
                  71
                  89
% identity
                  Oryza sativa 23 kDa polypeptide of photosystem II mRNA,
NCBI Description
                  complete cds
                   403072
Seq. No.
                  LIB3431-059-P1-N1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2570511
BLAST score
                  163
E value
                   3.0e-22
Match length
                   67
% identity
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                   403073
Seq. No.
                  LIB3431-059-P1-N1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20262
BLAST score
                  126
E value
                  2.0e-64
Match length
                  194
                  91
% identity
NCBI Description
                  O.sativa light-induced mRNA
Seq. No.
                  403074
Seq. ID
                  LIB3431-059-P1-N1-C8
Method
                  BLASTX
NCBI GI
                  q3885894
BLAST score
                  193
E value
                   1.0e-14
Match length
                  53
% identity
NCBI Description
                   (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
                  403075
Seq. No.
Seq. ID
                  LIB3431-059-P1-N1-C9
Method
                  BLASTX
NCBI GI
                  q3138799
BLAST score
                  263
E value
                  7.0e-23
Match length
                  60
% identity
                   (AB014058) beta 6 subunit of 20S proteasome [Oryza sativa]
NCBI Description
                  403076
Seq. No.
```

LIB3431-059-P1-N1-D10

```
Method
                   BLASTN
NCBI GI
                   g2072554
BLAST score
                   380
                   0.0e + 00
E value
Match length
                   380
% identity
                   100
                   Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   403077
Seq. No.
                   LIB3431-059-P1-N1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q671740
BLAST score
                   243
E value
                   1.0e-20
Match length
                   47
                   100
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   403078
Seq. No.
                   LIB3431-059-P1-N1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3915826
BLAST score
                   202
E value
                   9.0e-16
Match length
                   41
                   100
% identity
NCBI Description 60S RIBOSOMAL PROTEIN L5
Seq. No.
                   403079
                   LIB3431-059-P1-N1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q548605
BLAST score
                   386
E value
                   2.0e-37
Match length
                   80
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi_539055_pir__A48527 photosystem I protein psaK precursor
                   - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
                   403080
Seq. No.
                   LIB3431-059-P1-N1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   526
                   1.0e-53
E value
Match length
                   95
                   100
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
```

NCBI GI

E value Match length

BLAST score

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
sativa] >gi_226375_prf__1508256A ribulose bisphosphate
carboxylase S [Oryza sativa]

```
Seq. No.
                   403081
                  LIB3431-059-P1-N1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q347451
BLAST score
                  248
E value
                   4.0e-21
Match length
                   48
% identity
                   100
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                   sativa]
                   403082
Seq. No.
                  LIB3431-059-P1-N1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3894171
BLAST score
                   252
                   1.0e-21
E value
Match length
                   67
% identity
                   70
                   (AC005312) putative glutathione s-transferase [Arabidopsis
NCBI Description
                   thaliana]
                   403083
Seq. No.
                  LIB3431-059-P1-N1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g347451
BLAST score
                  248
                   4.0e-21
E value
Match length
                  48
% identity
                  100
NCBI Description
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
                  sativa]
                   403084
Seq. No.
                  LIB3431-059-P1-N1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3914466
BLAST score
                  163
                  2.0e-11
E value
Match length
                  46
                   67
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                   (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN
                  subunit precursor [Zea mays]
Seq. No.
                  403085
                  LIB3431-059-P1-N1-E10
Seq. ID
Method
                  BLASTX
```

g517500

2.0e-36

378

E value

7.0e-42

```
% identity
NCBI Description
                   (M87435) precursor of the oxygen evolving complex 17 kDa
                  protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
                  403086
Seq. No.
                  LIB3431-059-P1-N1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218209
BLAST score
                  149
E value
                   4.0e-78
Match length
                  316
% identity
                   97
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS2106
                  403087
Seq. No.
Seq. ID
                  LIB3431-059-P1-N1-E2
Method
                  BLASTX
NCBI GI
                  g548603
BLAST score
                  366
E value
                   5.0e-35
Match length
                  72
                  96
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                  >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                  barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                  403088
                  LIB3431-059-P1-N1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2198853
BLAST score
                  355
E value
                   9.0e-34
Match length
                  82
% identity
                   (AF007786) cystathionine gamma-synthase [Zea mays]
NCBI Description
                  403089
Seq. No.
Seq. ID
                  LIB3431-059-P1-N1-E5
Method
                  BLASTN
                  g1235663
NCBI GI
BLAST score
                  253
E value
                  1.0e-140
Match length
                  261
% identity
NCBI Description
                  Oryza sativa clone pFDRSC61 novel calmodulin-like protein
                  mRNA, complete cds
Seq. No.
                  403090
Seq. ID
                  LIB3431-059-P1-N1-E6
Method
                  BLASTX
NCBI GI
                  q1173275
BLAST score
                  425 -
```

Seq. ID

```
Match length
                    102
% identity
                    86
NCBI Description
                    CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
                    >gi_2119068_pir__S58630 ribosomal protein S7 - maize
chloroplast >gi_902274_emb_CAA60339_ (X86563) ribosomal
protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563)
                    ribosomal protein S7 [Zea mays]
Seq. No.
                    403091
Seq. ID
                    LIB3431-059-P1-N1-E7
Method
                    BLASTX
NCBI GI
                    q1835731
BLAST score
                    286
                    1.0e-25
E value
Match length
                    65
                    85
% identity
                    (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                    403092
Seq. No.
Seq. ID
                    LIB3431-059-P1-N1-E9
Method
                    BLASTX
NCBI GI
                    q733454
BLAST score
                    232
E value
                    3.0e-19
Match length
                    48
% identity
                    94
                    (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                    [Zea mays]
                    403093
Seq. No.
Seq. ID
                    LIB3431-059-P1-N1-F1
Method
                    BLASTX
NCBI GI
                    q1173347
BLAST score
                    216
                    2.0e-17
E value
Match length
                    47
% identity
                    SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                    (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7) P2ASE)
                    >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                    3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                    (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                    aestivum]
Seq. No.
                    403094
Seq. ID
                    LIB3431-059-P1-N1-F10
Method
                    BLASTX
NCBI GI
                    q2754849
BLAST score
                    199
E value
                    2.0e-15
Match length
                    45
% identity
                    (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                    [Fritillaria agrestis]
                    403095
Seq. No.
```

LIB3431-059-P1-N1-F4

Method

BLASTX

```
BLASTX
Method
NCBI GI
                  q3036951
BLAST score
                  199
                  9.0e-19
E value
                  52
Match length
                  98
% identity
                   (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                   [Nicotiana sylvestris]
Seq. No.
                  403096
                  LIB3431-059-P1-N1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q671740
BLAST score
                  336
E value
                  2.0e-31
Match length
                  64
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                  40.3097
Seq. ID
                  LIB3431-059-P1-N1-F7
Method
                  BLASTN
NCBI GI
                  q606816
BLAST score
                  306
E value
                  1.0e-172
Match length
                  326
                  98
% identity
                  Oryza sativa chloroplast carbonic anhydrase mRNA, complete
NCBI Description
                  403098
Seq. No.
Seq. ID
                  LIB3431-059-P1-N1-F8
Method
                  BLASTX
NCBI GI
                  q517500
BLAST score
                  378
E value
                  2.0e-36
Match length
                  91
% identity
NCBI Description
                   (M87435) precursor of the oxygen evolving complex 17 kDa
                  protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                  OE17 protein [Pisum sativum]
                  403099
Seq. No.
Seq. ID
                  LIB3431-059-P1-N1-G11
Method
                  BLASTX
NCBI GI
                  q4079798
BLAST score
                  326
E value
                  3.0e-30
Match length
                  65
% identity
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  satival
                  403100
Seq. No.
                  LIB3431-059-P1-N1-G2
Seq. ID
```

BLAST score

```
g347451
NCBI GI
                   248
BLAST score
                   4.0e-21
E value
Match length
                   48
                   100
% identity
                    (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   403101
                   LIB3431-059-P1-N1-G3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115787
                   329
BLAST score
                   1.0e-30
E value
Match length
                   63
                   100
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
                   403102
Seq. No.
                   LIB3431-059-P1-N1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3450889
BLAST score
                   279
E value
                   9.0e-25
Match length
                   63
% identity
                   86
                   (AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
NCBI Description
                   403103
Seq. No.
                   LIB3431-059-P1-N1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g21839
BLAST score
                   163
E value
                    3.0e-11
Match length
                   35
% identity
                    (X57952) phosphoribulokinase [Triticum aestivum]
NCBI Description
Seq. No.
                   403104
                   LIB3431-059-P1-N1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455232
BLAST score
                   151
                    9.0e-10
E value
Match length
                    36
% identity
                    75
                    (AL035523) putative protein [Arabidopsis thaliana]
NCBI Description
                    403105
Seq. No.
                   LIB3431-059-P1-N1-H10
Seq. ID
Method
                   BLASTX
                   q3345477
NCBI GI
```

```
3.0e-12
E value
Match length
                  32
                  97
% identity
NCBI Description (AB016283) carbonic anhydrase [Oryza sativa]
                  403106
Seq. No.
Seq. ID
                  LIB3431-059-P1-N1-H11
Method
                  BLASTX
NCBI GI
                  g21699
                  351
BLAST score
E value
                  3.0e-33
                  76
Match length
                  86
% identity
                  (X66013) cathepsin B [Triticum aestivum]
NCBI Description
                  403107
Seq. No.
                  LIB3431-059-P1-N1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  .g3510256
                  190
BLAST .score
E value
                  2.0e-14
Match length
                  40
% identity
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  403108
                  LIB3431-059-P1-N1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4512125
BLAST score
                  181
E value
                  3.0e-13
Match length
                  34
% identity
                  100
NCBI Description
                  (AF133340) putative chlorophyll a/b-binding protein
                  [Phalaenopsis sp. 'KCbutterfly']
Seq. No.
                  403109
                  LIB3431-059-P1-N1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q871931
BLAST score
                  144
E value
                  2.0e-13
Match length
                  43
% identity
NCBI Description (D30763) ferredoxin [Oryza sativa]
Seq. No.
                  403110
Seq. ID
                  LIB3431-059-P1-N1-H7
Method
                  BLASTX
NCBI GI
                  q131773
BLAST score
                  246
E value
                  6.0e-21
Match length
                  65
% identity
                  40S RIBOSOMAL PROTEIN S14 (CLONE MCH2)
NCBI Description
                  >gi 82724 pir B30097 ribosomal protein S14 (clone MCH2) -
```

maize

```
403111
Seq. No.
                  LIB3431-060-P1-K1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g417260
                  381
BLAST score
E value
                  1.0e-36
Match length
                  121
% identity
                  64
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                  lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                  light-regulated gene [Oryza sativa]
Seq. No.
                   403112
Seq. ID
                  LIB3431-060-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g729668
BLAST score
                  251
E value
                   2.0e-21
Match length
                  73
% identity
                   62
NCBI Description
                  HISTONE H1 >gi_2147479_pir__S65059 histone H1,
                  drought-inducible - Lycopersicon pennellii >gi 436823
                   (U01890) Solanum pennellii histone H1 [Solanum pennellii]
Seq. No.
                   403113
Seq. ID
                  LIB3431-060-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g3201632
BLAST score
                  223
E value
                   3.0e-18
Match length
                  112
% identity
NCBI Description
                   (AC004669) putative 2A6 protein [Arabidopsis thaliana]
Seq. No.
                  403114
Seq. ID
                  LIB3431-060-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q733454
BLAST score
                   417
E value
                   5.0e-41
Match length
                  101
% identity
                  79
NCBI Description
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
Seq. No.
                  403115
Seq. ID
                  LIB3431-060-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q4098250
BLAST score
                  161
E value
                  7.0e-11
Match length
                  69
% identity
NCBI Description
                   (U76611) similar to Solanum tuberosum ci21A gene product
                  encoded by the sequence presented in GenBank Accession
```

Number U76610 [Solanum tuberosum]

BLAST score

```
403116
Seq. No.
Seq. ID
                   LIB3431-060-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   g5262202
BLAST score
                   220
E value
                   8.0e-18
Match length
                   127
% identity
                   39
                   (AL080252) nodulin-like protein [Arabidopsis thaliana]
NCBI Description
                   403117
Seq. No.
                   LIB3431-060-P1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q671740
BLAST score
                   280
E value
                   8.0e-25
Match length
                   49
% identity
                   100
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
Seq. No.
                   403118
Seq. ID
                   LIB3431-060-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   q2673914
BLAST score
                   287
E value
                   1.0e-25
Match length
                   122
% identity
                   47
NCBI Description (AC002561) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   403119
Seq. ID
                   LIB3431-060-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   q3201612
BLAST score
                   153
E value
                   5.0e-10
Match length
                   60
% identity
NCBI Description (AC004669) putative 2A6 protein [Arabidopsis thaliana]
Seq. No.
                   403120
                   LIB3431-060-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2570511
BLAST score
                   637
E value
                   1.0e-66
Match length
                   120
% identity
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   403121
                   LIB3431-060-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115787
```

```
E value
                   2.0e-48
Match length
                   112
% identity
                   86
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   403122
Seq. No.
                   LIB3431-060-P1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   510
E value
                   8.0e-52
Match length
                   113
                   86
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza `sativa]
                   >gi 227611 prf 1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   403123
                   LIB3431-060-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3023816
BLAST score
                   592
E value
                   2.0e-61
Match length
                   115
                   98
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi 968996 (U31676) glyceraldehyde-3-phosphate
                   dehydrogenase [Oryza sativa]
Seq. No.
                   403124
Seq. ID
                   LIB3431-060-P1-K1-C1
Method
                   BLASTX
                   q3885888
NCBI GI
BLAST score
                   348
                   8.0e-33
E value
Match length
                   113
% identity
                   (AF093632) high mobility group protein [Oryza sativa]
NCBI Description
                   403125
Seq. No.
Seq. ID
                   LIB3431-060-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   q5091623
                   295
BLAST score
E value
                   1.0e-26
                   75
Match length
% identity
                   69
                   (ACO07454) Similar to gb U93048 somatic embryogenesis
NCBI Description
                   receptor-like kinase from Daucus carota, contains 4
                   PF 00560 Leucine Rich Repeat domains and a PF 00069
```

Eukaryotic protein kinase domain. [Arabidopsis thaliana]

Method

BLASTX

```
403126
Seq. No.
Seq. ID
                   LIB3431-060-P1-K1-C11
                   BLASTX
Method
NCBI GI
                   g2980641
BLAST score
                   174
                   2.0e-12
E value
Match length
                   76
% identity.
                   50
NCBI Description
                   (Y11250) multi resistance protein [Arabidopsis thaliana]
Seq. No.
                   403127
                   LIB3431-060-P1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3789954
BLAST score
                   610
E value
                   1.0e-63
Match length
                   113
% identity
                   100
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
Seq. No.
                   403128
Seq. ID
                   LIB3431-060-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   7.0e-20
Match length
                   44
                   100
% identity
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   403129
Seq. No.
Seq. ID
                   LIB3431-060-P1-K1-C6
Method
                   BLASTX
NCBI GI
                  · q3885886
BLAST score
                   632
E value
                   3.0e-66
Match length
                   123
% identity.
NCBI Description
                   (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
                   403130
Seq. No.
Seq. ID
                   LIB3431-060-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   q4200165
BLAST score
                   563
E value
                   5.0e-58
Match length
                   134
                   79
% identity
NCBI Description
                   (Y16262) neutral invertase [Daucus carota]
                   403131
Seq. No.
Seq. ID
                   LIB3431-060-P1-K1-C8
```

```
NCBI GI
                   q2244867
BLAST score
                   261
E value
                   1.0e-22
Match length
                   138
                   39
% identity
                   (Z97337) hydroxynitrile lyase like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   403132
                   LIB3431-060-P1-K1-D2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q266567
BLAST score
                   548
E value
                   3.0e-56
Match length
                   144
                   72
% identity
                   MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR
NCBI Description
                   (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II)
                   >gi_421956_pir__S23558 mitochondrial processing peptidase
(EC 3.4.99.41) alpha chain precursor - potato
                   >gi 21493 emb CAA46990 (X66284) mitochondrial processing
                   peptidase [Solanum tuberosum]
Seq. No.
                   403133
Seq. ID
                   LIB3431-060-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   a4098647
BLAST score
                   652
E value
                   2.0e-68
Match length
                   131
% identity
                   88
NCBI Description
                   (U80668) homogentisate 1,2-dioxygenase [Arabidopsis
                   thaliana]
Seq. No.
                   403134
Seq. ID
                   LIB3431-060-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   q733454
BLAST score
                   431
E value
                   1.0e-42
Match length
                   103
% identity
NCBI Description
                   (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
Seq. No.
                   403135
Seq. ID
                   LIB3431-060-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   q548605
BLAST score
                   534
E value
                   1.0e-54
Match length
                   133
% identity
                   82
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi 539055 pir A48527 photosystem I protein psaK precursor
                   - barley >gi 304220 (L12707) photosystem I PSI-K subunit
```

Method

BLASTX

[Hordeum vulgare] Seq. No. 403136 LIB3431-060-P1-K1-D7 Seq. ID BLASTN Method NCBI GI g20239 BLAST score 141 E value 3.0e-73 Match length 169 % identity 96 O.sativa (rice) shoot-specific GOS5 gene for a putative NCBI Description chloroplast transit peptide 403137 Seq. No. LIB3431-060-P1-K1-D8 Seq. ID Method BLASTX NCBI GI g4587579 BLAST score 251 E value 2.0e-21 Match length 143 35 % identity NCBI Description (AC006550) F1003.1 [Arabidopsis thaliana] Seq. No. 403138 LIB3431-060-P1-K1-D9 Seq. ID Method BLASTN NCBI GI a6015437 BLAST score 36 E value 4.0e-11 Match length 44 % identity 64 NCBI Description Homo sapiens PEX1 mRNA, complete cds 403139 Seq. No. LIB3431-060-P1-K1-E1 Seq. ID Method BLASTX NCBI GI g4559358 BLAST score 341 E value 5.0e-32 Match length 97 % identity NCBI Description (AC006585) putative steroid binding protein [Arabidopsis thaliana] 403140 Seq. No. LIB3431-060-P1-K1-E10 Seq. ID Method BLASTX NCBI GI g1488297 BLAST score 190 3.0e-14 E value 132 Match length % identity NCBI Description (U63530) osRAD23 [Oryza sativa] 403141 Seq. No. LIB3431-060-P1-K1-E2 Seq. ID

```
NCBI GI
                   q115787
BLAST score
                   498
E value
                   2.0e-50
Match length
                   117
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   403142
Seq. No.
Seq. ID
                   LIB3431-060-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   q4127456
BLAST score
                   244
E value
                   1.0e-20
Match length
                   62
% identity
                   (AJ010818) Cpn21 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403143
Seq. ID
                   LIB3431-060-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   q3288821
BLAST score
                   490
E value
                   2.0e-49
Match length
                   117
% identity
                   79
NCBI Description
                   (AF063901) alanine:glyoxylate aminotransferase;
                   transaminase [Arabidopsis thaliana]
                   >gi 4733989 gb AAD28669.1_AC007209_5 (AC007209)
                   alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
Seq. No.
                   403144
Seq. ID
                   LIB3431-060-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   q2754849
BLAST score
                   175
E value
                   1.0e-12
Match length
                   39
% identity
                   (AF039000) putative serine-glyoxylate aminotransferase
NCBI Description
                   [Fritillaria agrestis]
Seq. No.
                   403145
Seq. ID
                   LIB3431-060-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   500
E value
                   1.0e-50
Match length
                   111
% identity
                   86
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi 227611_prf__1707316A chlorophyll a/b binding protein 1
```

% identity

98

[Oryza sativa] Seq. No. 403146 Seq. ID LIB3431-060-P1-K1-E9 Method BLASTX NCBI GI g2995990 BLAST score 205 E value 4.0e-16 Match length 102 % identity 44 (AF053746) dormancy-associated protein [Arabidopsis NCBI Description thaliana] >gi 2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana] Seq. No. 403147 Seq. ID LIB3431-060-P1-K1-F11 Method BLASTX NCBI GI g3068713 BLAST score 549 E value 2.0e-56 Match length 139 % identity NCBI Description (AF049236) unknown [Arabidopsis thaliana] 403148 Seq. No. Seq. ID LIB3431-060-P1-K1-F2 Method BLASTX NCBI GI q4507223 BLAST score 215 E value 2.0e-27 Match length 95 % identity NCBI Description signal recognition particle receptor ('docking protein') >gi_134892_sp_P08240_SRPR_HUMAN SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA) >gi_88607_pir__A29440 signal recognition particle receptor - human >gi_30866_emb_CAA29608_ (X06272) docking protein [Homo sapiens] Seq. No. 403149 Seq. ID LIB3431-060-P1-K1-F4 Method BLASTN NCBI GI g2062705 BLAST score 35 E value 5.0e-10 Match length 35 % identity 100 NCBI Description Human butyrophilin (BTF5) mRNA, complete cds 403150 Seq. No. Seq. ID LIB3431-060-P1-K1-F5 Method BLASTX NCBI GI q3789952 BLAST score 516 E value 1.0e-52 Match length 103

```
(AF094775) chlorophyll a/b-binding protein presursor [Oryza
 NCBI Description
                    sativa]
 Seq. No.
                    403151
                    LIB3431-060-P1-K1-F6
 Seq. ID
Method
                    BLASTX
NCBI GI
                    q3386621
                    593
BLAST score
E value
                    2.0e-61
Match length
                    141
 % identity
                    81
                    (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                    403152
Seq. No.
                    LIB3431-060-P1-K1-F7
 Seq. ID
Method
                    BLASTX
                    g2281649
NCBI GI
BLAST score
                    198
E value
                    3.0e-15
Match length
                    42
 % identity
                    81
                    (AF003105) AP2 domain containing protein RAP2.12
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    403153
                    LIB3431-060-P1-K1-F8
Seq. ID
Method
                    BLASTN
                    g169133
NCBI GI
                    40
BLAST score
                    5.0e-13
E value
                    132
Match length
                    83
 % identity
                    Zea mays precursor of the oxygen evolving complex 17 kDa
NCBI Description
                    protein mRNA, complete cds
                    403154
Seq. No.
Seq. ID
                    LIB3431-060-P1-K1-F9
Method
                    BLASTX
NCBI GI
                    g417103
BLAST score
                    577
E value
                    1.0e-59
Match length
                    115
 % identity
                    100
                    HISTONE H3.2, MINOR >gi 282871 pir S24346 histone
NCBI Description
                    H3.3-like protein - Arabidopsis thaliana
                    >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
                    histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
                    (U09458) histone H3.2 [Medicago sativa] >gi_488567 (\overline{U}09460)
                    histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone
                    H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2
                    [Medicago sativa] >gi_488577 (U09465) histone H3.2
                    [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone
                    H3 [Lolium temulentum] >gi 1435157 emb_CAA58445_ (X83422)
                    histone H3 variant H3.3 [Lycopersicon esculentum]
                    >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum]
                    >gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana
```

tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469 gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana] >gi_6006364_dbj_BAA84794.1_ (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to histone H3 (AB015760) [Oryza sativa]

```
Seq. No.
                  403155
Seq. ID
                  LIB3431-060-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  232
E value
                  3.0e-19
Match length
                  43
                  100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  403156
Seq. No.
Seq. ID
                  LIB3431-060-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3789954
BLAST score
                  744
E value
                  3.0e-79
                  136
Match length
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                  sativa]
                  403157
Seq. No.
                  LIB3431-060-P1-K1-G12
Seq. ID
                  BLASTN
Method
NCBI GI
                  q5006852
BLAST score
                  176
E value
                  3.0e-94
Match length
                  336
% identity
                  Oryza sativa homeodomain leucine zipper protein (hox4)
NCBI Description
                  mRNA, complete cds
                  403158
Seq. No.
                  LIB3431-060-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131192
BLAST score
                  209
E value
                  2.0e-16
Match length
                  44
                  86
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_100606_pir__S20937
                  photosystem I chain V precursor - barley
                  >gi 19091 emb CAA42727 (X60158) photosystem I polypeptide
```

PSI-G precursor [Hordeum vulgare]

```
Seq. No.
                  403159
Seq. ID
                  LIB3431-060-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g2072555
BLAST score
                  237
E value
                  9.0e-20
Match length
                  44
% identity
                  100
NCBI Description
                  (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
                  403160
Seq. No.
Seq. ID
                  LIB3431-060-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  700
                  4.0e-74
E value
Match length
                  131
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                  subunit [Oryza sativa]
                  403161
Seq. No.
                  LIB3431-060-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2501189
BLAST score
                  257
E value
                  3.0e-22
Match length
                  121
% identity
                  58
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                  - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  403162
                  LIB3431-060-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4544428
BLAST score
                  214
E value
                  3.0e-17
Match length
                  51
% identity
                  (AC006955) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  403163
Seq. ID
                  LIB3431-060-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q1053047
BLAST score
                  591
                  3.0e-61
E value
Match length
                  118
% identity
                  100
                  (U38425) histone H3 [Glycine max] >gi 1053049 (U38426)
NCBI Description
                  histone H3 [Glycine max] >gi 1053051 (U38427) histone H3
```

[Glycine max]

Seq. ID

```
403164
Seq. No.
Seq. ID
                   LIB3431-060-P1-K1-H1
Method
                   BLASTX
NCBI GI
                   g6006270
BLAST score
                   196
                   5.0e-15
E value
Match length
                   66
% identity
                   47
                   (AB022692) TAF-Ibeta2 [Xenopus laevis]
NCBI Description
Seq. No.
                   403165
                   LIB3431-060-P1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   488
E value
                   3.0e-49
Match length
                   110
% identity
                   85
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403166
                   LIB3431-060-P1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   293
E value
                   1.0e-26
Match length
                   73
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   403167
Seq. ID
                   LIB3431-060-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   g2344889
BLAST score
                   297
E value
                   7.0e-27
Match length
                   133
% identity
                   44
NCBI Description
                   (AC002388) unknown protein [Arabidopsis thaliana]
                   >gi_4895255_gb_AAD32840.1_AC007659_22 (AC007659) unknown
                   protein [Arabidopsis thaliana]
Seq. No.
                   403168
                   LIB3431-060-P1-K1-H3
```

Match length

```
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  567
                  2.0e-58
E value
Match length
                  122
                  87
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  403169
Seq. No.
Seq. ID
                  LIB3431-060-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2306981
BLAST score
                  503
E value
                  5.0e-51
                  90
Match length
% identity
NCBI Description
                  (AF010321) photosystem I antenna protein [Oryza sativa]
Seq. No.
                  403170
Seq. ID
                  LIB3431-060-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g2501189
BLAST score
                  547
E value
                  3.0e-56
Match length
                  111
% identity
                  95
NCBI Description
                  THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
                  >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                  - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                  [Zea mays]
Seq. No.
                  403171
Seq. ID
                  LIB3431-060-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q3789952
BLAST score
                  560
E value
                  1.0e-57
Match length
                  112
% identity
NCBI Description
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                  sativa]
Seq. No.
                  403172
Seq. ID
                  LIB3431-060-P1-K1-H9
Method
                  BLASTN
NCBI GI
                  g2062705
BLAST score
                  35
E value
                  4.0e-10
```

% identity

```
% identity
NCBI Description
                  Human butyrophilin (BTF5) mRNA, complete cds
                  403173
Seq. No.
Seq. ID
                  LIB3431-060-P1-N1-A11
                  BLASTX
Method
NCBI GI
                  g417260
                  327
BLAST score
                  2.0e-30
E value
                  75
Match length
                  83
% identity
                  LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
NCBI Description
                  lir1 protein - rice >gi 20263_emb_CAA48706_ (X68807)
                  light-regulated gene [Oryza sativa]
                  403174
Seq. No.
                  LIB3431-060-P1-N1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2073379
BLAST score
                  154
E value
                  3.0e-81
Match length
                  173
                  97
% identity
NCBI Description
                  Rice CP26 mRNA, partial sequence
Seq. No.
                  403175
Seq. ID
                  LIB3431-060-P1-N1-A4
Method
                  BLASTX
NCBI GI
                  g4098250
BLAST score
                  160
E value
                   7.0e-11
Match length
                  56
                  50
% identity
                   (U76611) similar to Solanum tuberosum ci21A gene product
NCBI Description
                  encoded by the sequence presented in GenBank Accession
                  Number U76610 [Solanum tuberosum]
Seq. No.
                  403176
                  LIB3431-060-P1-N1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g218207 .
BLAST score
                  279
E value
                  1.0e-156
                  291
Match length
                  99
% identity
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
Seq. No.
                  403177
Seq. ID
                  LIB3431-060-P1-N1-B4
Method
                  BLASTN
NCBI GI
                  g11957
BLAST score
                  65
E value
                  5.0e-28
Match length
                  84
```

```
NCBI Description Rice complete chloroplast genome
Seq. No.
                  403178
                  LIB3431-060-P1-N1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g20181
BLAST score
                  163
E value
                  2.0e-86
Match length
                  177
                  98
% identity
NCBI Description
                  Rice cab2R gene for light harvesting chlorophyll
                  a/b-binding protein
                  403179
Seq. No.
Seq. ID
                  LIB3431-060-P1-N1-B7
Method
                  BLASTX
NCBI GI
                  q115787
BLAST score
                  559
E value
                  2.0e-57
Match length
                  111
                  97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding
                  protein 2R precursor - rice >gi_20182_emb_CAA32109
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                  [Oryza sativa]
Seq. No.
                  403180
                  LIB3431-060-P1-N1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3885887
BLAST score
                  221
                  1.0e-121
E value
Match length
                  296
                  93
% identity
NCBI Description
                  Oryza sativa high mobility group protein (HMG) mRNA,
                  complete cds
Seq. No.
                  403181 "
                  LIB3431-060-P1-N1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1619300
BLAST score
                  174
                  2.0e-12
E value
                  48
Match length
% identity
                  65
                  (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
                  403182
Seq. No.
Seq. ID
                  LIB3431-060-P1-N1-C11
Method
                  BLASTX
                  g2316016
NCBI GI
BLAST score
                  150
E value
                  2.0e-09
                  71
Match length
                  44
% identity
NCBI Description (U92650) MRP-like ABC transporter [Arabidopsis thaliana]
```

```
403183
Seq. No.
Seq: ID
                  LIB3431-060-P1-N1-C12
Method
                   BLASTN
NCBI GI
                   g3789953
BLAST score
                   298
E value
                   1.0e-167
                   298
Match length
                   100
% identity
                  Oryza sativa chlorophyll a/b-binding protein precursor
NCBI Description
                   (Cab26) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
                   403184
Seq. No.
Seq. ID
                   LIB3431-060-P1-N1-C2
                   BLASTN
Method
NCBI GI
                   g3885885
BLAST score
                   144
                   3.0e-75
E value
Match length
                   167
                   97
% identity
                  Oryza sativa Rieske Fe-S precursor protein (RISP) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   403185
                   LIB3431-060-P1-N1-C4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2072554
BLAST score
                   186
E value
                   1.0e-100
                   210
Match length
                   97
% identity
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   cds
Seq. No.
                   403186
Seq. ID
                   LIB3431-060-P1-N1-C6
                   BLASTX
Method
NCBI GI
                   g3885886
BLAST score
                   630
E value
                   9.0e-66
Match length
                   112
% identity
                   99
                   (AF093631) Rieske Fe-S precursor protein [Oryza sativa]
NCBI Description
Seq. No.
                   403187
Seq. ID
                   LIB3431-060-P1-N1-C9
Method
                  BLASTX
NCBI GI
                   g3184292
BLAST score
                  287
E value
                   1.0e-25
Match length
                  56
% identity
                   (AC004136) putative nucleic acid binding protein, 5'
NCBI Description
                  partial [Arabidopsis thaliana]
```

403188

Seq. No.

```
LIB3431-060-P1-N1-D1
Seq. ID
                   BLASTX
Method
                   g3913811
NCBI GI
BLAST score
                   367
                   4.0e-35
E value
Match length
                   91
% identity
                   GLUTAMYL-TRNA REDUCTASE PRECURSOR (GLUTR)
NCBI Description
                   >gi_2920320_dbj_BAA25003_ (AB011416) glutamyl-tRNA
                   reductase [Oryza sativa]
                   403189
Seq. No.
Seq. ID
                   LIB3431-060-P1-N1-D12
                   BLASTX
Method
NCBI GI
                   g3126854
BLAST score
                   345
E value
                   1.0e-32
Match length
                   65
% identity
                   100
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   403190
                   LIB3431-060-P1-N1-D2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q266567
BLAST score
                   306
E value
                   8.0e-28
Match length
                   87
% identity
                   MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR
NCBI Description
                   (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II)
                   >gi_421956_pir__S23558 mitochondrial processing peptidase (EC 3.4.99.41) alpha chain precursor - potato
                   >gi 21493 emb CAA46990 (X66284) mitochondrial processing
                   peptidase [Solanum tuberosum]
Seq. No.
                   403191
                   LIB3431-060-P1-N1-D4
Seq. ID
Method
                   BLASTX .
NCBI GI
                   g733456
BLAST score
                   352
E value
                   2.0e-33
                 ~~73
Match length
% identity
                   (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                   [Zea mays]
Seq. No.
                   403192
Seq. ID
                   LIB3431-060-P1-N1-D8
Method
                   BLASTX
NCBI GI
                   g3850577
BLAST score
                   185
E value
                   6.0e-16
Match length
                   120
% identity
                   41
                   (AC005278) This gene may be cut off. [Arabidopsis thaliana]
NCBI Description
```

```
Seq. No.
                  403193
                  LIB3431-060-P1-N1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5640111
BLAST score
                  305
E value
                  1.0e-27
Match length
                  83
                  72
% identity
NCBI Description (AJ243875) RAD23 protein [Lycopersicon esculentum]
                  403194
Seq. No.
Seq. ID
                  LIB3431-060-P1-N1-E7
Method
                  BLASTX
                  g289920
NCBI GI
BLAST score
                  319
                  2.0e-29
E value
Match length
                  61
% identity
                  100
                  (L07119) chlorophyll A/B binding protein [Gossypium
NCBI Description
                  hirsutum]
                                              Š.
                  403195
Seq. No.
Seq. ID
                  LIB3431-060-P1-N1-E8
Method
                  BLASTN
NCBI GI
                  q218171
BLAST score
                  40
E value
                  3.0e-13
Match length
                  -107
                  85
% identity
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
NCBI Description
                  a/b binding protein of photosystem II (LHCPII), complete
                  cds
                  403196
Seq. No.
Seq. ID
                  LIB3431-060-P1-N1-F1
Method
                  BLASTN
NCBI GI
                  q2773153
BLAST score
                  268
E value
                  1.0e-149
Match length
                  280
% identity
                  . 99
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                  (Asr1) mRNA, complete cds
Seq. No.
                  403197
Seq. ID
                  LIB3431-060-P1-N1-F2
Method
                  BLASTN
NCBI GI
                  q5106766
BLAST score
                  38
                  7.0e-12
E value
Match length
                  86
% identity
                  86
                  Arabidopsis thaliana BAC F17I23
NCBI Description
                  403198
Seq. No.
Seq. ID
                  LIB3431-060-P1-N1-F5
```

BLASTN

Method '

Method

BLASTN

```
NCBI GI
                   g3789951
BLAST score
                   186
E value
                   1.0e-100
Match length
                   379
% identity
                   98
                   Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                   complete cds
                   403199
Seq. No.
                   LIB3431-060-P1-N1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q517500
BLAST score
                   530
E value
                   4.0e-54
Match length
                   126
                   83
% identity
                   (M87435) precursor of the oxygen evolving complex 17 kDa
NCBI Description
                   protein [Zea mays] >gi_444338_prf__1906386A photosystem II
                   OE17 protein [Pisum, sativum]
                   403200
Seq. No.
Seq. ID
                   LIB3431-060-P1-N1-F9
Method
                   BLASTX
NCBI GI
                   q70753
BLAST score
                   219
E value
                   9.0e-18
Match length
                   44
                   100
% identity
                   histone H3 - garden pea >gi 82610 pir S00373 histone H3 -
NCBI Description
                   wheat
                   403201
Seq. No.
                   LIB3431-060-P1-N1-G1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2072554
BLAST score
                   288
                   1.0e-161
E value
                   292
Match length
                   100
% identity
                   Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   cds
                   403202
Seq. No.
Seq. ID
                   LIB3431-060-P1-N1-G11
Method
                   BLASTX
NCBI GI
                   g3789954
BLAST score
                   241
E value
                   2.0e-20
Match length
                   43
                   100
% identity
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
                   403203
Seq. No.
                   LIB3431-060-P1-N1-G12
Seq. ID
```

BLAST score

```
NCBI GI
                   q5006852
BLAST score
                   225
E value
                   1.0e-123
                   293
Match length
                   94
% identity
                  Oryza sativa homeodomain leucine zipper protein (hox4)
NCBI Description
                  mRNA, complete cds
Seq. No.
                   403204
Seq. ID
                   LIB3431-060-P1-N1-G2
Method
                   BLASTX
NCBI GI
                   g131192
BLAST score
                   209
E value
                   2.0e-16
Match length
                   44
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR
NCBI Description
                   (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi 100606 pir S20937
                   photosystem I chain V precursor - barley
                   >gi_19091_emb_CAA42727_ (X60158) photosystem I polypeptide
                   PSI-G precursor [Hordeum vulgare]
Seq. No.
                   403205
Seq. ID
                   LIB3431-060-P1-N1-G3
Method
                   BLASTX
NCBI GI
                   q2072555
BLAST score
                   237
                   1.0e-19
E value
                   44
Match length
% identity
                   100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   403206
Seq. No.
Seq. ID
                   LIB3431-060-P1-N1-G5
Method ·
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   186
E value
                   6.0e-14
Match length
                   35
% identity
                   100
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4.\overline{1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403207
                   LIB3431-060-P1-N1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4544428
```

```
Match length
                      81
% identity
                      69
                       (AC006955) unknown protein [Arabidopsis thaliana]
NCBI Description
                      403208
Seq. No.
Seq. ID
                      LIB3431-060-P1-N1-G8
Method
                      BLASTX
NCBI GI
                      g417103
                      283
BLAST score
                       4.0e-25
E value
Match length
                      58
% identity
                      HISTONE H3.2, MINOR >gi_282871 pir__S24346 histone
NCBI Description
                      H3.3-like protein - Arabidopsis thaliana
                      >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
                      histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
                       (U09458) histone H3.2 [Medicago sativa] >gi_488567 (\overline{U}09460)
                      histone H3.2 [Medicago sativa] >gi 488569 (\overline{U}09461) histone
                      H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911 emb_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi_1435157 emb_CAA58445 (X83422)
                      histone H3 variant H3.3 [Lycopersicon esculentum]
                      >gi 2558944 (AF024716) histone 3 [Gossypium hirsutum]
                      >qi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana
                      tabacum] >qi 3885890 (AF093633) histone H3 [Oryza sativa]
                      >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia
                      coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_
                       (AL035708) Histon H3 [Arabidopsis thaliana]
                      >gi_6006364_dbj_BAA84794.1_ (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to
                      histone H3 (AB015760) [Oryza sativa]
                      403209
Seq. No.
Seq. ID
                      LIB3431-060-P1-N1-H10
Method
                      BLASTX
NCBI GI
                      q671740
BLAST score
                      499
                      2.0e-50
E value
                      91
Match length
% identity
                       (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                      construct]
                      403210
Seq. No.
Seq. ID
                      LIB3431-060-P1-N1-H11
Method
                      BLASTX
NCBI GI
                      g3036951
BLAST score
                      282
E value
                      3.0e-25
Match length
                      54
% identity
                      100
                       (AB012639) light harvesting chlorophyll a/b-binding protein
NCBI Description
                       [Nicotiana sylvestris]
```

2.0e-26

E value

Seq. ID

```
Seq. No.
                  403211
Seq. ID
                  LIB3431-060-P1-N1-H12
                  BLASTX
Method
                  g3318613
NCBI GI
BLAST score
                  156
                  2.0e-10
E value
Match length
                  34
% identity
                  (AB016064) mitochondrial phosphate transporter [Zea mays]
NCBI Description
                  403212
Seq. No.
Seq. ID
                  LIB3431-060-P1-N1-H3
                  BLASTN
Method
NCBI GI
                  g218207
BLAST score
                  303
                  1.0e-170
E value
Match length
                  319
% identity
                  99
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
Seq. No.
                  403213
Seq. ID
                  LIB3431-060-P1-N1-H4
Method
                  BLASTX
NCBI GI
                  q551047
BLAST score
                  210
E value
                  9.0e-17
Match length
                  41
% identity
                  (X79277) type II LHCI [Lolium temulentum]
NCBI Description
Seq. No.
                  403214
Seq. ID
                  LIB3431-060-P1-N1-H7
Method
                  BLASTN
NCBI GI
                  g3789951
BLAST score
                  243
E value
                  1.0e-134
Match length
                  356
% identity
                  91
                  Oryza sativa chlorophyll a/b-binding protein presursor
NCBI Description
                   (Cab27) mRNA, nuclear gene encoding chloroplast protein,
                  complete cds
Seq. No.
                  403215
Seq. ID
                  LIB3431-061-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  g2696224
BLAST score
                  41
E value
                  9.0e-14
Match length
                  109
% identity
                  84
                  Oryza sativa mRNA for chitinase, complete cds
NCBI Description
Seq. No.
                  403216
                  LIB3431-061-P1-K1-A10
```

```
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  327
E value
                  8.0e-41
                  108
Match length
                  83
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208 dbj_BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >qi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403217
                  LIB3431-061-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3345477
BLAST score
                  232
E value
                  2.0e-19
Match length
                  85
% identity
NCBI Description
                  (AB016283) carbonic anhydrase [Oryza sativa]
                  403218
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q82080
BLAST score
                  310
E value
                  1.0e-28
Match length
                  90
% identity
NCBI Description
                  chlorophyll a/b-binding protein type III precursor - tomato
                  >gi 226872 prf 1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
Seq. No.
                  403219
Seq. ID
                  LIB3431-061-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g4455248
BLAST score
                  150
E value
                  1.0e-09
Match length
                  69
% identity
                  (AL035523) acyl carrier-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  403220
                  LIB3431-061-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3913018
BLAST score
                  570
E value
                  7.0e-59
Match length
                  115
% identity
                  100
```

NCBI Description FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR

```
aldolase [Oryza sativa]
                    403221
 Seq. No.
 Seq. ID
                    LIB3431-061-P1-K1-A4
 Method
                    BLASTN
 NCBI GI
                    g20262
 BLAST score
                    330
 E value
                    0.0e + 00
 Match length
                    346
                    99
 % identity
 NCBI Description
                    O.sativa light-induced mRNA
                    403222
 Seq. No.
                    LIB3431-061-P1-K1-A6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g2351846
 BLAST score
                    146
🗧 E value
                    3.0e-09
 Match length
                    123
 % identity
 NCBI Description
                    (U93050) poly(A) binding protein II [Mus musculus]
 Seq. No.
                    403223
                    LIB3431-061-P1-K1-A8
 Seq. ID
 Method
                    BLASTN
 NCBI GI
                    q3063523
 BLAST score
                    176
 E value
                    2.0e-94
 Match length
                    219
 % identity
                    95
                    Oryza sativa ribulose 1,5-bisphosphate carboxylase small
 NCBI Description
                    subunit mRNA, complete cds
                    403224
 Seq. No.
 Seq. ID
                    LIB3431-061-P1-K1-A9
 Method
                    BLASTX
 NCBI GI
                    q1709846
 BLAST score
                    163
 E value
                    4.0e-11
 Match length
                    118
 % identity
                    45
                    PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi 706853 (U04336)
 NCBI Description
                    22 kDa component of photosystem II [Lycopersicon
                    esculentum]
 Seq. No.
                    403225
 Seq. ID
                    LIB3431-061-P1-K1-B10
 Method
                    BLASTX
 NCBI GI
                    q115813
 BLAST score
                    243
 E value
                    1.0e-20
 Match length
                    55
 % identity
                    CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
 NCBI Description
                    CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III
                    chlorophyll a/b-binding protein [Lycopersicon esculentum]
```

(ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic

E value

1.0e-42

```
403226
Seq. No.
                   LIB3431-061-P1-K1-B11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4165550
BLAST score
                   567
E value
                   1.0e-58
Match length
                   121
% identity
                   88
NCBI Description
                   (AJ004915) apgm [Malus domestica]
Seq. No.
                   403227
Seq. ID
                   LIB3431-061-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   477
E value
                   5.0e-48
Match length
                   106
% identity
                   85
NCBI Description
                   chlorophyll a/b-binding protein I precursor - rice
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                   chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
Seq. No.
                   403228
Seq. ID
                   LIB3431-061-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   q3913192
BLAST score
                   142
E value
                   9.0e-09
Match length
                   70
                   47
% identity
                   CYTOCHROME P450 93A1 >gi_2129824_pir__S62899 cytochrome
P450 (CYP93 A1) - soybean >gi_1232111_dbj_BAA12159_
NCBI Description
                   (D83968) Cytochrome P-450 (CYP93A1) [Glycine max]
                   >gi 1588679 prf 2209281A cytochrome P450 [Glycine max]
Seq. No.
                   403229
Seq. ID
                   LIB3431-061-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   q400879
BLAST score
                   202
E value
                   6.0e-16
Match length
                   102
% identity
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                   (PSI-N) >gi_479690_pir__S35159 photosystem I chain psaN -
                   barley >gi_19095_emb_CAA47056_ (X66428) photosystem I
                   subunit N [Hordeum vulgare]
                   403230
Seq. No.
Seq. ID
                   LIB3431-061-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   q733454
BLAST score
                   431
```

```
103
Match length
% identity
                   81
NCBI Description (U23188) chlorophyll a/b-binding apoprotein CP26 precursor
                   [Zea mays]
                   403231
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-C10
Method
                  BLASTX
NCBI GI
                   q4586058
BLAST score
                   209
E value
                   2.0e-17
Match length
                  116
% identity
                   46
NCBI Description
                   (AC007020) unknown protein [Arabidopsis thaliana]
Seq. No.
                  LIB3431-061-P1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2072554
BLAST score
                   47
E value
                   3.0e-17
Match length
                  199
% identity
NCBI Description
                  Oryza sativa metallothionein-like protein mRNA, complete
Seq. No.
                   403233
Seq. ID
                  LIB3431-061-P1-K1-C2
Method
                  BLASTX
NCBI GI
                   g1052960
BLAST score
                   748
E value
                   1.0e-79
Match length
                  146
% identity
                   91
NCBI Description
                  (U37437) PNIL34 [Ipomoea nil]
Seq. No.
                   403234
                  LIB3431-061-P1-K1-C3
Seq. ID -
Method
                  BLASTN
NCBI GI
                   q1304214
BLAST score
                  51
E value
                   1.0e-19
Match length
                  95
% identity
NCBI Description
                  Rice mRNA for precursor of 22 kDa protein of photosystem II
                   (PSII-S), complete cds
Seq. No.
                   403235
Seq. ID
                  LIB3431-061-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g729668
BLAST score
                  197
E value
                   3.0e-15
                  58
Match length
% identity
                   60
                  HISTONE H1 >gi 2147479 pir S65059 histone H1,
NCBI Description
```

drought-inducible - Lycopersicon pennellii >gi 436823



Seq. No.

Seq. ID

Method NCBI GI 403236

BLASTX

g417154

LIB3431-061-P1-K1-C5

(U01890) Solanum pennellii histone H1 [Solanum pennellii]

```
BLAST score
                  370
E value
                  1.0e-35
                  98
Match length
% identity
                  HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock
NCBI Description
                  protein 82 - rice (strain Taichung Native One)
                  >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82
                   (HSP82) [Oryza sativa]
                  403237
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  g218207
BLAST score
                  191
E value
                  1.0e-103
Match length
                  191
% identity
                  100
NCBI Description
                  Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  p0SSS1139
                  403238
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4850382
BLAST score
                  152
E value
                  7.0e-10
Match length
                  70
% identity
NCBI Description
                   (ACO07357) Similar to gb D38124 EREBP-3 from Nicotiana
                  tabacum and contains PF 00847 AP2 domain. [Arabidopsis
                  thaliana]
Seq. No.
                  403239
Seq. ID
                  LIB3431-061-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  670
E value
                  1.0e-70
Match length
                  126
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                  403240
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3158476
BLAST score
                  310
E value
                  9.0e-35
Match length
                  109
% identity
                  64
```

NCBI Description

```
NCBI Description (AF067185) aquaporin 2 [Samanea saman]
                   403241
Seq. No.
                   LIB3431-061-P1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g320618
BLAST score
                   540
E value
                   2.0e-55
Match length
                   117
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                   [Oryza sativa]
                   403242
Seq. No.
Seq. ID
                   LIB3431-061-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   591
                   3.0e-61
E value
Match length
                   127
% identity
                   87
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403243
Seq. ID
                   LIB3431-061-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   q2864617
BLAST score
                   154
                   4.0e-10
E value
Match length
                   62
% identity
                   (AL021811) H+-transporting ATP synthase chain9 - like
NCBI Description
                   protein [Arabidopsis thaliana] >gi_5730141 emb_CAB52473.1_
                   (AJ245574) ATP synthase beta chain precursor (Subunit II)
                   [Arabidopsis thaliana]
Seq. No.
                   403244
Seq. ID
                   LIB3431-061-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g2293480
BLAST score
                   344
E value
                   2.0e-40
Match length
                   89
% identity
```

(AF011331) glycine-rich protein [Oryza sativa]

```
403245
Seq. No.
Seq. ID
                   LIB3431-061-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g3126854
BLAST score
                   612
E value
                   8.0e-64
Match length
                   114
% identity
                    100
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                    403246
Seq. No.
Seq. ID
                   LIB3431-061-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   q4115913
BLAST score
                   236
E value
                    1.0e-19
Match length
                   78
% identity
NCBI Description
                    (AF118222) contains similarity to Iron/Ascorbate family of
                   oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1) [Arabidopsis thaliana] >gi_4539409_emb_CAB40042.1_
                    (AL049524) putative flavanone 3-beta-hydroxylase
                    [Arabidopsis thaliana]
Seq. No.
                    403247
Seq. ID
                   LIB3431-061-P1-K1-D6
Method
                   BLASTN
NCBI GI
                   q505134
BLAST score
                   154
E value
                    5.0e-81
Match length
                   230
                   92
% identity
                   Rice mRNA for ferredoxin, complete cds
NCBI Description
Seq. No.
                    403248
Seq. ID
                   LIB3431-061-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g2407281
BLAST score
                   522
E value
                   3.0e-53
Match length
                   99
% identity
                    (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq. No.
                   403249
Seq. ID
                   LIB3431-061-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   q3047064
BLAST score
                   293
E value
                   2.0e-26
Match length
                   116
% identity
                    (AF058825) contains similarity to peptidyl-prolyl cis-trans
NCBI Description
                   isomerase (Pfam: pro_isomerase.hmm, score: 23.86 and 28.41
```

[Arabidopsis thaliana]

Seq. No.

```
403250
 Seq. No.
 Seq. ID
                    LIB3431-061-P1-K1-E1
 Method
                    BLASTX
 NCBI GI
                    g4803924
 BLAST score
                    571
                    6.0e-59
 E value
 Match length
                    141
 % identity
                    77
                    (AC006264) putative ER lumen protein retaining receptor
 NCBI Description
                    [Arabidopsis thaliana]
                    403251
 Seq. No.
                    LIB3431-061-P1-K1-E10
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q2492519
 BLAST score
                    401
 E value
                    1.0e-45
                    97
 Match length
                    86
 % identity
                    26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
 NCBI Description
                    7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase
                    subunit [Spinacia oleracea]
 Seq. No.
                    403252
 Seq. ID
                    LIB3431-061-P1-K1-E12
 Method
                    BLASTX
 NCBI GI
                    q3135751
 BLAST score
                    398
 E value
                    9.0e-39
 Match length
                    79
 % identity
                    (AJ006095) 26S protease regulatory subunit 6 [Cicer
 NCBI Description
                    arietinum]
                    403253
 Seq. No.
 Seq. ID
                    LIB3431-061-P1-K1-E2
 Method
                    BLASTX
 NCBI GI
                    q417260
 BLAST score
                    381
 E value
                    1.0e-36
 Match length
                    121
 % identity
                    LIGHT REGULATED PROTEIN PRECURSOR >gi 422003 pir S33632
 NCBI Description
                    lir1 protein - rice >gi 20263 emb CAA48706 (X68807)
                    light-regulated gene [Oryza sativa]
 Seq. No.
                    403254
 Seq. ID
                    LIB3431-061-P1-K1-E4
 Method
                    BLASTX
 NCBI GI
                    q2570511
 BLAST score
                    307
 E value
                    5.0e-28
 Match length
                    94
 % identity
                    (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
```

```
LIB3431-061-P1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115787
BLAST score
                   552
                   1.0e-56
E value
                   105
Match length
% identity
                   99
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                   (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                   [Oryza sativa]
                   403256
Seq. No.
Seq. ID
                   LIB3431-061-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g1881585
BLAST score
                   187
E value
                   5.0e-14
Match length
                   44
% identity
                   80
NCBI Description
                   (U72489) remorin [Solanum tuberosum]
Seq. No.
                   403257
Seq. ID
                   LIB3431-061-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   q401190
BLAST score
                   669
E value
                   2.0e-70
Match length
                   128
% identity
                   96
NCBI Description
                   THAUMATIN-LIKE PROTEIN PRECURSOR >gi 100715 pir S25551
                   thaumatin-like protein - rice >gi_20376_emb_CAA48278_
                   (X68197) thaumatin-like protein [Oryza sativa]
Seq. No.
                   403258
Seq. ID
                   LIB3431-061-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   q3775987
BLAST score
                   430
E value
                   2.0e-42.
Match length
                   112
% identity
NCBI Description
                   (AJ010457) RNA helicase [Arabidopsis thaliana]
                   403259
Seq. No.
Seq. ID
                   LIB3431-061-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   q131225-
BLAST score
                   311
E value
                   1.0e-28
Match length
                   105
% identity
                   65
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
                   V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                   precursor - barley >gi_167087 (M61146) photosystem I
```

hydrophobic protein [Hordeum vulgare]

```
403260
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-F12
Method
                  BLASTN
NCBI GI
                  g11957
                  47
BLAST score
                  2.0e-17
E value
Match length
                  87
% identity
                  44
NCBI Description
                  Rice complete chloroplast genome
                  403261
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2653558
BLAST score
                  606
E value
                   4.0e-63
Match length
                  124
% identity
                  93
                   (D50679) ferredoxin-sulfite reductase precursor [Zea mays]
NCBI Description
                  403262
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  q2072555
BLAST score
                  237
E value
                  8.0e-20
Match length
                  44
% identity
                  100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                  >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  403263
Seq. ID
                  LIB3431-061-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  q6006355
BLAST score
                  36
E value
                  1.0e-10
Match length
                  44
% identity
                  95
                  Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
NCBI Description
                  403264
Seq. No.
Seq. ID
                  LIB3431-061-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q2315363
BLAST score
                  212
E value
                  7.0e-17
Match length
                  115
                  38
% identity
NCBI Description
                   (AF016441) No definition line found [Caenorhabditis
                  elegans]
                  403265
Seq. No.
                  LIB3431-061-P1-K1-F8
Seq. ID
Method
                  BLASTN
```

E value

2.0e-22

```
q6015437
   NCBI GI
   BLAST score
                      36
                      1.0e-10
   E value
                      47
   Match length
                      65
    % identity
                      Homo sapiens PEX1 mRNA, complete cds
   NCBI Description
    Seq. No.
                      403266
    Seq. ID
                      LIB3431-061-P1-K1-F9
   Method
                      BLASTN
   NCBI GI
                      q6015437
   BLAST score
                      40
                      4.0e-13
   E value
   Match length
                      40
    % identity
                      100
   NCBI Description Homo sapiens PEX1 mRNA, complete cds
                      403267
   Seq. No.
   Seq. ID
                      LIB3431-061-P1-K1-G1
   Method
                      BLASTN
   NCBI GI
                      q4138289
   BLAST score
                      300
   E value
                      1.0e-168
   Match length
                      312
   % identity
                      99
NCBI Description
                      Oryza sativa mRNA for thioredoxin M
                      403268
    Seq. No.
   Seq. ID
                      LIB3431-061-P1-K1-G10
   Method
                      BLASTX
   NCBI GI
                      q4105561
   BLAST score
                      568
   E value
                      1.0e-58
   Match length
                      127
                      89
    % identity
                      (AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]
   NCBI Description
                      403269
   Seq. No.
   Seq. ID
                      LIB3431-061-P1-K1-G11
   Method
                      BLASTX
   NCBI GI
                      g320618
   BLAST score
                      409
   E value
                      5.0e-40
   Match length
                      98
    % identity
   NCBI Description
                      chlorophyll a/b-binding protein I precursor - rice
                      >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
                      chlorophyll a/b-binding protein [Oryza sativa]
                      >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                      [Oryza sativa]
                      403270
   Seq. No.
   Seq. ID
                      LIB3431-061-P1-K1-G12
   Method
                      BLASTX
   NCBI GI
                      q3057120
   BLAST score
                      256
```

 γ .

% identity -

```
Match length
                    67
% identity
                    66
                    (AF023159) starch synthase DULL1 [Zea mays]
NCBI Description
Seq. No.
                   403271
Seq. ID
                   LIB3431-061-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g3790102
                   594
BLAST score
E value
                   1.0e-61
Match length
                   133
                   84
% identity
                    (AF095521) pyrophosphate-dependent phosphofructokinase
NCBI Description
                   alpha subunit [Citrus X paradisi]
                   403272
Seq. No.
                   LIB3431-061-P1-K1-G4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1173275 .
BLAST score
                   159
E value
                    4.0e-11
Match length
                   47
                   70
% identity
                   CHLOROPLAST 30S RIBOSOMAL PROTEIN S7
NCBI Description
                   >gi_2119068_pir__S58630 ribosomal protein S7 - maize chloroplast >gi_902274_emb_CAA60339_ (X86563) ribosomal
                   protein S7 [Zea mays] >gi 902298 emb CAA60362 (X86563)
                   ribosomal protein S7 [Zea mays]
Seq. No.
                   403273
Seq. ID
                   LIB3431-061-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g1498315
BLAST score
                   355
E value
                   1.0e-33
Match length
                   126
% identity
                   58
                    (U56419) IAP100 [Pisum sativum]
NCBI Description
                   403274
Seq. No.
Seq. ID
                   LIB3431-061-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   g5931694
BLAST score
                   410
E value
                   3.0e-40
Match length
                   104
% identity
                   76
NCBI Description
                   (Y18470) Exportin1 (XPO1) protein [Arabidopsis thaliana]
                   403275
Seq. No.
Seq. ID
                   LIB3431-061-P1-K1-H10
Method
                   BLASTN
NCBI GI
                   q1144509
BLAST score
                   36
E value
                   1.0e-10
Match length
                   44
```

```
NCBI Description Oryza sativa wanderer mobile element linked to Xa21
Seq. No.
                  403276
                  LIB3431-061-P1-K1-H11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q81946
BLAST score
                  453
E value
                  2.0e-45
                  91 🐬
Match length
                  92 🗀
% identity
                  protochlorophyllide reductase (EC 1.3.1.33) precursor -
NCBI Description
                  garden pea
Seq. No.
                  403277
Seq. ID
                  LIB3431-061-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  g949979
BLAST score
                  36
E value
                  1.0e-10
Match length
                  60
% identity
                  90
NCBI Description
                  Z.mays Glossy2 locus DNA
Seq. No.
                  403278
Seq. ID
                  LIB3431-061-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q3789954
BLAST score
                  559
E value
                  1.0e-57
Match length
                  109
% identity
NCBI Description
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
                  sativa]
Seq. No.
                  403279
Seq. ID
                  LIB3431-061-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g2435511 -
BLAST score
                  474
E value
                  1.0e-47
Match length
                  111
% identity
                  (AF024504) contains similarity to prolyl 4-hydroxylase
NCBI Description
                  alpha subunit [Arabidopsis thaliana]
Seq. No.
                  403280
Seq. ID
                  LIB3431-061-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q3947448
BLAST score
                  212
                  5.0e-17
E value
Match length
                  102
% identity
                  (AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA
NCBI Description
                  EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3
                  comes from this gene; cDNA EST yk475f6.5 comes from this
```

gene; cDNA EST yk499g5.5 comes from this gene; cDNA EST ...

>gi_3947543_emb_CAA88952.1_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene; cDNA EST yk499g5.5 comes

```
403281
Seq. No.
Seq. ID
                   LIB3431-061-P1-K1-H6
Method
                   BLASTN
NCBI GI
                   g949979
BLAST score
                   49
                   1.0e-18
E value
                   97
Match length
% identity
                   88
NCBI Description Z.mays Glossy2 locus DNA
Seq. No.
                   403282
                   LIB3431-061-P1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1483213
BLAST score
                   308
E value
                   4.0e-28
Match length
                   108
% identity
                   56
                   (X96480) PAC [Arabidopsis thaliana]
NCBI Description
                   >gi_5729705_gb_AAD48512.1_AC007927_2 (AC007927) pale cress
                   protein [Arabidopsis thaliana]
                   403283
Seq. No.
Seq. ID
                   LIB3431-061-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q3075488
BLAST score
                   705
                   1.0e-74
E value
Match length
                   137
% identity
                   99
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
                   403284
Seq. No.
                   LIB3431-062-P1-K1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3885888
BLAST score
                   321
E value
                   1.0e-29
Match length
                   108
% identity
                   (AF093632) high mobility group protein [Oryza sativa]
NCBI Description
Seq. No.
                   403285
                   LIB3431-062-P1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3929545
BLAST score
                   425
                   9.0e-42
E value
Match length
                   107
% identity
                   84
                   (AF067194) S-adenosylmethionine decarboxylase [Oryza
NCBI Description
```

Seq. No.

```
sativa]
                   403286
Seq. No.
Seq. ID
                   LIB3431-062-P1-K1-A12
                   BLASTX
Method
NCBI GI
                   g5360591
BLAST score
                   476
                   9.0e-48
E value
                   149
Match length
                   60
% identity
                   (AB022328) nClpP3 [Arabidopsis thaliana]
NCBI Description
                   403287
Seq. No.
                   LIB3431-062-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g419742
BLAST score
                   624
E value
                   3.0e-65
Match length
                   127
% identity
                   91
NCBI Description
                   protochlorophyllide reductase (EC 1.3.1.33) precursor -
                   loblolly pine
Seq. No.
                   403288
Seq. ID
                   LIB3431-062-P1-K1-A3
Method
                   BLASTX
NCBI GI
                  q548603
BLAST score
                   434
E value
                   7.0e-43
Match length
                   130
% identity
                   70
NCBI Description
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR
                   (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D)
                   >gi_478404_pir__JQ2247 photosystem I chain D precursor -
                   barley >gi 167085 (M98254) PSI-D subunit [Hordeum vulgare]
Seq. No.
                  403289
                   LIB3431-062-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1835731
BLAST score
                   180
E value
                   9.0e-14
Match length
                   44
% identity
NCBI Description
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
Seq. No.
                   403290
Seq. ID
                   LIB3431-062-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   648
E value
                   1.0e-73
Match length
                   150
% identity
NCBI Description
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

Seq. ID

```
LIB3431-062-P1-K1-A9
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4138289
BLAST score
                   228
                   1.0e-125
E value
Match length
                   276
% identity
                   96
NCBI Description Oryza sativa mRNA for thioredoxin M
                   403292
Seq. No.
Seq. ID
                   LIB3431-062-P1-K1-B10
                   BLASTX
Method
NCBI GI
                   g131388
BLAST score
                   250
E value
                   2.0e-21
Match length
                   95
                   65
% identity
                   OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) (33 KD
NCBI Description
                   SUBUNIT OF OXYGEN EVOLVING SYSTEM OF PHOTOSYSTEM II) (33 KD
                   THYLAKOID MEMBRANE PROTEIN) >gi 100831 pir S16260
                   photosystem II oxygen-evolving complex protein 1 - common
                   wheat x Sanduri wheat >gi_21844_emb_CAA40670_ (X57408)
33kDa oxygen evolving protein of photosystem II [Triticum
                   aestivum]
                   403293
Seq. No. .
                   LIB3431-062-P1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4914411
BLAST score
                   363
E value
                   2.0e-34
Match length
                   105
% identity
                   68
NCBL Description
                   (AL050352) putative protein [Arabidopsis thaliana]
Seq. No.
                   403294
Seq. ID
                   LIB3431-062-P1-K1-B3
                   BLASTX
Method
NCBI GI
                   g4733937
BLAST score
                   264
E value
                   8.0e-23
Match length
                   146
% identity
                   42
                   (AF080245) sesquiterpene synthase [Elaeis oleifera]
NCBI Description
Seq. No.
                   403295
Seq. ID
                   LIB3431-062-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g1261917
BLAST score
                   339
E value
                   1.0e-31
Match length
                   96
% identity
NCBI Description
                   (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
                   403296
Seq. No.
```

LIB3431-062-P1-K1-B5

NCBI GI

```
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  298
                  7.0e-27
E value
Match length
                  76
% identity
                  75
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
                  403297
Seq. No.
                  LIB3431-062-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245015
BLAST score
                  463
E value
                  3.0e-46
                  107
Match length
                  80
% identity
NCBI Description
                  (Z97341) glucosyltransferase like protein [Arabidopsis
                  thaliana]
                  403298
Seq. No.
Seq. ID
                  LIB3431-062-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2286121
BLAST score
                  521
E value
                  5.0e-53
                  102
Match length
                  97
% identity
NCBI Description
                 (U88068) sec14 like protein [Oryza sativa]
                  403299
Seq. No.
                  LIB3431-062-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g871931
BLAST score
                  248
E value
                  6.0e-21
                  75
Match length
% identity
NCBI Description (D30763) ferredoxin [Oryza sativa]
Seq. No.
                  403300
Seq. ID
                  LIB3431-062-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g115772
BLAST score
                  156
E value
                  6.0e-11
Match length
                  32
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
NCBI Description
                  CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding
                  protein 1R precursor - rice >gi 20178 emb CAA32108
                  (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                  [Oryza sativa]
                  403301
Seq. No.
                  LIB3431-062-P1-K1-C12
Seq. ID
Method
                  BLASTX
```

J.

g5091520

% identity

```
204
BLAST score
E value
                  6.0e-16
Match length
                  130
                  45
% identity
                  (AB023482) ESTs AU058081(E30812), AU058365(E50679),
NCBI Description
                  AU030138(E50679) correspond to a region of the predicted
                  gene.; Similar to Spinacia oleracea mRNA for proteasome
                  37kD subunit.(X96974) [Oryza sativa]
                  403302
Seq. No.
Seq. ID
                  LIB3431-062-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  553
                  7.0e-57
E value
                  120
Match length
% identity
                  87
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094 pir __RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403303 🐠
                  LIB3431-062-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1854378
BLAST score
                  252
E value
                  1.0e-25
Match length
                  125
% identity
                  (AB001338) Sucrose-Phosphate Synthase [Saccharum
NCBI Description
                  officinarum]
                  403304
Seq. No.
Seq. ID
                  LIB3431-062-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4972111
BLAST score
                  546
E value
                  6.0e-56
Match length
                  151
% identity
                  (AL078579) protein phosphatase homolog (PPH1) [Arabidopsis
NCBI Description
                  thaliana]
                  403305
Seq. No.
Seq. ID
                  LIB3431-062-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  g2072554
BLAST score
                  188
E value
                  1.0e-101
Match length
                  196
```

NCBI GI

19. C

```
NCBI Description Oryza sativa metallothionein-like protein mRNA, complete
                  cds
                  403306
Seq. No.
                  LIB3431-062-P1-K1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2267594
                  49
BLAST score
E value
                  4.0e-19
Match length
                  49
                  100
% identity
                  Oryza sativa plastocyanin precursor, mRNA, complete cds
NCBI Description
                  403307
Seq. No.
Seq. ID
                  LIB3431-062-P1-K1-D11
                  BLASTX
Method
NCBI GI
                  g1835731
BLAST score
                  461
E value
                  5.0e-46
                  95
Match length
                  95
% identity
                  (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
                  403308
Seq. No.
Seq. ID
                  LIB3431-062-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q2244965
BLAST score
                  307
E value
                  3.0e-28
Match length
                  85
% identity
                  68
                  (Z97340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  403309
Seq. ID
                  LIB3431-062-P1-K1-D2
Method
                  BLASTN
NCBI GI
                  g6015437
BLAST score
                  35
E value
                  3.0e-10
Match length
                  35
% identity
                  100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                  403310
Seq. No.
                  LIB3431-062-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g21695
                  361
BLAST score
                  3.0e-34
E value
Match length
                  110
% identity
                   62
NCBI Description
                  (X66014) cathepsin B [Triticum aestivum]
Seq. No.
                  403311
                  LIB3431-062-P1-K1-D4
Seq. ID
Method
                  BLASTX
```

g4585882

```
BLAST score
                   444
                   2.0e-45
E value
Match length
                   141
                   70
% identity
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   403312
                   LIB3431-062-P1-K1-D5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3290022
BLAST score
                   434
E value
                   9.0e-43
                   142
Match length
                   58
% identity
                   (AF044173) cysteine synthase; CS-B; O-acetylserine (thiol)
NCBI Description
                   lyase; plastidic isoform [Solanum tuberosum]
Seq. No.
                   403313
Seq. ID
                   LIB3431-062-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g3201969
                   225
BLAST score
                   2.0e-18
E value
Match length
                   43
% identity
                   98
                   (AF068332) submergence induced protein 2A [Oryza sativa]
NCBI Description
Seq. No.
                   403314
                   LIB3431-062-P1-K1-E1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2624325
BLAST score
                   86
E value
                   9.0e-41
Match length
                   110
% identity
                   95
                   Oryza sativa mRNA for glycine-rich RNA-binding protein
NCBI Description
                   (OsGRP1)
                   403315
Seq. No.
Seq. ID
                   LIB3431-062-P1-K1-E11
                   BLASTN
Method
NCBI GI
                   g218209
BLAST score
                   155
E value
                   1.0e-81
Match length
                   281
% identity
                   96
                  Oryza sativa mRNA for the small subunit of
NCBI Description
                   ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
Seq. No.
                   403316
Seq. ID
                   LIB3431-062-P1-K1-E12
                   BLASTX
Method
NCBI GI
                   g3618310
BLAST score
                   331
```

6.0e-31

E value

E value

3.0e-15

```
101
Match length
                    65
% identity
NCBI Description
                    (AB001883) zinc finger protein [Oryza sativa]
Seq. No.
                    403317
Seq. ID
                   LIB3431-062-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   q320618
BLAST score
                   476 ·
E value
                   8.0e-48
Match length
                   115
                   80
% identity
                   chlorophyll a/b-binding protein I precursor - rice
NCBI Description
                   >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting
chlorophyll a/b-binding protein [Oryza sativa]
                   >gi_227611_prf__1707316A chlorophyll a/b binding protein 1
                    [Oryza sativa]
Seq. No.
                   403318
Seq. ID
                   LIB3431-062-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   q2832606
BLAST score
                   214
E value
                   5.0e-17
Match length
                   90
% identity
NCBI Description
                    (AL021635) predicted protein [Arabidopsis thaliana]
                   >gi 3292810 emb CAA19800.1 (AL031018) putative protein
                    [Arabidopsis thaliana]
Seq. No.
                   403319
Seq. ID
                   LIB3431-062-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   q2306981
BLAST score
                   409
E value
                   2.0e-44
Match length
                   98
% identity
NCBI Description
                    (AF010321) photosystem I antenna protein [Oryza sativa]
                   403320
Seq. No.
Seq. ID
                   LIB3431-062-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   g4512705
BLAST score
                   483
E value
                   1.0e-48
Match length
                   144
% identity
NCBI Description
                    (AC006569) putative serine/threonine protein kinase
                    [Arabidopsis thaliana]
                   403321
Seq. No.
Seq. ID
                   LIB3431-062-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   g2739375
BLAST score
                   197
```

Method

BLASTX

```
109
Match length
% identity `
                   46
NCBI Description
                   (AC002505) unknown protein [Arabidopsis thaliana]
Seq. No.
                   403322 .
                   LIB3431-062-P1-K1-E8
Seq. ID
Method
                   BLASTN
NCBI GI
                   g5042437
BLAST score
                   287
                                                                               E value
                   1.0e-160
Match length
                   358
                   99
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
Seq. No.
                   403323
Seq. ID
                   LIB3431-062-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   q4079798
BLAST score
                   227
E value
                   4.0e-20
Match length
                   92
% identity
NCBI Description
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
                   sativa]
Seq. No.
                   403324
Seq. ID
                   LIB3431-062-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   270
E value
                   4.0e-24
Match length
                   79
                   71
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf · 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   403325
Seq. No.
Seq. ID
                   LIB3431-062-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   q5042462
BLAST score
                   221
E value
                   9.0e-18
Match length
                   109
                   47
% identity
NCBI Description
                   (AC007789) putative negatively light-regulated protein
                   [Oryza sativa]
Seq. No.
                   403326
                   LIB3431-062-P1-K1-F12
Seq. ID
```

```
NCBI GI
                   g2407281
BLAST score
                   775
E value
                   7.0e-83
Match length
                   145
                   99
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq: No.
                   403327
Seq. ID
                   LIB3431-062-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g3885894 .
BLAST score
                   302
E value
                   1.0e-27
                   90
Match length
                   72
% identity
NCBI Description
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
Seq. No.
                   403328
Seq. ID
                   LIB3431-062-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   q3789952
BLAST score
                   290
E value
                   2.0e-26
Match length
                   71
% identity
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                   sativa]
Seq. No.
                   403329
Seq. ID
                   LIB3431-062-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g2407281
BLAST score
                   614
E value
                   5.0e-64
Match length
                   126
% identity
                   90
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq. No.
                   403330
                   LIB3431-062-P1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   391
E value
                   7.0e-38
Match length
                   108
                   75
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
```

BLAST score

```
Seq. No.
                   403331
Seq. ID
                   LIB3431-062-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g2462834
BLAST score
                   293
E value
                   3.0e-26
Match length
                   106
% identity
                   57
                   (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   403332
Seq. No.
Seq. ID
                   LIB3431-062-P1-K1-G10
Method
                   BLASTN
NCBI GI
                   g1835730
BLAST score
                   156
                   1.0e-82
E value
Match length
                   164
                   99
% identity
NCBI Description
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
                   complete cds
Seq. No.
                   403333
Seq. ID
                   LIB3431-062-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   g3126854
                   289
BLAST score
                   2.0e-26
E value
                   57
Match length
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   403334 、
Seq. No.
                   LIB3431-062-P1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3885892
BLAST score
                   667
E value
                   3.0e-70
Match length
                   136
% identity
                   (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
NCBI Description
                   403335
Seq. No.
                   LIB3431-062-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5031281
BLAST score
                   356
E value
                   1.0e-33
Match length
                   121
% identity
                   (AF139499) unknown [Prunus armeniaca]
NCBI Description
                   403336
Seq. No.
                   LIB3431-062-P1-K1-G3
Seq. ID
Method
                   BLASTX
                   q2072555
NCBI GI
```

```
9.0e-20
E value
Match length
                   44
% identity
                   100
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   403337
Seq. ID
                   LIB3431-062-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   q5123711
BLAST score
                   467
E value
                   1.0e-46
Match length
                   148
% identity
                   62
                   (AL079347) putative protein [Arabidopsis thaliana]
NCBI Description
                   403338
Seq. No.
Seq. ID
                   LIB3431-062-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   751
E value
                   6.0e-80
Match length
                   164
% identity
                   88
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403339
Seq. ID
                   LIB3431-062-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   q4973264
BLAST score
                   376
E value
                   4.0e-36
                   93
Match length
% identity
                   (AF144391) thioredoxin-like 5 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403340
                   LIB3431-062-P1-K1-G7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3913018
BLAST score
                   515
E value
                   3.0e-52
Match length
                   125
% identity
                   81
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi 218155 dbj BAA02730_ (D13513) chloroplastic
```

aldolase [Oryza sativa]

Method

NCBI GI

BLASTN

g6015437

```
Seq. No.
                   403341
Seq. ID
                   LIB3431-062-P1-K1-G8
Method .
                   BLASTN
NCBI GI
                   g20369
BLAST score
                   388
                   0.0e + 00
E value
                   396
Match length
% identity
                   99
NCBI Description
                   Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
                   synthetase (EC 6.3.1.2) (clone lambda-GS31)
                   >gi 2170909 dbj_E02681 E02681 cDNA encoding precursor of
                   chloroplast localising glutamine synthetase
Seq. No.
                   403342
                   LIB3431-062-P1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3289002
BLAST score
                   590
E value
                   4.0e-61
Match length
                   170
% identity
                   42
NCBI Description
                   (AF073522) CRP1 [Zea mays]
Seq. No.
                   403343
Seq. ID
                   LIB3431-062-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   1.0e-19
Match length
                   44
% identity
                   100
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   403344
Seq. ID
                   LIB3431-062-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                   606
E value
                   5.0e-63
Match length
                   131
                   87
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   403345
Seq. No.
Seq. ID
                   LIB3431-062-P1-K1-H9
```

NCBI GI

```
BLAST score
                   35
E value
                   3.0e-10
Match length
                  35
                  100
% identity
                  Homo sapiens PEX1 mRNA, complete cds
NCBI Description
                   403346
Seq. No.
                  LIB3431-062-P1-N1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3885887
BLAST score
                   465
                  0.0e + 00
E value
Match length
                   473
% identity
                   100
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                  complete cds
Seq. No.
                   403347
Seq. ID
                  LIB3431-062-P1-N1-A10
Method
                  BLASTX
NCBI GI
                  g3913426
BLAST score
                  362
E value
                   2.0e-34
Match length
                   67
% identity
                  100
NCBI Description
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
                   (SAMDC) >gi_1532048_emb_CAA69074_ (Y07766)
                  S-adenosylmethionine decarboxylase [Oryza sativa]
Seq. No.
                   403348
Seq. ID
                  LIB3431-062-P1-N1-A2
Method
                  BLASTX
NCBI GI
                  g2598151
BLAST score
                  251
E value
                  2.0e-21
Match length
                  50
% identity
NCBI Description
                   (AF027350) NADPH:protochlorophyllide oxidoreductase porB
                   [Pinus taeda]
Seq. No.
                  403349
Seq. ID
                  LIB3431-062-P1-N1-A6
Method
                  BLASTX
NCBI GI
                  g131225
BLAST score
                  360
E value
                  3.0e-34
Match length
                  99
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi 167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
Seq. No.
                  403350
Seq. ID
                  LIB3431-062-P1-N1-A7
Method
                  BLASTN
```

g1835730

```
BLAST score
                   162
                   6.0e-86
E value
Match length
                   282
% identity
                   89
NCBI Description
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
                   complete cds
                   403351
Seq. No.
Seq. ID
                   LIB3431-062-P1-N1-A8
Method
                   BLASTX
NCBI GI
                   g2570513
BLAST score
                   172
E value
                   2.0e-12
Match length
                   32
% identity
NCBI Description
                   (AF022739) chlorophyll a-b binding protein [Oryza sativa]
Seq. No.
                   403352
                  LIB3431-062-P1-N1-A9.
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4138290
BLAST score
                   313
E value
                   1.0e-28
Match length
                   63
% identity
NCBI Description
                   (AJ005841) thioredoxin M [Oryza sativa]
Seq. No.
                   403353
                  LIB3431-062-P1-N1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g5931625
BLAST score
                   529
                   6.0e-54
E value
Match length
                   111
% identity
NCBI Description
                   (AB032761) rab5B [Oryza sativa]
Seq. No.
                   403354
Seq. ID
                  LIB3431-062-P1-N1-B10
Method
                  BLASTX
NCBI GI
                   q482311
BLAST score
                   398
E value
                   1.0e-38
                   79
Match length
                   100
% identity
NCBI Description
                  photosystem II oxygen-evolving complex protein 1 - rice
                   (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving
                  complex protein 1 [Oryza sativa]
                   403355
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-B11
Method
                  BLASTX
NCBI GI
                  q3158476
BLAST score
                   166
E value
                   2.0e-11
Match length
                  43
% identity
                  70
```

```
NCBI Description (AF067185) aquaporin 2 [Samanea saman]
Seq. No.
                  403356
                  LIB3431-062-P1-N1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4914411
BLAST score
                  245
E value
                  1.0e-20 .
Match length
                  85
% identity
                  59
NCBI Description (AL050352) putative protein [Arabidopsis thaliana]
                  403357
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-B3
Method
                  BLASTX
NCBI GI
                  g3108343
BLAST score
                  159
E value
                  1.0e-10
Match length
                  102
% identity
                  29
NCBI Description (AF061285) sesquiterpene cyclase [Capsicum annuum]
Seq. No.
                  403358
Seq. ID
                  LIB3431-062-P1-N1-B4
Method
                  BLASTX
NCBI GI
                  g1261917
BLAST score
                  218
                  2.0e-17
E-value
Match length
                  59
% identity
                  64
NCBI Description (X96979) lipid transfer protein 7a2b [Hordeum vulgare]
                  403359
Seq. No.
                  LIB3431-062-P1-N1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1617197
BLAST score
                  300
                  3.0e-27
E value
Match length
                  71
% identity
NCBI Description (Z72488) CP12 [Nicotiana tabacum]
                  403360
Seq. No.
                  LIB3431-062-P1-N1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2286121
BLAST score
                  534
E value
                  1.0e-54
Match length
                  102
% identity
NCBI Description (U88068) sec14 like protein [Oryza sativa]
```

Seq. No. 403361

Seq. ID LIB3431-062-P1-N1-B8

Method BLASTN NCBI GI g2305114 BLAST score 225

```
1.0e-123
E value
Match length
                    352
% identity
                    91
                   Oryza sativa ferredoxin mRNA, complete cds
NCBI Description
Seq. No.
                    403362
Seq. ID
                   LIB3431-062-P1-N1-B9
Method
                   BLASTX
NCBI GI
                   q132105
BLAST score
                    411
                    4.0e-40
E value
                   76
Match length
                    99
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
Seq. No.
                    403363
Seq. ID
                   LIB3431-062-P1-N1-C11
Method
                   BLASTX
NCBI GI
                    q115787
BLAST score
                    403
E value
                    3.0e-39
Match length
                    76
% identity
                    100
                   CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-2) (LHCP) >gi_82461_pir__S03706 chlorophyll a/b-binding protein 2R precursor - rice >gi_20182_emb_CAA32109_
                    (X13909) chlorophyll a/b-binding preprotein (AA -28 to 235)
                    [Oryza sativa]
                    403364
Seq. No.
                   LIB3431-062-P1-N1-C12
Seq. ID
Method
                   BLASTN
NCBI GI
                    g20262
BLAST score
                    108
E value
                    1.0e-53
Match length
                   220
                   87
% identity
NCBI Description
                   O.sativa light-induced mRNA
Seq. No.
                    403365
Seq. ID
                   LIB3431-062-P1-N1-C5
Method
                   BLASTN
NCBI GI
                    q218207
BLAST score
                   256
E value
                    1.0e-142
Match length
                   284
                    98
% identity
NCBI Description
                   Oryza sativa mRNA for the small subunit of
```

ribulose-1,5-bisphosphate carboxylase, complete cds, clone

Seq. No.

```
pOSSS1139
Seq. No.
                   403366
                  LIB3431-062-P1-N1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1854378
BLAST score
                  275
E value
                   4.0e-24
Match length
                  60
% identity
                  87
                   (AB001338) Sucrose-Phosphate Synthase [Saccharum
NCBI Description
                  officinarum]
Seq. No.
                   403367
Seq. ID
                  LIB3431-062-P1-N1-C7
Method
                  BLASTX
NCBI GI
                  g3643090
BLAST score
                   337
E value
                   2.0e-31
Match length
                   96
% identity
                   (AF075582) protein phosphatase-2C; PP2C [Mesembryanthemum
NCBI Description
                  crystallinum]
Seq. No.
                   403368
Seq. ID
                  LIB3431-062-P1-N1-C8
Method
                  BLASTX
NCBI GI
                   q451193
                   397
BLAST score
E value
                   2.0e-38
Match length
                   109
% identity
NCBI Description
                   (L28008) wali7 [Triticum aestivum]
                  >gi 1090845 prf 2019486B wali7 gene [Triticum aestivum]
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-C9
Method
                  BLASTN
NCBI GI
                   q2072554
BLAST score
                   317
E value
                   1.0e-178
Match length
                   325
% identity
                   99
                  Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
Seq. No.
                   403370
                  LIB3431-062-P1-N1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2267594
BLAST score
                   43
E value
                   1.0e-15
Match length
                   43
% identity
                   100
                  Oryza sativa plastocyanin precursor, mRNA, complete cds
NCBI Description
```

```
LIB3431-062-P1-N1-D11
Seq. ID
                    BLASTX
Method
NCBI GI
                    g131400
                    243
BLAST score
                    3.0e-27
E value
                    93
Match length
                    67
% identity
                    PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                    >gi_81471_pir__S00409 photosystem II 10K protein precursor
- spinach >gi_170127 (J03887) 10kd polypeptide precursor
                    [Spinacia oleracea]
                    403372
Seq. No.
                    LIB3431-062-P1-N1-D12
Seq. ID
                    BLASTX
Method
NCBI GI
                    q2244965
BLAST score
                    157
E value
                    2.0e-10
Match length
                    37
% identity
                    81
NCBI Description (297340) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                    403373
Seq. ID
                    LIB3431-062-P1-N1-D3
Method
                    BLASTN
NCBI GI
                    q21692
BLAST score
                    43
E value
                    9.0e-15
                    75
Match length
% identity
NCBI Description T.aestivum mRNA 1 for cathepsin B (2529)
Seq. No.
                    403374
Seq. ID
                    LIB3431-062-P1-N1-D4
Method
                    BLASTX
NCBI GI
                    q115813
BLAST score
                    280
E value
                    8.0e-25
Match length
                    68
% identity
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN 8 PRECURSOR (LHCI TYPE III
                   CAB-8) >gi_19182_emb_CAA33330_ (X15258) Type III chlorophyll a/b-binding protein [Lycopersicon esculentum]
                    403375
Seq. No.
Seq. ID
                    LIB3431-062-P1-N1-D5
Method
                    BLASTX
NCBI GI
                    q399333
BLAST score
                    289
E value
                    8.0e-26
Match length
                    66
% identity
                   CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYLSERINE
NCBI Description
                    SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE)
                    >gi 322740_pir__A43407 cysteine synthase (EC 4.2.99.8)
                   precursor - pepper >gi_17944_emb_CAA46086_ (X64874)
```

O-acetylserine (thiol)-lyase [Capsicum annuum]

Match length

% identity

155

88

```
Seq. No.
Seq. ID
                   LIB3431-062-P1-N1-D6
Method
                   BLASTX
NCBI GI
                   g2498397
                   217
BLAST score
E value
                   2.0e-17
Match length
                   48
 % identity
                   83
                   FERREDOXIN-THIOREDOXIN REDUCTASE, VARIABLE CHAIN (FTR-V)
NCBI Description
                   (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT A) (FTR-A)
                   403377
Seq. No.
                   LIB3431-062-P1-N1-D7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3201968
BLAST score
                   235
E value
                   1.0e-129
Match length
                   307
                   94
% identity
NCBI Description
                   Oryza sativa submergence induced protein 2A mRNA, complete
Seq. No.
                   403378
Seq. ID
                   LIB3431-062-P1-N1-E1
Method
                   BLASTN
NCBI GI
                   q2624325
BLAST score
                   179
E value
                   4.0e-96
Match length
                   273
% identity
                   92
NCBI Description
                   Oryza sativa mRNA for glycine-rich RNA-binding protein
                   (OsGRP1)
Seq. No.
                   403379
Seq. ID
                   LIB3431-062-P1-N1-E10
Method
                   BLASTX
NCBI GI
                   g1173347
BLAST score
                   184
E value
                   1.0e-13
Match length
                   40
% identity
NCBI Description
                   SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                   >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                   3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                   aestivum]
                   403380
Seq. No.
Seq. ID
                   LIB3431-062-P1-N1-E11
Method
                   BLASTN
NCBI GI
                   q218209
BLAST score
                   44
E value
                   1.0e-15
```

403376

```
NCBI Description Oryza sativa mRNA for the small subunit of
                  ribulose-1,5-bisphosphate carboxylase, complete cds, clone
                  pOSSS2106
Seq. No.
                  403381
                  LIB3431-062-P1-N1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3618310
BLAST score
                  378
E value
                  3.0e-36
Match length
                  72
% identity
                  100
                   (AB001883) zinc finger protein [Oryza sativa]
NCBI Description
Seq. No.
                  403382
                  LIB3431-062-P1-N1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1617197
BLAST score
                  274
E value
                   4.0e-24
Match length
                  67
% identity
                  73
                  (Z72488) CP12 [Nicotiana tabacum]
NCBI Description
Seq. No.
                   403383
Seq. ID
                  LIB3431-062-P1-N1-E3
Method
                  BLASTX
                  q693920
NCBI GI
                   386
BLAST score
                   3.0e-37
E value
Match length
                   77
% identity
                   (U21113) chlorophyll a/b binding protein [Solanum
NCBI Description
                   tuberosum]
Seq. No.
                   403384
Seq. ID
                  LIB3431-062-P1-N1-E5
Method
                  BLASTX
NCBI GI
                   a1076724
BLAST score
                   404
                   3.0e-39
E value
Match length
                   77
                   95
% identity
                  LHCI-680, photosystem I antenna protein - barley
NCBI Description
                  >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                   403385
Seq. ID
                  LIB3431-062-P1-N1-E7
Method
                  BLASTX
                   a2739375
NCBI GI
BLAST score
                   162
E value
                   6.0e-11
Match length
                   93
                   42
% identity
                   (AC002505) unknown protein [Arabidopsis thaliana]
NCBI Description
```

```
Seq. No.
                  403386
Seq. ID
                  LIB3431-062-P1-N1-E8
Method
                  BLASTN
NCBI GI
                  g5042437
BLAST score
                  283
E value
                  1.0e-158
Match length
                  342
                  100
% identity
NCBI Description Oryza sativa BAC T49B20 genomic sequence, complete sequence
                  403387
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-F1
Method
                  BLASTX
NCBI GI
                  g4079798
BLAST score
                  455
                  3.0e-45
E value
Match length
                  88
% identity
                  100
                   (AF052203) 23 kDa polypeptide of photosystem II [Oryza
NCBI Description
                  sativa]
                  403388
Seq. No.
Seq. ID
                  LIB3431-062-P1-N1-F12
Method
                  BLASTX
                  q347451
NCBI GI
BLAST score
                  154
E value
                  4.0e-10
                  29
Match length
                  100
% identity
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                  sativa]
                  403389
Seq. No.
                  LIB3431-062-P1-N1-F3
Seq. ID
Method
                  BLASTX
                  q3885894
NCBI GI
BLAST score
                  330
                  1.0e-30
E value
                  77
Match length
% identity
                  (AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]
NCBI Description
                  403390
Seq. No.
                  LIB3431-062-P1-N1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2997591
BLAST score
                  306
E value
                  8.0e-28
                  74
Match length
                  80
% identity
                  (AF020814) glucose-6-phosphate/phosphate-translocator
NCBI Description
                  precursor [Pisum sativum]
                  403391
Seq. No.
                  LIB3431-062-P1-N1-F7
Seq. ID
Method
                  BLASTX
```

q3789952

Seq. ID

```
BLAST score
                  193
                  1.0e-14
E value
Match length
                  35
                  100
% identity
                 (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
                  403392
Seq. No.
                  LIB3431-062-P1-N1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g132105
BLAST score
                  556
E value
                  3.0e-57
                  101
Match length
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  403393
Seq. No.
                  LIB3431-062-P1-N1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462834
BLAST score
                  244
E value
                  1.0e-20
Match length
                  107
% identity
NCBI Description
                  (AF000657) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  403394
                  LIB3431-062-P1-N1-G10
Seq. ID
Method
                  BLASTX-
NCBI GI
                  g1835731
BLAST score
                  426
E value
                  6.0e-42
Match length
                  92
% identity
                 (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                  403395
Seq. ID
                  LIB3431-062-P1-N1-G11
Method
                  BLASTX
NCBI GI
                  g3126854
BLAST score
                  370
E value
                  2.0e-35
Match length
                  70
% identity
                 (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                  403396
```

LIB3431-062-P1-N1-G12

E value

4.0e-36

```
Method
                   BLASTX
NCBI GI
                   g3885892
BLAST score
                   208
E value
                   1.0e-16
Match length
                   41
                   100
% identity
NCBI Description
                   (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
                   403397
Seq. No.
                  LIB3431-062-P1-N1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g5031281
BLAST score
                   223
                   4.0e-18
E value
                   47
Match length
% identity
                   81
                  (AF139499) unknown [Prunus armeniaca]
NCBI Description
Seq. No.
                   403398
Seq. ID
                   LIB3431-062-P1-N1-G3
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   1.0e-19
Match length
                   44
% identity
                  100
                 (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   403399
Seq. ID
                   LIB3431-062-P1-N1-G4
Method
                  BLASTX
NCBI GI
                   g5123711
BLAST score
                   280
E value
                   9.0e-25
                   90
Match length
% identity
                   (AL079347) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403400
Seq. ID
                   LIB3431-062-P1-N1-G5
Method
                  BLASTX
NCBI GI
                   g347451
BLAST score
                  220
E value
                   9.0e-18
Match length
                  65
% identity
                   (L22155) ribulose 1,5-bisphosphate carboxylase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   403401
                   LIB3431-062-P1-N1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4973264
BLAST score
                   376
```

```
93
Match length
                   73
% identity
NCBI Description
                   (AF144391) thioredoxin-like 5 [Arabidopsis thaliana]
Seq. No.
                   403402
                   LIB3431-062-P1-N1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2407279
BLAST score
                   206
E value
                   4.0e-16
Match length
                   42
                   100
% identity
NCBI Description
                  (AF017362) aldolase [Oryza sativa]
Seq. No.
                   403403
                   LIB3431-062-P1-N1-G8
Seq. ID
Method
                   BLASTN
NCBI GI
                   q20369
BLAST score
                   381
E value
                   0.0e + 00
                   385
Match length
                   100
% identity
NCBI Description
                   Oryza sativa shoot GS2 mRNA for chloroplastic glutamine
                   synthetase (EC 6.3.1.2) (clone lambda-GS31)
                   >gi_2170909_dbj_E02681_E02681 cDNA encoding precursor of
                   chloroplast localising glutamine synthetase
Seq. No.
                   403404
                   LIB3431-062-P1-N1-G9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3885887
BLAST score
                   269
E value
                   1.0e-149
Match length
                   397
                   92
% identity
                  Oryza sativa high mobility group protein (HMG) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   403405
                   LIB3431-062-P1-N1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q451193
BLAST score
                   412
E value
                   3.0e-40
Match length
                   114
% identity
                   (L28008) wali7 [Triticum aestivum]
NCBI Description
                   >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]
Seq. No.
                   403406
                   LIB3431-062-P1-N1-H3
Seq. ID
Method

∠ BLASTX

NCBI GI
                   g3250697
BLAST score
                   377
E value
                   3.0e-36
Match length
                   91
```

76

% identity

E value

BLAST score

g2072555

7.0e-20

```
NCBI Description (AL024486) putative protein [Arabidopsis thaliana]
                   403407
Seq. No.
                   LIB3431-062-P1-N1-H5
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2072554
BLAST score
                   285
E value
                   1.0e-159
Match length
                   301
                   99
% identity
                   Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
                   cds
                   403408
Seq. No.
Seq. ID
                   LIB3431-062-P1-N1-H7
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   402
E value
                   4.0e-39
                   73
Match length
                   100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403409
Seq. ID
                   LIB3431-062-P1-N1-H9
Method
                   BLASTN
NCBI GI
                   q5051932
BLAST score
                   200
E value
                   1.0e-108
Match length
                   254
% identity
                   100
NCBI Description Oryza sativa MADS-box protein FDRMADS8 mRNA, complete cds
Seq. No.
                   403410
Seq. ID
                   LIB3431-063-P1-K1-A1
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   41
E value
                   1.0e-13
Match length
                   41
% identity
                   100
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                   403411
Seq. No.
Seq. ID
                   LIB3431-063-P1-K1-A11
Method
                   BLASTX
```

Seq. ID

```
44
Match length
                   100
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   403412
Seq. No.
                   LIB3431-063-P1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   392
E value
                   2.0e-38
Match length
                   74
% identity
                   100
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   403413
                   LIB3431-063-P1-K1-A2
Seq. ID
Method
                   BLASTX ·
NCBI GI
                   g132105
BLAST score
                   363
E value
                   1.0e-34
                   101
Match length
% identity
                   74
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403414
                   LIB3431-063-P1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2407281
BLAST score
                   696
E value
                   1.0e-73
Match length
                   144
                   93
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq. No.
                   403415
                   LIB3431-063-P1-K1-A4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3819202
BLAST score
                   51
E value
                   2.0e-19
Match length
                   191
                   82
% identity
                   Hordeum vulgare partial mRNA; clone cMWG0680.rev
NCBI Description
Seq. No.
                   403416
```

LIB3431-063-P1-K1-A5

```
Method
                   BLASTX
NCBI GI
                   g548605
BLAST score
                   469
                   5.0e-47
E value
Match length
                   112
                   85
% identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >gi 539055 pir A48527 photosystem I protein psaK precursor
                   - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                   [Hordeum vulgare]
                   403417
Seq. No.
Seq. ID
                   LIB3431-063-P1-K1-A7
                   BLASTN
Method
NCBI GI
                   g2773153
BLAST score
                   181
                   2.0e-97
E value
Match length
                   197
                   98
% identity
                   Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                   (Asr1) mRNA, complete cds
Seq. No.
                   403418
Seq. ID
                   LIB3431-063-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   q4973254
BLAST score
                   436
E value
                   4.0e-43
Match length
                   100
% identity
                   80
NCBI Description
                   (AF144386) thioredoxin f2 [Arabidopsis thaliana]
                   403419
Seq. No.
Seq. ID
                   LIB3431-063-P1-K1-A9
Method
                   BLASTN
NCBI GI
                   q3819198
BLAST score
                   67
E value
                   4.0e-29
                   95
Match length
% identity
                   93
NCBI Description
                  Hordeum vulgare partial mRNA; clone cMWG0676.rev
                   403420
Seq. No.
Seq. ID
                   LIB3431-063-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   664
E value
                   8.0e-70
Match length
                   143
% identity
                   88
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
```

E value

BLAST score

Match length

g2570511

2.0e-22

256

57

```
sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   403421
Seq. No.
                   LIB3431-063-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4220533
                   220 -
BLAST score
                   2.0e-18
E value
                   56
Match length
% identity
                   77
                   (AL035356) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
                   403422
Seq. No.
                   LIB3431-063-P1-K1-B11
Seq. ID
                   BLASTN.
Method
NCBI GI
                   g6015437
BLAST score
                   38
E value
                   1.0e-12
Match length
                   38
                   100
% identity
                   Homo sapiens PEX1 mRNA, complete cds
NCBI Description
Seq. No.
                   403423
                   LIB3431-063-P1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3929924
BLAST score
                   479
E value
                   4.0e-48
                   93
Match length
% identity
                   98
NCBI Description
                   (AB020502) catalase [Oryza sativa]
Seq. No.
                   403424
Seq. ID
                   LIB3431-063-P1-K1-B3
Method
                   BLASTX --
NCBI GI
                   q4103987
BLAST score
                   486
E value
                   6.0e-49
Match length
                   115
% identity
                   (AF030516) 5,10-methylenetetrahydrofolate
NCBI Description
                   dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase
                   [Pisum sativum] >gi_6002383_emb_CAB56756.1_ (AJ011589)
                   5,10-methylenetetrahydrofolate dehydrogenase:
                   5,10-methenyltetrahydrofolate cyclohydrolase [Pisum
                   sativum]
Seq. No.
                   403425
Seq. ID
                   LIB3431-063-P1-K1-B5
Method
                   BLASTX
```

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

```
% identity
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
NCBI Description
                   403426
Seq. No.
                   LIB3431-063-P1-K1-B6
Seq. ID
                   BLASTN
Method
                   g20177
NCBI GI
BLAST score
                   47
E value
                   1.0e-17
Match length
                   115
                   85
% identity
                   Rice cab1R gene for light harvesting chlorophyll
NCBI Description
                   a/b-binding protein
Seq. No.
                   403427
                   LIB3431-063-P1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3126854
BLAST score
                   434
E value
                   5.0e-43
Match length
                   84
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
                   403428
Seq. No.
Seq. ID
                   LIB3431-063-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   a5803266
BLAST score
                   425
E value
                   7.0e-42
Match length
                   84
% identity
                   (AP000399) ESTs AU078063(S15496), C97608(C60475),
NCBI Description
                   C28255(C60475) correspond to a region of the predicted
                   gene; similar to plastid transketolase 2 (Y15782) [Oryza
                   sativa]
. 4
                   403429
Seq. No.
Seq. ID
                   LIB3431-063-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   q2245120
BLAST score
                   372
E value
                   1.0e-35
Match length
                   121
                   60
% identity
NCBI Description
                   (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   403430
Seq. ID
                   LIB3431-063-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   q2264373
BLAST score
                   163
E value
                   1.0e-11
Match length
                   41
% identity
                   (AC002354) putative NAM/no apical meristem protein
NCBI Description
```

[Arabidopsis thaliana]

E value

7.0e-26

```
Seq. No.
                   403431
                   LIB3431-063-P1-K1-C12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g6015437
BLAST score
                   37
E value
                   2.0e-11
Match length
                   48
                   66
% identity .
NCBI Description Homo sapiens PEX1 mRNA, complete cds
                   403432
Seq. No.
Seq. ID
                   LIB3431-063-P1-K1-C3
Method
                   BLASTN
NCBI GI
                   g2305114
BLAST score
                   92
E value
                   1.0e-44
Match length
                   108
% identity
                   96
NCBI Description Oryza sativa ferredoxin mRNA, complete cds
Seq. No.
                   403433
Seq. ID
                   LIB3431-063-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   271
E value
                   1.0e-40
Match length
                   84
                   95
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403434
Seq. ID
                   LIB3431-063-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g3913018
BLAST score
                   547
E value
                   3.0e-56
Match length
                   112
% identity
                   95
                   FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                   aldolase [Oryza sativa]
Seq. No.
                 403435
Seq. ID
                   LIB3431-063-P1-K1-C8
Method
                   BLASTN
NCBI GI
                   g2570514
BLAST score
                   61
```

```
77
```

```
Match length
                  .95
% identity
NCBI Description Oryza sativa glycolate oxidase (GOX) mRNA, complete cds
                  403436
Seq. No.
                  LIB3431-063-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4038695
BLAST score
                  198
E value
                  3.0e-18
                  63
Match length
                  78
% identity
                  (AB020945) ribulose-1,5-bisphosphate carboxylase/oxygenase
NCBI Description
                  small subunit [Avena sativa]
Seq. No.
                  403437
                  LIB3431-063-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  518
E value
                  6.0e-53
Match length
                  99
% identity
                  95
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375_prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403438
Seq. ID
                  LIB3431-063-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q5734636
BLAST score
                  238
E value
                  5.0e-20
Match length
                  71
% identity
                  (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                  sativa]
Seq. No.
                  403439
Seq. ID
                  LIB3431-063-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q2407281
```

BLAST score 159 E value 3.0e-11 Match length 39 % identity

(AF017363) ribulose 1,5-bisphosphate carboxylase small NCBI Description

subunit [Oryza sativa]

Seq. No. 403440

Seq. ID LIB3431-063-P1-K1-D6

```
Method
                  BLASTX
NCBI GI
                  g6014934
BLAST score
                  540
E value
                  3.0e-55
Match length
                  118
% identity
                  81
                  DCL PROTEIN, CHLOROPLAST PRECURSOR (DEFECTIVE CHLOROPLASTS
NCBI Description
                  AND LEAVES PROTEIN) >gi_1305531 (U55219) defective
                  chloroplasts and leaves; required for chloroplast
                  development and palisade cell differentiation in leaves
                   [Lycopersicon esculentum] >gi 1323698 (U55278) DCL [Solanum
                  lycopersicum]
Seq. No.
                  403441
Seq. ID
                  LIB3431-063-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g3549665
BLAST score
                  175
E value
                  1.0e-12
Match length
                  37
% identity
NCBI Description
                   (AL031394) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  403442
Seq. ID
                  LIB3431-063-P1-K1-E11
Method -
                  BLASTX
NCBI GI
                  q3738329
BLAST score
                  257
E value
                  2.0e-22
Match length
                  65
% identity
                  75
NCBI Description
                   (AC005170) unknown protein [Arabidopsis thaliana]
                  403443
Seq. No.
Seq. ID
                  LIB3431-063-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  q451192
BLAST score
                  47
E value
                  1.0e-17
Match length
                  119
% identity
                  85
NCBI Description
                  Triticum aestivum (wali7) mRNA, 3' end, partial cds
                  403444
Seq. No.
Seq. ID
                  LIB3431-063-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g3914423
BLAST score
                  183
E value
                  8.0e-14
Match length
                  37
% identity
NCBI Description PROFILIN 4 > gi 2642324 (AF032370) profilin [Zea mays]
                  403445
Seq. No.
Seq. ID
                  LIB3431-063-P1-K1-E7
Method
                  BLASTN
```

g6015437

```
BLAST score
                  35
E value
                  2.0e-10
Match length
                  35
                  100
% identity
NCBI Description Homo sapiens PEX1 mRNA, complete cds
Seq. No.
                  403446
Seq. ID
                  LIB3431-063-P1-K1-E8
Method
                  BLASTX
                  g2182029
NCBI GI
BLAST score
                  522
E value
                  2.0e-53
Match length
                  99
                  96
% identity
NCBI Description (Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]
                  403447
Seq. No.
Seq. ID
                  LIB3431-063-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g473980
BLAST score
                  45
E value
                  1.0e-16
Match length
                  73
% identity
                  89
NCBI Description Rice mRNA, partial homologous to glycine-rich protein gene
Seq. No.
                  403448
Seq. ID
                  LIB3431-063-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2130069
                  788
BLAST score
E value
                  2.0e-84
Match length
                  143
% identity
                  99
NCBI Description
                  catalase (EC 1.11.1.6) catA - rice
                  >gi 1261858 dbj BAA06232 (D29966) catalase [Oryza sativa]
                  403449
Seq. No.
Seq. ID
                  LIB3431-063-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g2244867
BLAST score
                  314
E value
                  9.0e-29
Match length
                  156
% identity
                  40
NCBI Description
                  (Z97337) hydroxynitrile lyase like protein [Arabidopsis
                  thaliana]
Seq. No.
                  403450
Seq. ID
                  LIB3431-063-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2570515
BLAST score
                  568
E value
                  1.0e-58
Match length
                  121
                  93
% identity
                 (AF022740) glycolate oxidase [Oryza sativa]
NCBI Description
```

```
403451
Seq. No.
Seq. ID
                   LIB3431-063-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   g3953471
BLAST score
                   207
E value
                   3.0e-16
Match length
                   62
% identity
                   (AC002328) F2202.16 [Arabidopsis thaliana]
NCBI Description
                   403452
Seq. No.
Seq. ID
                   LIB3431-063-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g3075488
BLAST score
                   197
E value
                   2.0e-15
Match length
                   58
% identity
NCBI Description
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
Seq. No.
                   403453
Seq. ID
                   LIB3431-063-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   q5911907
BLAST score
                   337
E value
                   1.0e-31
Match length
                   118
% identity
                   56
NCBI Description
                   (AL117455) hypothetical protein [Homo sapiens]
                   403454
Seq. No.
Seq. ID
                   LIB3431-063-P1-K1-F5
Method
                   BLASTN
NCBI GI
                   g218171
BLAST score
                   90
E value
                   4.0e-43
Match length
                   113
% identity
                   96
NCBI Description
                  Oryza sativa mRNA for type I light-harvesting chlorophyll
                   a/b binding protein of photosystem II (LHCPII), complete
                   cds
                   403455
Seq. No.
Seq. ID
                  LIB3431-063-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1076724
BLAST score
                  586
E value
                   9.0e-61
Match length
                  125
% identity
                  84
NCBI Description
                  LHCI-680, photosystem I antenna protein - barley
                  >gi 666054 emb CAA59049 (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                   403456
                  LIB3431-063-P1-K1-F7
Seq. ID
```

BLAST score

```
BLASTN
Method
NCBI GI
                  g218154
BLAST score
                  39
E value
                   4.0e-13
Match length
                  59
                  92
% identity
                  Oryza sativa gene for cytoplasmic aldolase, complete cds,
NCBI Description
                  clone:Aldp,
                   403457
Seq. No.
                  LIB3431-063-P1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3126854
BLAST score
                  388
                  1.0e-37
E value
                  82
Match length
% identity
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   403458
                  LIB3431-063-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1184774
BLAST score
                  502
E value
                  8.0e-51
Match length
                  114
% identity
                  88
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                  GAPC3 [Zea mays]
Seq. No.
                   403459
                  LIB3431-063-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3913018
BLAST score
                  698
E value
                  7.0e-74
Match length
                  139
% identity
                   99
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (ALDP) >gi 218155 dbj BAA02730 (D13513) chloroplastic
                  aldolase [Oryza sativa]
Seq. No.
                   403460
                  LIB3431-063-P1-K1-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q11957
BLAST score
                  342
E value
                  0.0e + 00
Match length
                  362
% identity
                  99
NCBI Description Rice complete chloroplast genome
Seq. No.
                   403461
                  LIB3431-063-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3695005
```

```
E value
                  2.0e-62
Match length
                  145
                  89
% identity
                  (AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2
NCBI Description
                  [Zea mays]
Seq. No.
                  403462
Seq. ID
                  LIB3431-063-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  534
E value
                  7.0e-55
                  96
Match length
                  100
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir_RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403463
                  LIB3431-063-P1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1777375
BLAST score
                  527
E value
                  6.0e-54
Match length
                  105
% identity
                  99
                  (D78573) aspartate kinase-homoserine dehydrogenase [Oryza
NCBI Description
                  sativa]
Seq. No.
                  403464
Seq. ID
                  LIB3431-063-P1-K1-H2
                  BLASTX
Method
NCBI GI
                  q2688828
BLAST score
                  197
E value
                  3.0e-15
                  81
Match length
% identity
                  (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus
NCBI Description
                  armeniaca]
Seq. No.
                  403465
Seq. ID
                  LIB3431-063-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  741
E value
                  7.0e-79
Match length
                  140
% identity
                  (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
```

subunit [Oryza sativa]

```
403466
  Seq. No.
  Seq. ID
                    LIB3431-063-P1-K1-H4
  Method
                    BLASTX
  NCBI GI
                    g3832512
  BLAST score
                    374
                     5.0e-36
  E value
  Match length
                    110
  % identity
                     69
                     (AF097922) granule-bound glycogen (starch) synthase
  NCBI Description
                     [Astragalus membranaceus]
                     403467
  Seq. No.
  Seq. ID
                    LIB3431-063-P1-K1-H5
                    BLASTX
  Method
  NCBI GI
                    g131225
  BLAST score
                    179
                     2.0e-13
  E value
  Match length
                     59
  % identity
                    PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
  NCBI Description
                    V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein
                    precursor - barley >gi 167087 (M61146) photosystem I
                    hydrophobic protein [Hordeum vulgare]
Seq. No.
                     403468
  Seq. ID
                    LIB3431-063-P1-N1-A11
  Method
                    BLASTX
  NCBI GI
                    g2072555
  BLAST score
                    237
  E value
                    7.0e-20
  Match length
                     44
                     100
  % identity
                     (AF001396) metallothionein-like protein [Oryza sativa]
  NCBI Description
                    >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                    protein [Oryza sativa]
                    403469
  Seq. No.
                    LIB3431-063-P1-N1-A12
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    g3126854
  BLAST score
                    393
  E value
                    5.0e-38
  Match length
                    78
  % identity
                     (AF061577) chlorophyll a/b binding protein [Oryza sativa]
  NCBI Description
  Seq. No.
                    403470
                    LIB3431-063-P1-N1-A2
  Seq. ID
 Method
                    BLASTX
                    g132105
  NCBI GI
  BLAST score
                    508
  E value
                    2.0e-51
 Match length
                    91
                    100
  % identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
  NCBI Description
                     (RUBISCO SMALL SUBUNIT C) >gi 68094_pir__RKRZS9
```

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain

Match length

% identity

389 99

```
sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
 Seq. No.
                   403471
                   LIB3431-063-P1-N1-A3
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
 BLAST score
                   713
 E value
                   2.0e-75
Match length
                   131
                   99
 % identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                    (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4.\overline{1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208:dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf_ 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   403472
 Seq. No.
                   LIB3431-063-P1-N1-A4
 Seq. ID
 Method
                   BLASTX
                   g5541681
 NCBI GI
 BLAST score
                   202
                   9.0e-16
 E value
                   83
Match length
 % identity
                    (AL096859) putative protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                   403473
                   LIB3431-063-P1-N1-A5
 Seq. ID
                   BLASTX`
 Method
 NCBI GI
                   q548605
 BLAST score
                   570
                    9.0e-59
 E value
                                                                          ٠.,
                   127
 Match length
                   89
 % identity
                   PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 NCBI Description
                    (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                   >qi 539055 pir A48527 photosystem I protein psaK precursor
                    - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                    [Hordeum vulgare]
                    403474
 Seq. No.
 Seq. ID
                   LIB3431-063-P1-N1-A7
Method
                   BLASTN
 NCBI GI
                   g2773153
                   373
 BLAST score
                   0.0e + 00
 E value
```

precursor (clone pOSSS1139) - rice >gi_218208 dbj BAA00538_

carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

(D00643) small subunit of ribulose-1,5-bisphosphate

BLAST score

```
NCBI Description Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
                   403475
Seq. No.
Seq. ID
                   LIB3431-063-P1-N1-A8
Method
                   BLASTX
NCBI GI
                   g4973254
BLAST score
                   396
                   2.0e-38
E value
                   94
Match length
                   79
% identity
NCBI Description (AF144386) thioredoxin f2 [Arabidopsis thaliana]
                   403476
Seq. No.
Seq. ID
                   LIB3431-063-P1-N1-A9
Method
                   BLASTN
NCBI GI
                   g3819197
BLAST score
                   55
                   7.0e-22
E value
Match length
                   200
                   82
% identity
NCBI Description Hordeum vulgare partial mRNA; clone cMWG0676.uni
                   403477
Seq. No.
Seq. ID
                   LIB3431-063-P1-N1-B1
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   426
E value
                   7.0e-42
Match length
                   77
                   100
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf_ 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403478
Seq. ID
                   LIB3431-063-P1-N1-B10
Method
                   BLASTX
NCBI GI
                   q4544443
BLAST score
                   172
E value
                   3.0e-12
Match length
                   45
                   71
% identity
                   (AC006592) putative mitochondrial uncoupling protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   403479
Seq. ID
                   LIB3431-063-P1-N1-B11
Method
                   BLASTX
NCBI GI
                   q1076724
```

Seq. No.

```
4.0e-47
E value
Match length
                   89
% identity
                   LHCI-680, photosystem I antenna protein - barley
NCBI Description
                   >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                   antenna protein [Hordeum vulgare]
Seq. No.
                   403480
                   LIB3431-063-P1-N1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3929924
                   357
BLAST score
                   8.0e-34
E value
Match length
                   67
% identity
                   (AB020502) catalase [Oryza sativa]
NCBI Description
                   403481
Seq. No.
Seq. ID
                   LIB3431-063-P1-N1-B3
Method
                   BLASTX
NCBI GI
                   g4103987
BLAST score
                   486
E value
                   6.0e-49
Match length
                   115
% identity
NCBI Description
                   (AF030516) 5,10-methylenetetrahydrofolate
                   dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase
                   [Pisum sativum] >gi 6002383 emb CAB56756.1 (AJ011589)
                   5,10-methylenetetrahydrofolate dehydrogenase:
                   5,10-methenyltetrahydrofolate cyclohydrolase [Pisum
                   sativum]
Seq. No.
                   403482
Seq. ID
                   LIB3431-063-P1-N1-B5
Method
                   BLASTX
NCBI GI
                   g115793
BLAST score
                   229
E value
                   3.0e-23
Match length
                   65
% identity
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR
                   (CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_
                   (X63197) type III LHCII CAB precursor protein [Hordeum
                   vulgare]
Seq. No.
                   403483
Seq. ID
                   LIB3431-063-P1-N1-B8
Method
                   BLASTX
NCBI GI
                   q3126854
BLAST score
                   410
E value
                   4.0e-40
                   78
Match length
% identity
NCBI Description
                   (AF061577) chlorophyll a/b binding protein [Oryza sativa]
```

```
LIB3431-063-P1-N1-B9
Seq. ID
Method
                   BLASTN
                   g5803242
NCBI GI
BLAST score
                   388
E value
                   0.0e + 00
                   484
Match length
                   100
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
Seq. No.
                   403485
Seq. ID
                  LIB3431-063-P1-N1-C12
Method
                   BLASTX
NCBI GI
                   q6103011
BLAST score
                   478
                   5.0e-48
E value
                   104
Match length
% identity
                   46
                   (X84225) precursor of photosystem II subunit (22KDa)
NCBI Description
                   [Nicotiana tabacum]
Seq. No.
                   403486
Seq. ID
                   LIB3431-063-P1-N1-C3
Method
                   BLASTX
NCBI GI
                   g871931
BLAST score
                   220
E value
                   8.0e-18
Match length
                   59
% identity
                   71
NCBI Description (D30763) ferredoxin [Oryza sativa]
Seq. No.
                   403487
Seq. ID
                   LIB3431-063-P1-N1-C4
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   144
E value
                   5.0e-09
Match length
                   36
                   81
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403488
Seq. ID.
                   LIB3431-063-P1-N1-C9
Method
                   BLASTX
NCBI GI
                   q4098250
BLAST score
                   164
E value
                   3.0e-11
Match length
                   71
% identity
                   41
NCBI Description (U76611) similar to Solanum tuberosum ci21A gene product
```

E value

BLAST score

Match length

g902200

3.0e-26

62

182

, å,

```
encoded by the sequence presented in GenBank Accession
                   Number U76610 [Solanum tuberosum]
                   403489
Seq. No.
                   LIB3431-063-P1-N1-D11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g671740
                   473
BLAST score
E value
                   2.0e-47
                   86
Match length
                   100
% identity
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   403490
Seq. No.
                   LIB3431-063-P1-N1-D12
Seq. ID
                   BLASTN -
Method
NCBI GI
                   g2950394
BLAST score
                   35
                   5.0e-10
E value
                   51
Match length
% identity
                   92
NCBI Description Zea mays me gene, exons 1 to
                   403491
Seq. No.
Seq. ID
                   LIB3431-063-P1-N1-D2
Method
                   BLASTX
NCBI GI
                   q5734636
BLAST score
                   173
E value
                   3.0e-12
                   53
Match length
% identity
                   (AP000391) Similar to putative lipase (AC006232) [Oryza
NCBI Description
                   sativa]
Seq. No.
                   403492
Seq. ID
                   LIB3431-063-P1-N1-D6
Method
                   BLASTX
NCBI GI
                   q6014934
BLAST score
                   381
E value
                   1.0e-36
Match length
                   84
% identity
                   DCL PROTEIN, CHLOROPLAST PRECURSOR (DEFECTIVE CHLOROPLASTS
NCBI Description
                   AND LEAVES PROTEIN) >gi_1305531 (U55219) defective chloroplasts and leaves; required for chloroplast
                   development and palisade cell differentiation in leaves
                   [Lycopersicon esculentum] >gi_1323698 (U5,5278) DCL [Solanum
                   lycopersicum]
Seq. No.
                   403493
Seq. ID
                   LIB3431-063-P1-N1-D7
Method
                   BLASTN
```

Seq. ID

```
% identity
NCBI Description Z.mays complete chloroplast genome
                   403494
                  LIB3431-063-P1-N1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g451193
BLAST score
                  314
E value
                   2.0e-33
Match length
                  120
% identity
                   68
                   (L28008) wali7 [Triticum aestivum]
NCBI Description
                  >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]
Seq. No.
                   403495
                  LIB3431-063-P1-N1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1835731
BLAST score
                   438
E value
                   2.0e-43
Match length
                  102
% identity
                  85
NCBI Description
                   (U86018) photosystem II 10 kDa polypeptide [Oryza sativa]
                   403496
Seq. No.
Seq. ID
                  LIB3431-063-P1-N1-E8
Method
                  BLASTN
NCBI GI
                  q2182028
BLAST score
                  324
E value
                   0.0e + 00
Match length
                  324
                   100
% identity
NCBI Description Oryza sativa mRNA for shaggy-like kinase etha
                   403497
Seq. No.
Seq. ID
                  LIB3431-063-P1-N1-E9
Method
                  BLASTN
NCBI GI
                  q2331130
BLAST score
                  226
E value
                  1.0e-124
Match length
                  226
% identity
                  100
NCBI Description
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
Seq. No.
                  403498
Seq. ID
                  LIB3431-063-P1-N1-F10
Method
                  BLASTX
NCBI GI
                  g1705624
BLAST score
                  180
E value
                  4.0e-13
Match length
                  41
% identity
                  88
NCBI Description
                  CATALASE ISOZYME A (CAT-A)
                  403499
Seq. No.
```

LIB3431-063-P1-N1-F12

E value

6.0e-47

```
BLASTX
Method
NCBI GI
                   q2570515
BLAST score
                   159
                   9.0e-11
E value
Match length
                   34
                   97
% identity
NCBI Description
                   (AF022740) glycolate oxidase [Oryza sativa]
Seq. No.
                   403500
Seq. ID
                   LIB3431-063-P1-N1-F2
Method
                   BLASTX
NCBI GI
                   q3953471
BLAST score
                   207
E value
                   3.0e-16
Match length
                   62
% identity
NCBI Description
                   (AC002328) F2202.16 [Arabidopsis thaliana]
Seq. No.
                   403501
Seq. ID
                   LIB3431-063-P1-N1-F3
Method
                   BLASTX
NCBI GI
                   q3075488
BLAST score
                   227
E value
                   2.0e-18
Match length
                   44
% identity
                   (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
NCBI Description
Seq. No.
                   403502
Seq. ID
                  LIB3431-063-P1-N1-F5
Method
                  BLASTX
NCBI GI
                   q3036946
BLAST score
                   307
E value
                   4.0e-28
Match length
                   60
% identity
NCBI Description
                   (AB012637) light harvesting chlorophyll a/b-binding protein
                   [Nicotiana sylvestris]
Seq. No.
                   403503
Seq. ID
                  LIB3431-063-P1-N1-F6
Method
                  BLASTX
NCBI GI
                  q1076724
BLAST score
                  278
E value
                  1.0e-24
Match length
                  56
% identity
                  93
NCBI Description
                  LHCI-680, photosystem I antenna protein - barley
                  >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I
                  antenna protein [Hordeum vulgare]
Seq. No.
                   403504
Seq. ID
                  LIB3431-063-P1-N1-F7
Method
                  BLASTX
NCBI GI
                  g2407279
BLAST score
                  469
```

Seq. No.

```
Match length
                    96
% identity
                    95
NCBI Description
                    (AF017362) aldolase [Oryza sativa]
Seq. No.
                    403505
                    LIB3431-063-P1-N1-F9
Seq. ID
Method
                    BLASTX
NCBI GI
                    g115802
BLAST score
                    189
E value
                    3.0e-14
Match length
                    36
% identity
                    97
                    CHLOROPHYLL A-B BINDING PROTEIN 36 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-36) (LHCP) >gi_100311_pir__S21827 chlorophyll a/b-binding protein (cab-36) - common tobacco
                    >gi 19827 emb CAA41188 (X58230) chlorophyll a/b binding
                    protein [Nicotiana tabacum]
Seq. No.
                    403506
Seq. ID
                    LIB3431-063-P1-N1-G1
Method
                    BLASTX
NCBI GI
                    q120668
BLAST score
                    469
E value
                    7.0e-47
Match length
                    102
% identity
NCBI Description
                    GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_82399_pir__A24159 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
                    >gi 167044 (M36650) glyceraldehyde-3-phosphate
                    dehydrogenase [Hordeum vulgare] >gi 225347 prf 1301218A
                    dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var.
                    distichum]
Seq. No.
                    403507
Seq. ID
                    LIB3431-063-P1-N1-G10
Method
                    BLASTX
NCBI GI
                    q21839
BLAST score
                   595
E value
                    7.0e-62
Match length
                    118
% identity
                    (X57952) phosphoribulokinase [Triticum aestivum]
NCBI Description
Seq. No.
                    403508
Seq. ID
                    LIB3431-063-P1-N1-G11
Method
                   BLASTX
NCBI GI
                    q517500
BLAST score
                   273
E value
                    3.0e-24
Match length
                    68
% identity
NCBI Description
                    (M87435) precursor of the oxygen evolving complex 17 kDa
                   protein [Zea mays] >gi 444338 prf 1906386A photosystem II
                   OE17 protein [Pisum sativum]
```

NCBI Description

```
LIB3431-063-P1-N1-G12
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2407279
BLAST score
                   398
E value
                   1.0e-38
Match length
                   75
                   100
% identity
NCBI Description
                   (AF017362) aldolase [Oryza sativa]
Seq. No.
                   403510
                   LIB3431-063-P1-N1-G2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4138290
BLAST score
                   283
E value
                   3.0e-25
Match length
                   55
% identity
                   100
                   (AJ005841) thioredoxin M [Oryza sativa]
NCBI Description
Seq. No.
                   403511
Seq. ID
                   LIB3431-063-P1-N1-G7
Method
                   BLASTX
NCBI GI
                   g2191138
BLAST score
                   275
E value
                   3.0e-24
Match length
                   84
% identity
                   (AF007269) A IG002N01.18 gene product [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   403512
                   LIB3431-063-P1-N1-G8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   429
E value
                   3.0e-42
                   79
Match length
% identity
                   99
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403513
Seq. ID
                   LIB3431-063-P1-N1-H1
Method
                   BLASTX
NCBI GI
                   q693920
BLAST score
                   419
E value
                   5.0e-41
Match length
                   80
% identity
                   97
```

(U21113) chlorophyll a/b binding protein [Solanum

% identity

tuberosum]

```
Seq. No.
                   403514
                   LIB3431-063-P1-N1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q121291
BLAST score
                   295
E value
                   2.0e-30
Match length
                   79
                   90
% identity
                   GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT
NCBI Description
                   (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE)
                   (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE)
                   >gi 82596 pir S05079 glucose-1-phosphate
                   adenylyltransferase (EC 2.7.7.27) (clone AGA.1) - wheat
                   (fragment) >gi 21677 emb CAA32531 (X14348) ADP-glucose
                   pyrophosophorylase [Triticum aestīvum]
                   >gi 226873 prf 1609236A ADP glucose pyrophosphatase AGA.1
                   [Triticum aestivum]
Seq. No.
                   403515
Seq. ID
                   LIB3431-063-P1-N1-H12
Method
                   BLASTX
NCBI GI
                   q1777375
BLAST score
                   152
E value
                   6.0e-10
Match length
                   31
% identity
                   9.7
NCBI Description
                   (D78573) aspartate kinase-homoserine dehydrogenase [Oryza
                   sativa]
Seq. No.
                   403516
Seq. ID
                   LIB3431-063-P1-N1-H3
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   709
E value
                   5.0e-75
Match length
                   130
% identity
                   99
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403517
Seq. ID
                   LIB3431-063-P1-N1-H5
Method
                   BLASTX
NCBI GI
                   g131225
BLAST score
                   216
                   2.0e-17
E value
Match length
                   56
                   73
```

```
PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT
NCBI Description
                  V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein
                  precursor - barley >gi_167087 (M61146) photosystem I
                  hydrophobic protein [Hordeum vulgare]
                  403518
Seq. No.
Seq. ID
                  LIB3431-063-P1-N1-H6
Method
                  BLASTX
NCBI GI
                  g2462750
BLAST score
                  154
E value
                  4.0e-10
Match length
                  52
                  62
% identity
                   (AC002292) Highly similar to auxin-induced protein
NCBI Description
                   (aldo/keto reductase family) [Arabidopsis thaliana]
                  403519
Seq. No.
                  LIB3432-001-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q600771
BLAST score
                  198
E value
                  1.0e-15
Match length
                  63
% identity
                  68
NCBI Description (L35844) G protein alpha subunit [Oryza sativa]
                  403520
Seq. No.
                  LIB3432-002-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5002357
BLAST score
                  156
E value
                  6.0e-11
Match length
                  56
% identity
                  59
NCBI Description
                   (AF150957) heat-shock protein ClpP [Azospirillum
                  brasilense]
                  403521
Seq. No.
                  LIB3432-002-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2739382
BLAST score
                  215
E value
                  3.0e-17
Match length
                  141
% identity
NCBI Description
                   (AC002505) myosin heavy chain-like protein [Arabidopsis
                  thaliana]
Seq. No.
                  403522
                  LIB3432-003-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5263320
BLAST score
                  677
E value
                  3.0e-71
Match length
                  147
% identity
                  91
NCBI Description
                  (AC007727) Similar to gb M87339 replication factor C,
```

Seq. No.

403528

37-kDa subunit from Homo sapiens and is a member of PF_00004 ATPases associated with various cellular activities. [Arabidopsis thaliana]

```
403523
Seq. No.
Seq. ID
                   LIB3432-005-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g5912299
BLAST score
                   587
                   7.0e-61
E value
Match length
                   123
% identity
                   93
                   (AJ133787) gigantea homologue [Oryza sativa]
NCBI Description
                   403524
Seq. No.
Seq. ID
                   LIB3432-006-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   g871931
BLAST score
                   492
                   8.0e-50
E value
Match length
                   116
% identity
                   88
                   (D30763) ferredoxin [Oryza sativa]
NCBI Description
Seq. No.
                   403525
                   LIB3432-006-P1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2827524
BLAST score
                   215
E value
                   2.0e-17
Match length
                   44
                   77
% identity
                   (AL021633) predicted protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403526
Seq. ID
                   LIB3432-007-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   q1244566
BLAST score
                  <sup>-</sup>719
E value
                   3.0e-76
Match length
                   145
% identity
NCBI Description
                   (U39321) acetyl-CoA carboxylase [Triticum aestivum]
                   >gi 1588584 prf 2208491A Ac-CoA carboxylase [Triticum
                   aestivum]
Seq. No.
                   403527
Seq. ID
                   LIB3432-007-P1-K1-C1
Method
                   BLASTN
NCBI GI
                   q577352
BLAST score
                   55
E value
                   6.0e-22
Match length
                   148
% identity
                  Streptococcus equi M protein (emmSzW60) gene, complete cds
NCBI Description
```

Method

BLASTX

```
LIB3432-007-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g5230785
BLAST score
                   214
E value
                   5.0e-17
                   63
Match length
% identity
                   (AF107024) histone H1 WH1B.1 [Triticum aestivum]
NCBI Description
                   403529
Seq. No.
                   LIB3432-007-P1-K1-E12
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3417451
BLAST score
                   155
                   3.0e-10
E value
Match length
                   39
% identity
                   74
                   (AB013728) light-harvesting chlorophyll a/b-binding protein
NCBI Description
                   of photosystem II [Cryptomeria japonica]
                   403530
Seq. No.
                   LIB3432-007-P1-K1-E5
Seq. ID
Method-
                   BLASTX
NCBI GI
                   q3980378
BLAST score
                   373
                   1.0e-35
E value
Match length
                   140
% identity
                   55
                   (ACO04561) putative RNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   403531
Seq. No.
                   LIB3432-007-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g166835
BLAST score
                   623
E value
                   4.0e-65
                   135
Match length
                   89
% identity
                   (M86720) ribulose bisphosphate carboxylase/oxygenase
NCBI Description
                   activase [Arabidopsis thaliana] >gi 2642170 (AC003000)
                   Rubisco activase [Arabidopsis thaliana]
Seq. No.
                   403532
                   LIB3432-007-P1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3789952
BLAST score
                   562
E value
                   5.0e-58
Match length
                   112
% identity
                   93
NCBI Description
                   (AF094775) chlorophyll a/b-binding protein presursor [Oryza
                   sativa]
                   403533
Seq. No.
                   LIB3432-007-P1-K1-H6
Seq. ID
```

```
g3914603
 NCBI GI
 BLAST score
                    317
 E value
                    4.0e-29
                    145
Match length
                    50
 % identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE,
 NCBI Description
                    CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 1778414
                    (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase
                    activase [Oryza sativa]
                    403534
 Seq. No.
 Seq. ID
                    LIB3432-009-P1-K1-A2
 Method
                    BLASTX
 NCBI GI
                    q3367594
 BLAST score
                    194
                    1.0e-14
 E value
                    70
 Match length
                    53
 % identity
NCBI Description
                    (AL031135) putative protein [Arabidopsis thaliana]
 Seq. No.
                    403535
 Seq. ID
                    LIB3432-009-P1-K1-A7
 Method
                    BLASTX
 NCBI GI
                    q4574139
 BLAST score
                    159
 E value
                    2.0e-17
                    83
 Match length
 % identity
                    (AF073697) cysteine synthase [Oryza sativa]
 NCBI Description
 Seq. No.
                    403536
                    LIB3432-010-P1-K1-B11
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q940288
 BLAST score
                    381
 E value
                    1.0e-36
 Match length
                    137
% identity
                    57
                    (L43510) protein localized in the nucleoli of pea nuclei;
 NCBI Description
                    ORF; putative [Pisum sativum]
                    403537
 Seq. No.
 Seq. ID
                    LIB3432-010-P1-K1-G11
                    BLASTX
 Method
 NCBI GI
                    g606817
 BLAST score
                    329
 E value
                    2.0e-30
                    78
 Match length
 % identity
                    (U08404) carbonic anhydrase [Oryza sativa]
 NCBI Description
                    >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic
                    anhydrase 3 [Oryza sativa]
 Seq. No.
                    403538
 Seq. ID
                    LIB3432-010-P1-K1-G2
                    BLASTX
 Method
```

g2072555

E value

476.5

1.0e-17

```
BLAST score
                   215
                   4.0e-17
E value
Match length
                   44
                   91
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
                   403539
Seq. No.
Seq. ID
                   LIB3432-010-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g6041833
BLAST score
                   180
E value
                   5.0e-13
                   125
Match length
                   36
% identity
                   (AC009853) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403540
                   LIB3432-010-P1-K1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1353352
BLAST score
                   190
E value
                   1.0e-14
Match length
                   61
% identity
                   (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                   reinhardtii]
Seq. No.
                   403541
                   LIB3432-011-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2407281
BLAST score
                   680
E value
                   1.0e-71
Match length
                   139
% identity
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
NCBI Description
                   subunit [Oryza sativa]
Seq. No.
                   403542
                   LIB3432-011-P1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g733458
                   340
BLAST score
E value
                   6.0e-32
Match length
                   90
% identity
NCBI Description
                   (U23190) chlorophyll a/b-binding apoprotein CP24 precursor
                   [Zea mays]
Seq. No.
                   403543
Seq. ID
                   LIB3432-012-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g1632822
BLAST score
                   214
```

```
44
Match length
% identity
                   95
                   (Y08962) transmembrane protein [Oryza sativa] >gi 1667594
NCBI Description
                   (U77297) transmembrane protein [Oryza sativa]
                   403544
Seq. No.
Seq. ID
                  LIB3432-012-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g4056490
BLAST score
                  189
E value
                   2.0e-14
                  90
Match length
% identity
                   42
NCBI Description
                   (AC005896) hypothetical protein [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3432-012-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  g20155
BLAST score
                  65
E value
                   3.0e-28
Match length
                  85
% identity
                  94
NCBI Description
                  O.sativa random single-copy DNA fragment 12RG214R
Seq. No.
                   403546
Seq. ID
                  LIB3432-012-P1-K1-F3
Method
                  BLASTX
NCBI GI
                   g4662632
BLAST score
                  230
E value
                   6.0e-19
Match length
                  71
% identity
NCBI Description
                   (AC007267) unknown protein [Arabidopsis thaliana]
Seq. No.
                  403547
Seq. ID
                  LIB3432-012-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  q5257255
BLAST score
                  83
E value
                   1.0e-38
Match length
                  168
% identity
                  86
NCBI Description
                  Oryza sativa genomic DNA, chromosome 8, clone:P0026F07
                   403548
Seq. No.
Seq. ID
                  LIB3432-012-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q3885892
BLAST score
                  262
E value
                  1.0e-22
Match length
                  67
% identity
NCBI Description
                  (AF093634) photosystem-1 F subunit precursor [Oryza sativa]
Seq. No.
Seq. ID
                  LIB3432-012-P1-K1-H7
```

```
BLASTX
Method
NCBI GI
                   g4455680
                   150
BLAST score
                   4.0e-10
E value
Match length
                   66
                   47
% identity
                   (AL035472) putative prolyl tRNA synthetase [Mycobacterium
NCBI Description
                                                                          Seq. No.
                   403550
                  LIB3432-013-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2373403
BLAST score
                   157
E value
                   5.0e-11
Match length
                   42
% identity
NCBI Description
                   (D85193) similar to the membrane protein RD28 [Arabidopsis
                   thaliana]
                   403551
Seq. No.
Seq. ID
                  LIB3432-014-P1-K1-H6
Method
                  BLASTX
NCBI GI
                   q4006855
BLAST score
                   215
E value
                   2.0e-17
Match length
                   76
                   57
% identity
                   (Z99707) Cu2+-transporting ATPase-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   403552
Seq. No.
                  LIB3432-015-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1173347
BLAST score
                   618
E value
                   1.0e-64
Match length
                   120
% identity
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC
                   3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                   aestivum]
Seq. No.
                   403553
Seq. ID
                  LIB3432-015-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q2281115
BLAST score
                   631
E value
                   6.0e-66
Match length
                  154
% identity
                  76
NCBI Description
                   (AC002330) putative cullin-like 1 protein [Arabidopsis
```

thaliana]

Seq. ID

```
Seq. No.
                   403554
Seq. ID
                   LIB3432-016-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g1617197
BLAST score
                   275
E value
                   3.0e-24
                   71
Match length
% identity
                   75
NCBI Description
                   (Z72488) CP12 [Nicotiana tabacum]
Seq. No.
                   403555
Seq. ID
                   LIB3432-016-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   q2501189
BLAST score
                   192
E value
                   1.0e-14
Match length
                   82
                   56
% identity
                   THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR
NCBI Description
                   >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1
                   - maize >gi_596078 (U17350) thiamine biosynthetic enzyme
                   [Zea mays]
Seq. No.
                   403556
                   LIB3432-016-P1-K1-H6
Seq. ID
Method
                   BLASTX
                   g2072555
NCBI GI
BLAST score
                   233
                   2.0e-19
E value
Match length
                   44
% identity
                   98
NCBI Description
                   (AF001396) metallothionein-like protein [Oryza sativa]
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   403557
Seq. ID
                  LIB3432-017-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q2253092
BLAST score
                   196
                   3.0e-20
E value
Match length
                   68
% identity
                   66
NCBI Description
                   (Y14198) hypothetical protein [Spinacia oleracea]
                   403558
Seq. No.
Seq. ID
                  LIB3432-018-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q4587524
BLAST score
                   159
E value
                   1.0e-10
Match length
                  42
% identity
                   69
NCBI Description
                   (AC007060) T5I8.13 [Arabidopsis thaliana]
Seq. No.
                   403559
```

LIB3432-018-P1-K1-D2

```
BLASTX
Method
NCBI GI
                   g4567273
BLAST score
                   433
E value
                   9.0e-43
Match length
                   140
% identity
                   60
                   (AC006841) putative vacuolar proton ATPase subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   403560
                   LIB3432-019-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   479
E value
                   3.0e-48
Match length
                   109
                   85
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403561
Seq. ID
                   LIB3432-019-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   g2570497
BLAST score
                   206
E value
                   3.0e-16
Match length
                   123
% identity
NCBI Description
                   (AF022731) H protein subunit of glycine decarboxylase
                   [Oryza sativa]
Seq. No.
                   403562
Seq. ID
                   LIB3432-020-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g3281853
BLAST score
                   536
E value
                   7.0e-55
Match length
                   139
% identity
NCBI Description (AL031004) putative protein [Arabidopsis thaliana]
Seq. No.
                   403563
                   LIB3432-020-P1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4104056
BLAST score
                   279
E value
                   1.0e-24
Match length
                   62
% identity
```

NCBI Description (AF031194) S276 [Triticum aestivum]

```
403564
Seq. No.
                   LIB3432-020-P1-K1-D4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q5852170
BLAST score
                   108
                   7.0e-54
E value
Match length
                   179
% identity
                   89
                   Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC
NCBI Description
                   clone:t17804
                   403565
Seq. No.
                   LIB3432-020-P1-K1-D5
Seq. ID
Method
                   BLASTX
                   q1173347
NCBI GI
                   189
BLAST score
                   1.0e-14
E value
                   79
Match length
                   54
% identity
                   SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7) P2ASE)
                   >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC _
                   3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_
                   (X65540) sedoheptulose-1,7-bisphosphatase [Triticum
                   aestivum]
Seq. No.
                   403566
                   LIB3432-021-P1-K1-A2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q6063530
                   39
BLAST score
E value
                   5.0e-13
Match length
                   43
                   98
'% identity
NCBI Description
                  Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
Seq. No.
                   403567
Seq. ID
                   LIB3432-021-P1-K1-A3
Method
                   BLASTX
                   q6063542
NCBI GI
BLAST score
                   273
                   3.0e-24
E value
Match length
                   61
% identity
                   85
                   (APO00615) EST C74302(E30840) corresponds to a region of
NCBI Description
                   the predicted gene.; similar to glyceraldehyde-3-phosphate
                   dehydrogenase. (M64118) [Oryza sativa]
Seq. No.
                   403568
                   LIB3432-021-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   a115766
                   316
BLAST score
                   1.0e-29
E value
                   71
Match length
                   76
% identity
```

*3:

NCBI Description

```
CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCI TYPE II
  NCBI Description
                     CAB) >gi_82243_pir__S00442 chlorophyll a/b-binding protein
                     precursor - garden petunia >gi 169214 (M21317) chlorophyll
                    binding protein precursor [Petunia hybrida]
                     >gi_226259 prf__1503272A chlorophyll binding protein
                     [Petunia sp.]
Seq. No.
                     403569
  Seq. ID
                    LIB3432-022-P1-K1-E1
  Method
                    BLASTX
  NCBI GI
                     q166835
  BLAST score
                     464
  E value
                     1.0e-46
  Match length
                     92
  % identity
                     96
  NCBI Description
                     (M86720) ribulose bisphosphate carboxylase/oxygenase
                     activase [Arabidopsis thaliana] >gi 2642170 (AC003000)
                    Rubisco activase [Arabidopsis thaliana]
  Seq. No.
                     403570
  Seq. ID
                    LIB3432-023-P1-K1-H11
  Method
                    BLASTX
  NCBI GI
                    q2754849
  BLAST score
                     324
  E value
                     6.0e-30
  Match length
                     96
  % identity
                     68
                     (AF039000) putative serine-glyoxylate aminotransferase
  NCBI Description
                     [Fritillaria agrestis]
  Seq. No.
                     403571
                    LIB3432-024-P1-K1-B12
  Seq. ID
  Method
                    BLASTX
  NCBI GI
                    q132105
  BLAST score
                    183
  E value
                     6.0e-14
  Match length
                    59
  % identity
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
  NCBI Description
                     (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                    ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                     (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
  Seq. No.
                    403572
  Seq. ID
                    LIB3432-024-P1-K1-H5
  Method
                    BLASTX
  NCBI GI
                    q1353352
  BLAST score
                    191
  E value
                    1.0e-14
  Match length
                    57
  % identity
```

(U31975) alanine aminotransferase [Chlamydomonas

BLAST score

Match length

NCBI Description

% identity

E value

627

136 88

2.0e-65

reinhardtii] 403573 Seq. No. Seq. ID LIB3432-026-P1-K1-D2 Method BLASTN NCBI GI q2072554 BLAST score 142 E value 4.0e-74 Match length 166 98 % identity Oryza sativa metallothionein-like protein mRNA, complete NCBI Description 403574 Seq. No. Seq. ID LIB3432-026-P1-K1-H6 Method BLASTX q5912588 NCBI GI BLAST score 716 7.0e-76 E value Match length 152 % identity 86 (AJ249607) MGDG synthase A [Spinacia oleracea] NCBI Description 403575 Seq. No. LIB3432-028-P1-K1-A3 Seq. ID Method BLASTX NCBI GI q585551 BLAST score 236 3.0e-20 E value Match length 58 % identity NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) NCBI Description >gi_629798_pir__S43330 nucleoside-diphosphate kinase (EC 2.7.4.6) - rice >gi_303849_dbj_BAA03798_ (D16292) nucleoside diphosphate kinase [Oryza sativa] Seq. No. 403576 Seq. ID LIB3432-028-P1-K1-C11 Method BLASTX NCBI GI a5091509 BLAST score 816 E value 1.0e-87 Match length 147 % identity NCBI Description (AB023482) EST AU065533(C2174) corresponds to a region of the predicted gene.; Similar to Homo sapiens splicing factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa] Seq. No. 403577 LIB3432-028-P1-K1-D6 Seq. ID Method BLASTX NCBI GI q132105

RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR

NCBI GI

(RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

```
403578
  Seq. No.
  Seq. ID
                    LIB3432-028-P1-K1-G5
  Method
                    BLASTX
  NCBI GI
                     q729535
  BLAST score
                    160
                     9.0e-11
  E value
                     78
  Match length
                     46
  % identity
                    FERREDOXIN-THIOREDOXIN REDUCTASE, CATALYTIC CHAIN PRECURSOR
  NCBI Description
                     (FTR-C) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT B)
                     (FTR-B)
  Seq. No.
                     403579
  Seq. ID
                    LIB3432-028-P1-K1-H3
  Method
                    BLASTX
  NCBI GI
                     g1217967
  BLAST score
                     438
  E value
                     3.0e-43
  Match length .
                     124
  % identity
                     (X96431) high affinity sulphate transporter [Hordeum
  NCBI Description
                     vulgare]
                     403580
  Seq. No.
                     LIB3432-029-P1-K1-E3
  Seq. ID
  Method
                    BLASTN
                     g5803242
  NCBI GI
  BLAST score
                    221
E value
                     1.0e-121
  Match length
                     334
                     97
  % identity
  NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
                     403581
  Seq. No.
                    LIB3432-030-P1-K1-A1
  Seq. ID
  Method
                    BLASTN
  NCBI GI
                     g1835730
  BLAST score
                     129
  E value
                     3.0e-66
                    285
  Match length
  % identity
                    Oryza sativa photosystem II 10 kDa polypeptide mRNA,
  NCBI Description
                     complete cds
                     403582
  Seq. No.
                    LIB3432-030-P1-K1-A11
  Seq. ID
  Method
                    BLASTN
```

g1835730

403587

BLAST score

```
E value
                  1.0e-93
Match length
                  351
                  87
% identity
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
NCBI Description
                  complete cds
Seq. No.
                  403583
                  LIB3432-030-P1-K1-D4
Seq. ID
Method
                  BLASTX
                  g3413511
NCBI GI
BLAST score
                  256
                  2.0e-22
E value
Match length
                  77
% identity
                  (AJ000265) glucose-6-phosphate isomerase [Spinacia
NCBI Description
                  oleracea]
Seq. No.
                  403584
Seq. ID
                  LIB3432-032-P2-K1-G1
Method
                  BLASTN
NCBI GI
                  q4138731
BLAST score
                  44
E value
                  3.0e-15
Match length
                  166
% identity
                  28
NCBI Description
                  Zea mays mRNA for proline-rich protein
                  403585
Seq. No.
Seq. ID
                  LIB3432-032-P2-K1-H11
Method
                  BLASTX
NCBI GI
                  q2288969
BLAST score
                  182
E value
                  2.0e-19
Match length
                  120
% identity
NCBI Description
                  (Y12862) glutathione transferase [Zea mays]
                  403586
Seq. No.
Seq. ID
                  LIB3432-034-P2-K1-H12
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  563
E value
                  5.0e-58
Match length
                  122
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
```

NCBI GI

g132081

```
Seq. ID
                  LIB3432-034-P2-K1-H5
Method
                  BLASTX
NCBI GI
                  g5007084
BLAST score
                  696
                  1.0e-73
E value
Match length
                  133
% identity
                   (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
                  sativa]
                  403588
Seq. No.
Seq. ID
                  LIB3432-034-P2-K1-H6
Method
                  BLASTX
NCBI GI
                  q4895183
BLAST score
                  272
                  6.0e-24
E value
                  105
Match length
                   49
% identity
                   (AC007661) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  403589
Seq. No.
                  LIB3432-035-P2-K1-A2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g304219
BLAST score
                  70
E value
                  3.0e-31
Match length
                  173
                  86
% identity
                  Hordeum vulgare chloroplast photosystem I PSK-I subunit
NCBI Description
                  mRNA, complete cds
                  403590
Seq. No.
Seq. ID
                  LIB3432-035-P2-K1-A3
Method
                  BLASTX
NCBI GI
                  q3913018
BLAST score
                  819
E value
                  6.0e-88
Match length
                  163
                  96
% identity
NCBI Description
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
                   (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
Seq. No.
                  403591
Seq. ID
                  LIB3432-035-P2-K1-C7
Method
                  BLASTN
                  q4959460
NCBI GI
BLAST score
                  35
E value
                  2.0e-10
                  35
Match length
% identity
                  100
NCBI Description Zea mays RACB small GTP binding protein mRNA, complete cds
                  403592
Seq. No.
Seq. ID
                  LIB3432-035-P2-K1-G6
Method
                  BLASTX
```

Method

NCBI GI

BLASTX

g4582783

```
BLAST score
                   300
E value.
                   1.0e-27
Match length
                   82
% identity
                   76
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN PRECURSOR
                   (RUBISCO SMALL SUBUNIT) >gi_68093_pir__RKRZS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor - rice >gi_20341_emb_CAA30393_ (X07515) ribulose
                   bisphosphate carboxylase [Oryza sativa]
Seq. No.
                   403593
Seq. ID
                   LIB3432-035-P2-K1-H6
Method
                   BLASTX
NCBI GI
                   q1350986
BLAST score
                   592
                   2.0e-61
E value
Match length
                   115
                   99
% identity
NCBI Description
                   40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN)
                   >gi 483431_dbj BAA05059 (D26060) cyc07 [Oryza sativa]
Seq. No.
                   403594
Seq. ID
                   LIB3432-035-P2-K1-H8
Method
                   BLASTN
                   q473980
NCBI GI
BLAST score
                   44
                   7.0e-16
E value
                   56
Match length
                   93
% identity
                   Rice mRNA, partial homologous to glycine-rich protein gene
NCBI Description
Seq. No.
                   403595
                   LIB3432-037-P1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2293480
BLAST score
                   162
E value
                   4.0e-11
Match length
                   45
                   73
% identity
NCBI Description
                   (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                   403596
                   LIB3432-037-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2804280
BLAST score
                   653
E value
                   1.0e-68
Match length
                   136
% identity
                   (AB003687) 6-4 photolyase [Arabidopsis thaliana]
NCBI Description
                   >gi 3929918 dbj BAA34711 (AB017331) 6-4 photolyase
                   [Arabidopsis thaliana]
                   403597
Seq. No.
Seq. ID
                   LIB3432-037-P1-K1-E1
```

```
BLAST score
                   167
E value
                   3.0e-13
Match length
                   73
                   55
% identity
                   (AJ006752) starch synthase, isoform V [Vigna unguiculata]
NCBI Description
Seq. No.
                   403598
Seq. ID
                   LIB3432-037-P1-K1-E3
Method
                   BLASTX
                   g4850330
NCBI GI
BLAST score
                   332
E value
                   7.0e-31
Match length
                   63
% identity
                   100
                   (AB027123) cytochrome c oxidase subunit 5c [Oryza sativa]
NCBI Description
                   403599
Seq. No.
                   LIB3432-037-P1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2773154
BLAST score
                   217
                   6.0e-18
E value
Match length
                   71
                   62
% identity
NCBI Description
                   (AF039573) abscisic acid- and stress-inducible protein
                   [Oryza sativa]
                   403600
Seq. No.
                   LIB3432-039-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3122572
BLAST score
                   519
E value
                   8.0e-53
Match length
                   148
% identity
                   67
                   NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I
                   SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato
                   >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial
                   complex I subunit [Solanum tuberosum]
                   403601
Seq. No.
Seq. ID
                   LIB3432-039-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g5091509
BLAST score
                   719
E value
                   3.0e-76
Match length
                   134
                   100
% identity
                   (AB023482) EST AU065533(C2174) corresponds to a region of
NCBI Description
                   the predicted gene.; Similar to Homo sapiens splicing
                   factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa]
```

Seq. No. Seq. ID LIB3432-039-P1-K1-H12 ·

403602

Method **BLASTN**

E value

3.0e-50

```
NCBI GI
                    g1661159
 BLAST score
                    232
 E value
                    1.0e-128
                    232
 Match length
                    100
 % identity
                    Oryza sativa chlorophyll a/b binding protein (kcdl895)
 NCBI Description
                    mRNA, complete cds
 Seq. No.
                    403603
 Seq. ID
                    LIB3432-039-P1-K1-H4
 Method
                    BLASTX
 NCBI GI
                    g733456
 BLAST score
                    527
 E value
                    9.0e-54
                    122
 Match length
 % identity
                    84
                    (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
 NCBI Description
                    [Zea mays]
 Seq. No.
                    403604
 Seq. ID
                    LIB3432-040-P1-K1-A12
 Method
                    BLASTN
 NCBI GI
                    g2072554
 BLAST score
                    36
 E value
                    1.0e-10
 Match length
                    36
 % identity
                    100
NCBI Description
                    Oryza sativa metallothionein-like protein mRNA, complete
 Seq. No.
                    403605
 Seq. ID
                    LIB3432-040-P1-K1-A6
 Method
                    BLASTN
 NCBI GI
                    q6103440
 BLAST score
                    50
 E value
                    8.0e-20
 Match length
                    50
 % identity
                    100
 NCBI Description
                    Oryza sativa metallothionein-like protein (ML2) mRNA,
                    complete cds
 Seq. No.
                    403606
 Seq. ID
                    LIB3432-040-P1-K1-D10
 Method
                    BLASTX
 NCBI GI
                    g22240
 BLAST score
                    307
 E value
                    2.0e-28
                    79
 Match length
 % identity
 NCBI Description
                    (X07157) GADPH (383 AA) [Zea mays]
                    403607
 Seq. No.
 Seq. ID
                    LIB3432-040-P1-K1-G8
 Method
                    BLASTX
 NCBI GI
                    g132105
 BLAST score
                    495
```

```
91
Match length
                  98
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
                  403608
Seq. No.
                  LIB3432-041-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g671740
                  542
BLAST score
E value
                  2.0e-55
Match length
                  98
% identity
                  100
                  (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                  construct]
Seq. No.
                  403609
Seq. ID
                  LIB3432-042-P2-K1-A1
Method
                  BLASTN
NCBI GI
                  q1835730
BLAST score
                  219
E value
                  1.0e-120
Match length
                  235
% identity
                  98
                  Oryza sativa photosystem II 10 kDa polypeptide mRNA,
NCBI Description
                  complete cds
Seq. No.
                  403610
Seq. ID
                  LIB3432-042-P2-K1-A10
Method
                  BLASTX
NCBI GI
                  q733456
BLAST score
                  343
E value
                  4.0e-32
Match length
                  66
% identity
                  (U23189) chlorophyll a/b-binding apoprotein CP26 precursor
NCBI Description
                  [Zea mays]
Seq. No.
                  403611
Seq. ID
                  LIB3432-042-P2-K1-A12
Method
                  BLASTX
NCBI GI
                  q3789952
BLAST score
                  575
E value
                  1.0e-59
Match length
                  108
% identity
                  (AF094775) chlorophyll a/b-binding protein presursor [Oryza
NCBI Description
                  sativa]
```

Seq. ID

403617

LIB3432-042-P2-K1-C11

```
LIB3432-042-P2-K1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2662310
BLAST score
                   219
                   3.0e-18
E value
Match length
                   66
% identity
NCBI Description
                   (AB009307) bpw1 [Hordeum vulgare]
Seq. No.
                   403613
                  LIB3432-042-P2-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3643607
BLAST score
                   260
E value
                   8.0e-23
Match length
                   62
% identity
NCBI Description
                   (AC005395) unknown protein [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   LIB3432-042-P2-K1-B3
Method
                   BLASTX
NCBI GI
                   q2129675
BLAST score
                   555
E value
                   4.0e-57
Match length .
                   122 .
                   89
% identity
NCBI Description
                  probable chlorophyll synthetase G4 - Arabidopsis thaliana
                  >gi 972938 (U19382) putative chlorophyll synthetase
                   [Arabidopsis thaliana] >gi 3068709 (AF049236) putative
                   chlorophyll synthetase [Arabidopsis thaliana]
Seq. No.
                   403615
Seq. ID
                  LIB3432-042-P2-K1-B4
Method
                   BLASTN
NCBI GI
                   q167086
BLAST score
                   52
E value
                   2.0e-20
Match length
                   148
% identity
NCBI Description
                  Hordeum vulgare photosystem I protein (PSI-L) mRNA,
                   complete cds
                   403616
Seq. No.
Seq. ID
                  LIB3432-042-P2-K1-B7
Method
                  BLASTX
NCBI GI
                   q82080
BLAST score
                   200
E value
                   7.0e-16
Match length
                  72
                  60
% identity
                  chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                  >gi_226872_prf__1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
```

```
Method
                  BLASTX
NCBI GI
                  g1168537
BLAST score
                   448
E value
                  1.0e-44
Match length
                  96
% identity
                  89
NCBI Description
                  ASPARTIC PROTEINASE PRECURSOR >gi 82458 pir JS0732
                  aspartic proteinase (EC 3.4.23.-) - rice
                  >gi 218143_dbj_BAA02242_ (D12777) aspartic proteinase
                   [Oryza sativa]
Seq. No.
                  403618
Seq. ID
                  LIB3432-042-P2-K1-C5
Method
                  BLASTX
NCBI GI
                  g4557093
BLAST score
                  188
E value
                   6.0e-14
Match length
                  46
                  78
% identity
NCBI Description (AF001136) zinc finger protein [Pinus radiata]
                  403619
Seq. No.
Seq. ID
                  LIB3432-042-P2-K1-C9
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  455
E value
                  2.0e-45
Match length
                  92
% identity
                  91
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{\text{EC}} 4\overline{.1}.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403620
Seq. ID
                  LIB3432-042-P2-K1-D1
Method
                  BLASTX
NCBI GI
                  g3540182
BLAST score
                  182
E value
                  3.0e-15
                  77
Match length
% identity
NCBI Description (AC004122) Unknown protein [Arabidopsis thaliana]
                  403621
Seq. No.
Seq. ID
                  LIB3432-042-P2-K1-D11
Method
                  BLASTX
NCBI GI
                  g2407281
BLAST score
                  337
E value
                  7.0e-33
Match length .
                  78
% identity
                  89
```

```
NCBI Description
                   (AF017363) ribulose 1,5-bisphosphate carboxylase small
                   subunit [Oryza sativa]
                   403622
Seq. No.
                   LIB3432-042-P2-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1808694
BLAST score
                   480
E value
                   2.0e-48
                   109
Match length
                   87
% identity
                   (Y10787) hypothetical protein [Sporobolus stapfianus]
NCBI Description
Seq. No.
                   403623
Seq. ID
                   LIB3432-042-P2-K1-D9
                   BLASTX
Method
NCBI GI
                   g4204267
BLAST score
                   341
E value
                   3.0e-32
Match length
                   94
% identity
                   (AC005223) 55585 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403624
Seq. ID
                   LIB3432-042-P2-K1-E10
Method
                   BLASTX
NCBI GI
                   g2130082
BLAST score
                   338
E value
                   2.0e-31
Match length
                   157
                   49
% identity
                   protein kinase Xa21 (EC 2.7.1.-) - rice >gi_1122443
NCBI Description
                   (U37133) receptor kinase-like protein [Oryza sativa]
                   >gi 2586085 (U72723) receptor kinase-like protein [Oryza
                   longistaminata] >gi 1586408 prf 2203451A receptor
                   kinase-like protein [Oryza sativa]
                   403625
Seq. No.
                   LIB3432-042-P2-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g549063
BLAST score
                   339
E value
                   3.0e - 32
Match length
                   67
                   97
% identity
NCBI Description
                   TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                   >gi_1072464_pir__A38958 IgE-dependent histamine-releasing
factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626)
                   21kd polypeptide [Oryza sativa]
Seq. No.
                   403626
Seq. ID
                   LIB3432-042-P2-K1-E4
Method
                   BLASTX
NCBI GI
                   g2072555
BLAST score
                   237
E value
                   1.0e-19
Match length
                   44
```

```
% identity
                  (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                  >gi 6103441 gb AAF03603.1 (AF147786) metallothionein-like
                  protein [Oryza sativa]
Seq. No.
                  403627
Seq. ID
                  LIB3432-042-P2-K1-F11
Method
                  BLASTX
NCBI GI
                  g2497746
BLAST score
                  191
                  5.0e-15
E value
Match length
                  37
                  100
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2)
NCBI Description
                  >qi 951334 (U31766) lipid transfer protein precursor [Oryza
                  sativa]
                  403628
Seq. No.
Seq. ID
                  LIB3432-042-P2-K1-F4
Method
                  BLASTX
NCBI GI
                  g4006893
                  170
BLAST score
E value
                  2.0e-12
Match length
                  54
% identity
                  54
                 (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
NCBI Description
                  403629
Seq. No.
Seq. ID
                  LIB3432-042-P2-K1-F5
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  490
E value
                  8.0e-50
Match length
                  92
% identity
                  97
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208_dbj_BAA00538
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi 226375 prf 1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403630
Seq. ID
                  LIB3432-042-P2-K1-F6
Method
                  BLASTN
NCBI GI
                  q6041757
BLAST score
                  122
E value
                  5.0e-62
Match length
                  307
                  85
% identity
                  Genomic Sequence For Oryza sativa Clone 10P20, Lemont
NCBI Description
                  Strain, Complete Sequence, complete sequence
```

```
LIB3432-042-P2-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   a3212852
BLAST score
                   329
                   9.0e-31
E value
Match length
                   111
% identity
NCBI Description
                   (AC004005) unknown protein [Arabidopsis thaliana]
                   403632
Seq. No.
Seq. ID
                   LIB3432-042-P2-K1-G4
Method
                   BLASTX
NCBI GI
                   q82080
BLAST score
                   533
E value
                   2.0e-54
                   131
Match length
                   74
% identity
                   chlorophyll a/b-binding protein type III precursor - tomato
NCBI Description
                   >gi 226872 prf__1609235A chlorophyll a/b binding protein
                   [Lycopersicon esculentum]
                   403633
Seq. No.
Seq. ID
                   LIB3432-042-P2-K1-G5
Method
                   BLASTN
NCBI GI
                   q4733953
BLAST score
                   36
                   9.0e-11
E value
                   72
Match length
                   88
% identity
                   Arabidopsis thaliana chromosome I BAC F13011 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   403634
                   LIB3432-042-P2-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115772
BLAST score
                   571
                   4.0e-59
E value
                   114
Match length
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
NCBI Description
                   CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108_
                   (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                   [Oryza sativa]
Seq. No.
                   403635
Seq. ID
                   LIB3432-042-P2-K1-H2
Method
                   BLASTX
NCBI GI
                   q2072727
BLAST score
                   425
                   3.0e-42
E value
Match length
                   82
% identity
                   (Y12595) Fd-GOGAT protein [Oryza sativa]
NCBI Description
```

403636

Seq. No.

```
LIB3432-042-P2-K1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                   g132105
BLAST score
                   492
                   1.0e-49
E value
                   122
Match length
                   80
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi 68094 pir RKRZS9
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
                   403637
Seq. No.
Seq. ID
                   LIB3432-042-P2-K1-H4
Method
                   BLASTX
NCBI GI
                   g6006853
BLAST score
                   464
E value
                   2.0e-46
Match length
                   126
% identity
                   (AC009540) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Seq. ID
                   LIB3432-042-P2-K1-H6
Method
                   BLASTN
NCBI GI
                   g596077
BLAST score
                   47
E value
                   5.0e-18
Match length
                   79
                   91
% identity
                   Zea mays thiamine biosynthetic enzyme (thi1-1) mRNA,
NCBI Description
                   complete cds
Seq. No.
                   403639
Seq. ID
                   LIB3432-042-P2-K1-H7
Method
                   BLASTX
NCBI GI
                   g132105
BLAST score
                   558
E value
                   1.0e-57
Match length
                   103
                   98
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf 1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
```

Match length

```
Seq. ID
                   LIB3432-043-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g3582333
BLAST score
                   147
                   7.0e-10
E value
                   57
Match length
                   58
% identity
NCBI Description
                   (AC005496) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   403641
                   LIB3432-043-P1-K1-H12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g6063530
BLAST score
                   402
E value
                   0.0e + 00
Match length
                   414
% identity
                   99
NCBI Description
                   Oryza sativa genomic DNA, chromosome 3, clone:P0043E01
Seq. No.
                   403642
Seq. ID
                   LIB3432-043-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   q1929998
BLAST score
                   333
E value
                   3.0e - 31
Match length
                   89
                   78
% identity
NCBI Description
                   (U77463) NADPH-dependent HC-toxin reductase [Hordeum
                   vulgare]
Seq. No.
                   403643
Seq. ID
                   LIB3432-044-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   q2570511
BLAST score
                   280
E value
                   6.0e-25
Match length
                   110
% identity
NCBI Description
                   (AF022738) chlorophyll a-b binding protein [Oryza sativa]
Seq. No.
                   403644
Seq. ID
                   LIB3432-044-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   q435942
BLAST score
                   383
E value
                   5.0e-37
Match length
                   107
% identity
                   71
NCBI Description
                   (U04295) DNA-binding factor of bZIP class [Oryza sativa]
                   403645
Seq. No.
Seq. ID
                  LIB3432-044-P1-K1-G1
Method
                  BLASTX
NCBI GI
                   q3885884
BLAST score
                  371
E value
                   1.0e-35
```

```
% identity
                   (AF093630) 60S ribosomal protein L21 [Oryza sativa]
NCBI Description
                  403646
Seq. ID
                  LIB3432-044-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g5912424
BLAST score
                  512
E value
                  5.0e-52
Match length
                  150
% identity
                  71
                  (AJ242970) BTF3b-like factor [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  403647
                  LIB3432-045-P1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3367536
BLAST score
                  296
E value
                   5.0e-27
                  77
Match length
                  77
% identity
NCBI Description
                   (AC004392) Contains similarity to symbiosis-related like
                  protein F1N20.80 gi_2961343 from A. thaliana BAC
                  gb AL022140. EST gb T04695 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   403648
                  LIB3432-045-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g804973
BLAST score
                  147
E value
                   3.0e-09
Match length
                   48
% identity
NCBI Description (X81376) L-ascorbate peroxidase [Capsicum annuum]
Seq. No.
                   403649
Seq. ID
                  LIB3432-045-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q4056502
BLAST score
                  414
                  1.0e-40
E value
                  105
Match length
% identity
NCBI Description (AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
Seq. No.
                  403650
                  LIB3432-045-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2911358
BLAST score
                  521
E value
                  5.0e-53
Match length
                  142
% identity
                  70
NCBI Description
                  (AF041043) NADPH HC toxin reductase [Zea mays]
```

```
Seq. ID
                    LIB3432-046-P1-K1-F7
 Method
                    BLASTX
 NCBI GI
                    g132105
 BLAST score
                    749
 E value
                    9.0e-80
 Match length
                    159
 % identity
                    90
 NCBI Description
                    RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                    (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                    precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                    (D00643) small subunit of ribulose-1,5-bisphosphate
                    carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                    ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                    sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                    carboxylase S [Oryza sativa]
                    403652
 Seq. No.
 Seq. ID
                    LIB3432-047-P2-K11-G6
 Method
                    BLASTN
 NCBI GI
                    g6103440
 BLAST score
                    246
 E value
                    1.0e-136
 Match length
                    277
                    98
 % identity
                    Oryza sativa metallothionein-like protein (ML2) mRNA,
 NCBI Description
                    complete cds
 Seq. No.
                    403653
                    LIB3432-048-P2-K1-D6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g4469011
 BLAST score
                    392
                    5.0e-38
 E value
 Match length
                    103
 % identity
 NCBI Description
                     (AL035602) carbohydrate kinase-like protein [Arabidopsis
                    thaliana]
                    403654
 Seq. No.
                    LIB3432-048-P2-K1-E3
Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3786009
 BLAST score
                    401
                    3.0e-39
 E value
 Match length
                    103
 % identity
                    (AC005499) unknown protein [Arabidopsis thaliana]
 NCBI Description
 Seq. No.
                    403655
                    LIB3432-048-P2-K1-F12
 Seq. ID
 Method
                    BLASTN
                    g5670155
 NCBI GI
 BLAST score
                    58
 E value
                    3.0e-24
 Match length
                    58
```

100

% identity

```
NCBI Description
                    Oryza sativa subsp. japonica BAC clone 34K24, complete
                    sequence
                    403656
 Seq. No.
                    LIB3432-048-P2-K1-F6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3126854
 BLAST score
                    247
_E value
                                                     915
                    5.0e-26
 Match length
                    77
 % identity
                    (AF061577) chlorophyll a/b binding protein [Oryza sativa]
 NCBI Description
                    403657
 Seq. No.
 Seq. ID
                    LIB3432-049-P1-K1-C3
 Method
                    BLASTN
                    g218154
 NCBI GI
 BLAST score
                    77
 E value
                    4.0e-35
 Match length
                    77
                    100
 % identity
                    Oryza sativa gene for cytoplasmic aldolase, complete cds,
 NCBI Description
                    clone:Aldp
                    403658
 Seq. No.
 Seq. ID
                    LIB3432-049-P1-K1-E8
 Method
                    BLASTX
 NCBI GI
                    a115772
 BLAST score
                    170
                    1.0e-12
 E value
 Match length
                    37
                    97
 % identity
                    CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I
 NCBI Description
                    CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding
                    protein 1R precursor - rice >gi_20178_emb_CAA32108
                    (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235)
                    [Oryza sativa]
                    403659
 Seq. No.
 Seq. ID
                    LIB3432-049-P1-K1-H9
 Method
                    BLASTX
 NCBI GI
                    q2342683
 BLAST score
                    161
                    3.0e-11
 E value
 Match length
                    42
 % identity
 NCBI Description
                    (AC000106) Contains similarity to Bos beta-mannosidase
                    (gb_U46067). [Arabidopsis thaliana]
                    403660
 Seq. No.
                    LIB3432-050-P1-K1-A2
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g132105
 BLAST score
                    155
 E value
                    8.0e-11
 Match length
                    50
                  :~ 68
 % identity
```

```
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
                  ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                  sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                  carboxylase S [Oryza sativa]
Seq. No.
                  403661
Seq. ID
                  LIB3432-050-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q4115379
BLAST score
                  254
                  9.0e-22
E value
Match length
                  116
% identity
                  45
                  (AC005967) putative carbonyl reductase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  403662
Seq. ID
                  LIB3432-050-P1-K1-E3
Method
                  BLASTX
                  g2754849
NCBI GI
BLAST score
                  227
E value
                  3.0e-19
Match length
                  52
                  85
% identity
NCBI Description
                  (AF039000) putative serine-glyoxylate aminotransferase
                  [Fritillaria agrestis]
Seq. No.
                  403663
Seq. ID
                  LIB3432-051-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  g4158220
BLAST score
                  45
E value
                  3.0e-16
Match length
                  49
% identity
NCBI Description Oryza sativa mRNA for reversibly glycosylated polypeptide
Seq. No.
                  403664
Seq. ID
                  LIB3432-051-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g132105
BLAST score
                  168
E value
                  3.0e-12
Match length
                  50
% identity
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
                  (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                  ribulose-bisphosphate carboxylase (\overline{\text{EC 4.1.1.39}}) small chain
                  precursor (clone pOSSS1139) - rice >gi 218208 dbj BAA00538_
                  (D00643) small subunit of ribulose-1,5-bisphosphate
                  carboxylase (RuBPC) [Oryza sativa] >gi 2407283 (AF017364)
```

ribulose 1,5-bisphosphate carboxylase small subunit [Oryza

NCBI Description

```
carboxylase S [Oryza sativa]
                   403665
Seq. No.
                  LIB3432-051-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4519671
BLAST score
                  353
E value
                   3.0e - 33
Match length
                  127
% identity
NCBI Description
                   (AB017693) transfactor [Nicotiana tabacum]
                   403666
Seq. No.
Seq. ID
                  LIB3432-051-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q3913641
BLAST score
                  290
E value
                  2.0e-26
Match length
                  63
                  92
.% identity
                  FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
NCBI Description
                   (D-FRUCTOSE-1, 6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi_3041777_dbj_BAA25423_ (AB007194)
                  fructose-1,6-bisphosphatase [Oryza sativa]
Seq. No.
                  403667
                  LIB3432-051-P1-K1-G8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3885891
BLAST score
                  79
E value
                  8.0e-37
Match length
                  114
                  93
% identity
NCBI Description
                  Oryza sativa photosystem-1 F subunit precursor (PSI-F)
                  mRNA, complete cds
Seq. No.
                  403668
Seq. ID
                  LIB3432-052-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g2921158
BLAST score
                  228
E value
                  9.0e-19
Match length
                  73
% identity
                  66
NCBI Description
                  (AF022909) ClpC [Arabidopsis thaliana]
Seq. No.
                  403669
Seq. ID
                  LIB3432-052-P1-K1-F9
Method
                  BLASTX
                  g5306242
NCBI GI
BLAST score
                  204
E value
                  5.0e-16
Match length
                  46
                  78
% identity
```

sativa] >qi 226375 prf 1508256A ribulose bisphosphate

(AC006438) unknown protein [Arabidopsis thaliana]

BLAST score

```
403670
Seq. No.
Seq. ID
                   LIB3432-053-P1-K1-H1
                   BLASTX
Method
NCBI GI
                   g671740
                   602
BLAST score
                   2.0e-62
E value
Match length
                   110
% identity
                   100
                   (X84730) ribulose-bisphosphate carboxylase [synthetic
NCBI Description
                   construct]
                   403671
Seq. No.
Seq. ID
                   LIB3432-056-P1-K1-H2
Method
                   BLASTX
                   g4467116
NCBI GI
BLAST score
                   154
                   3.0e-10
E value
                   74
Match length
% identity
                   (AL035538) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   403672
Seq. No.
                   LIB3432-057-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q439879
BLAST score
                   300
E value
                   4.0e-27
Match length
                   124
% identity
                   54
NCBI Description
                   (L15194) [Golden delicious apple fruit expressed mRNA,
                   complete cds.], gene product [Malus domestica]
Seq. No.
                   403673
Seq. ID
                   LIB3432-057-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   q2369766
BLAST score
                   168
E value
                   9.0e-12
Match length
                   84
% identity
                   42
NCBI Description (AJ001304) hypothetical protein [Citrus x paradisi]
Seq. No.
                   403674
                   LIB3432-057-P1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1483563
BLAST score
                   247
E value
                   6.0e-27
Match length
                   65
% identity
NCBI Description (X99825) leucine aminopeptidase [Petroselinum crispum]
Seq. No.
                   403675
                   LIB3432-058-P1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2708741
```

E value

1.0e-43

```
1.0e-62
  E value
                     159
  Match length
                     72
  % identity
                     (AC003952) hypothetical protein [Arabidopsis thaliana]
  NCBI Description
                     403676
  Seq. No.
  Seq. ID
                     LIB3432-058-P1-K1-C10
  Method
                     BLASTN
  NCBI GI
                     g21843
  BLAST score
                     43
  E value
                     4.0e-15
                     73
  Match length
  % identity
                     90
                     Wheat PsbO mRNA for 33kDa oxygen evolving protein of
  NCBI Description
                     photosystem II
                     403677
  Seq. No.
  Seq. ID
                     LIB3432-058-P1-K1-G5
  Method
                     BLASTX
  NCBI GI
                     g1805654
  BLAST score
                     265
E value
                     5.0e-23
  Match length
                     101
  % identity
                     49
  NCBI Description
                     (X99972) calmodulin-stimulated calcium-ATPase [Brassica
                     oleracea]
                     403678
  Seq. No.
                     LIB3432-058-P1-K1-G6
  Seq. ID
  Method
                     BLASTX
  NCBI GI
                     g2765081
  BLAST score
                     636
  E value
                     5.0e-71
  Match length
                     154
  % identity
                     84
  NCBI Description
                     (Y10557) g5bf [Arabidopsis thaliana]
  Seq. No.
                     403679
  Seq. ID
                     LIB3432-058-P1-K1-H5
  Method
                     BLASTX
  NCBI GI
                     g548605
  BLAST score
                     401
  E value
                     2.0e-39
  Match length
                     90
                     89
  % identity
  NCBI Description
                     PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
                     (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K)
                     >gi 539055 pir A48527 photosystem I protein psaK precursor
                     - barley >gi 304220 (L12707) photosystem I PSI-K subunit
                     [Hordeum vulgare]
  Seq. No.
                     403680
  Seq. ID
                     LIB3432-059-P1-K1-A8
  Method
                     BLASTX
  NCBI GI
                     g3914466
  BLAST score
                     440
```

E value

Match length

1.0e-63 127

```
Match length
                  90
% identity
                  91
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
NCBI Description
                  (PSI-N) >gi 2981214 (AF052429) photosystem I complex PsaN
                  subunit precursor [Zea mays]
Seq. No.
                  403681
Seq. ID
                  LIB3432-059-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q2388911
BLAST score
                  159
E value
                  6.0e-11
Match length
                  62
                  50
% identity
                  (Z98974) hypothetical PSU1-like protein
NCBI Description
                  [Schizosaccharomyces pombe]
Seq. No.
                  403682
                  LIB3432-059-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4006872
BLAST score
                  182
E value
                  1.0e-13
Match length
                  50
% identity
                  (Z99707) methionyl aminopeptidase-like protein [Arabidopsis ]
NCBI Description
                  thaliana]
Seq. No.
                  403683
                  LIB3432-059-P1-K1-G2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3913018
BLAST score
                  657
                  5.0e-69
E value
Match length
                  137
                  98
% identity
                  FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR
NCBI Description
                  (ALDP) >gi 218155 dbj BAA02730_ (D13513) chloroplastic
                  aldolase [Oryza sativa]
                  403684
Seq. No.
                  LIB3432-059-P1-K1-H1
Seq. ID
                  BLASTX
Method
                  g4760483
NCBI GI
BLAST score
                  506
E value
                  1.0e-51
                  104
Match length
                  94
% identity
                  (AB026731) monodehydroascorbate reductase [Oryza sativa]
NCBI Description
                  403685
Seq. No.
                  LIB3432-059-P1-K1-H12
Seq. ID
                  BLASTN
Method
                  g2072554
NCBI GI
BLAST score
                  124
```

NCBI Description

```
% identity
                   Oryza sativa metallothionein-like protein mRNA, complete
NCBI Description
Seq. No.
                   403686
Seq. ID
                   LIB3432-059-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   g134022
BLAST score
                   143
E value
                   2.0e-09
Match length
                   30
                   100
% identity
                   CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi 70914 pir R3RZ8
NCBI Description
                   ribosomal protein S8 - rice chloroplast >gi_12022_emb_CAA33931_ (X15901) ribosomal protein S8
                   [Oryza sativa] >gi_226643_prf__1603356BT ribosomal protein
                   S8 [Oryza sativa]
                   403687
Seq. No.
Seq. ID
                   LIB3432-059-P1-K1-H6
Method
                   BLASTX
                   q2072555
NCBI GI
BLAST score
                   183
E value
                   6.0e-14
Match length
                   35
% identity
                   (AF001396) metallothionein-like protein [Oryza sativa]
NCBI Description
                   >gi_6103441_gb_AAF03603.1_ (AF147786) metallothionein-like
                   protein [Oryza sativa]
Seq. No.
                   403688
                   LIB3432-060-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132105
                   387
BLAST score
E value
                   1.0e-37
Match length
                   98
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9
                   ribulose-bisphosphate carboxy\overline{l}ase (\overline{E}C 4.\overline{1}.1.39) small chain
                   precursor (clone pOSSS1139) - rice >gi 218208 dbj_BAA00538_
                   (D00643) small subunit of ribulose-1,5-bisphosphate
                   carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364)
                   ribulose 1,5-bisphosphate carboxylase small subunit [Oryza
                   sativa] >gi_226375_prf__1508256A ribulose bisphosphate
                   carboxylase S [Oryza sativa]
Seq. No.
                   403689
                   LIB3432-060-P1-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   a733456
BLAST score
                   650
E value
                   4.0e-68
                   145
Match length
% identity
```

(U23189) chlorophyll a/b-binding apoprotein CP26 precursor

Method

BLASTN

```
[Zea mays]
Seq. No.
                   403690
                   LIB3432-060-P1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3789954
BLAST score
                   685
E value
                   3.0e-72
Match length
                   132
% identity
                   96
                   (AF094776) chlorophyll a/b-binding protein precursor [Oryza
NCBI Description
                   sativa]
Seq. No.
                   403691
                   LIB3432-060-P1-K1-H6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3868756
BLAST score
                   509
E value
                   6.0e-52
Match length
                   95
% identity
NCBI Description
                   (D86611) catalase [Oryza sativa]
Seq. No.
                   403692
Seq. ID
                   LIB3433-001-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   q2739366
BLAST score
                   167
E value
                   6.0e-12
Match length
                   67
% identity
                   49
NCBI Description
                   (AC002505) SF16 like protein [Arabidopsis thaliana]
                   403693
Seq. No.
Seq. ID
                   LIB3433-001-P1-K1-D6
Method
                   BLASTN
                   g1815625
NCBI GI
BLAST score
                   75
E value
                   3.0e-34
Match length
                   135
% identity
                   89
NCBI Description
                   Oryza sativa metallothionein-like type 1 (OsMT-1) mRNA,
                   complete cds
Seq. No.
                   403694
Seq. ID
                   LIB3433-001-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g3540195
BLAST score
                   250
E value
                   2.0e-21
Match length
                   108
% identity
NCBI Description
                   (AC004260) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   403695
                   LIB3433-001-P1-K1-H10
Seq. ID
```

Match length

```
NCBI GI
                   q556557
                   70
BLAST score
                   6.0e-31
E value
                   246
Match length
                   82
% identity
                   Rice mRNA for homologue of Tat binding protein, complete
NCBI Description
Seq. No.
                   403696
                   LIB3433-001-P1-K1-H6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2984709
BLAST score
                   181
E value
                   1.0e-13
Match length
                   71
% identity
                   (AF053468) DnaJ-related protein ZMDJ1 [Zea mays]
NCBI Description
Seq. No.
                   403697
Seq. ID
                   LIB3433-003-Q6-K6-C4
Method
                   BLASTX
NCBI GI
                   q4335755
BLAST score
                   143
E value
                   5.0e-09
Match length
                   66
% identity
                   (AC006284) putative hydroxyproline-rich glycoprotein
NCBI Description
                   [Arabidopsis thaliana]
                   403698
Seq. No.
Seq. ID
                   LIB3433-003-Q6-K6-D6
Method
                   BLASTX
NCBI GI
                   g121528
BLAST score
                   307
E value
                   4.0e-28
Match length
                   106
% identity
                   63
                   GOS9 PROTEIN >gi_100683 pir S19115 GOS9 protein - rice
NCBI Description
                   >gi 20242 emb CAA36189 (X51909) GOS9 [Oryza sativa]
Seq. No.
                   403699
Seq. ID
                   LIB3433-003-Q6-K6-E11
Method
                   BLASTX
NCBI GI
                   q5360230
BLAST score
                   475
E value
                   9.0e-48
Match length
                   99
% identity
                   (AB015287) Ran [Oryza sativa]
NCBI Description
                   403700
Seq. No.
Seq. ID
                   LIB3433-003-Q6-K6-E5
Method
                   BLASTX
NCBI GI
                   q3236242
BLAST score
                   336
                   3.0e-31
E value
```

```
% identity
                   (AC004684) putative ribosomal protein L36 [Arabidopsis
NCBI Description
                  thaliana]
                  403701
Seq. No.
Seq. ID
                  LIB3433-003-Q6-K6-E9
Method
                  BLASTN
NCBI GI
                  g2624325
BLAST score
                  88
                  7.0e-42
E value
                  238
Match length
% identity
                  Oryza sativa mRNA for glycine-rich RNA-binding protein
NCBI Description
                   (OsGRP1)
                  403702
Seq. No.
Seq. ID
                  LIB3433-003-Q6-K6-F3
Method
                  BLASTN
NCBI GI
                  q5441872
BLAST score
                  319
E value
                  1.0e-179
Match length
                  354
% identity
                  98
                  Oryza sativa genomic DNA, chromosome 2, clone:P0437H03
NCBI Description
                  (contig a)
                  403703
Seq. No.
                  LIB3433-003-Q6-K6-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4835235
BLAST score
                  242
                  2.0e-20
E value
Match length
                  132
% identity
                  45
                  (AL049862) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  403704
                  LIB3433-003-Q6-K6-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4103987
BLAST score
                  289
E value
                  4.0e-26
                  96
Match length
% identity
                   (AF030516) 5,10-methylenetetrahydrofolate
NCBI Description
                  dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase
                  [Pisum sativum] >gi_6002383_emb_CAB56756.1_ (AJ011589)
                  5,10-methylenetetrahydrofolate dehydrogenase:
                  5,10-methenyltetrahydrofolate cyclohydrolase [Pisum
                  sativum]
                  403705
Seq. No.
Seq. ID
                  LIB3433-003-Q6-K6-H5
Method
                  BLASTX
NCBI GI
                  g2293480
                  209
BLAST score
```

9.0e-17

E value

Match length

```
52
Match length
% identity
                  81
NCBI Description
                   (AF011331) glycine-rich protein [Oryza sativa]
Seq. No.
                  403706
                  LIB3433-005-Q6-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1729971
BLAST score
                  199
E value
                   9.0e-16
                  71
Match length
% identity
                  59
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                  rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                   403707
Seq. No.
Seq. ID
                  LIB3433-005-Q6-K1-E4
Method
                  BLASTN
NCBI GI
                  q5902929
BLAST score
                  78
E value
                   5.0e-36
Match length
                  212
% identity
NCBI Description
                  Oryza sativa mRNA for small GTP-binding protein OsRac3,
                  complete cds
Seq. No.
                  403708
Seq. ID
                  LIB3433-006-Q6-K6-A4
Method
                  BLASTX
NCBI GI
                  g2982251
BLAST score
                  169
E value
                  1.0e-11
Match length
                  101
% identity
NCBI Description
                   (AF051208) putative RNA-binding protein [Picea mariana]
                  403709
Seq. No.
Seq. ID
                  LIB3433-006-06-K6-B4
Method
                  BLASTX
NCBI GI
                  q5734720
BLAST score
                  304
E value
                  1.0e-27
Match length
                  123
% identity
NCBI Description
                   (AC008075) Contains PF 01426 BAH (bromo-adjacent homology)
                  domain. ESTs gb_N96349, gb_T42710, gb_H77084, gb_AA395147
                  and gb_AA605500 come from this gene. [Arabidopsis thaliana]
                  403710
Seq. No.
Seq. ID
                  LIB3433-006-Q6-K6-B6
Method
                  BLASTX
NCBI GI
                  q1084461
BLAST score
                  384
E value
                  6.0e-37
```

```
% identity
                  RCc3 protein - rice >gi 786132 (L27208) RCc3 [Oryza sativa]
NCBI Description
Seq. No.
                  403711
                  LIB3433-006-Q6-K6-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g283008
BLAST score
                  775
E value
                  7.0e-83
Match length
                  144
                  99
% identity
                  sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                  >qi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                  403712
Seq. No.
Seq. ID
                  LIB3433-006-Q6-K6-C8
Method
                  BLASTX
NCBI GI
                  q82308
BLAST score
                  239
E value
                  2.0e-26
Match length
                  66
% identity
                  80
                  myb protein 308 - garden snapdragon
NCBI Description
Seq. No.
                  403713
                  LIB3433-006-Q6-K6-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3121849
BLAST score
                  167
E value
                  1.0e-20
Match length
                  65
% identity
                  89
                  CALMODULIN >gi 1773321 (U79736) calmodulin [Helianthus
NCBI Description
                  annuus]
Seq. No.
                  403714
                  LIB3433-006-Q6-K6-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1084461
BLAST score
                  271
                  6.0e-24
E value
Match length
                  93
% identity
                  62
NCBI Description RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]
Seq. No.
                  403715
Seq. ID
                  LIB3433-006-Q6-K6-D7
Method
                  BLASTX
NCBI GI
                  q4850384
BLAST score
                  469
                  5.0e-47
E value
Match length
                  114
% identity
                  74
                  (AC007357) F3F19.3 [Arabidopsis thaliana]
NCBI Description
```

403716

Seq. No.

```
LIB3433-006-Q6-K6-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3660467
BLAST score
                  341
E value
                  5.0e-32
Match length
                  89
% identity
NCBI Description
                   (AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis
                  thaliana]
Seq. No.
                  403717
Seq. ID
                  LIB3433-006-Q6-K6-E11
Method
                  BLASTX
NCBI GI
                  q2407287
BLAST score
                  188
E value
                  4.0e-14
Match length
                  59
% identity
                   (AF017366) metallothionein-like protein [Oryza sativa]
NCBI Description
Seq. No.
                  403718
                  LIB3433-006-Q6-K6-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q21839
BLAST score
                  469
E value
                  4.0e-47
                  108
Match length
% identity
                  (X57952) phosphoribulokinase [Triticum aestivum]
NCBI Description
Seq. No.
                  403719
                  LIB3433-006-Q6-K6-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g548770
BLAST score
                  511
E value
                  5.0e-52
Match length
                  121
% identity
                  83
                  60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal
NCBI Description
                  protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630)
ribosomal protein L3 [Oryza sativa]
Seq. No.
                  403720
                  LIB3433-006-Q6-K6-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g5042453
BLAST score
                  646
E value
                  1.0e-67
Match length
                  126
% identity
NCBI Description
                   (AC007789) putative pathogenesis related protein [Oryza
                  sativa]
Seq. No.
                  403721
                  LIB3433-006-Q6-K6-E9
Seq. ID
Method
                  BLASTN
```

g170784

NCBI GI

NCBI Description

thaliana]

```
BLAST score .
E value
                   4.0e-13
Match length
                   71
                   89
% identity
NCBI Description Wheat ubiquitin carrier protein (UBC1) mRNA, complete cds
Seq. No.
                   403722
Seq. ID
                   LIB3433-006-Q6-K6-F3
Method
                   BLASTX
NCBI GI
                   g5360230
BLAST score
                   751
E value
                   4.0e-80
Match length
                   141
% identity
                   98
NCBI Description
                  (AB015287) Ran [Oryza sativa]
                   403723
Seq. No.
Seq. ID
                   LIB3433-006-Q6-K6-H4
Method
                   BLASTN-
NCBI GI
                   q5803242
BLAST score
                   353
E value
                   0.0e+00
Match length
                   353
% identity
                   100
                  Oryza sativa genomic DNA, chromosome 6, clone:P0535G04
NCBI Description
                   403724
Seq. No.
                   LIB3433-007-Q6-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                   g218140
BLAST score
                   74
                   2.0e-33
E value
Match length
                   274
                   88
% identity
NCBI Description Rice mRNA abundantly expressed at microspore stage
Seq. No.
                   403725
                   LIB3433-008-Q6-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3935169
BLAST score
                   170
E value
                   5.0e-12
Match length
                   69
% identity
                   59
                   (AC004557) F17L21.12 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403726
Seq. ID
                  LIB3433-011-Q6-K1-A7
Method
                  BLASTX
NCBI GI
                  q3212879
BLAST score
                   611
E value
                   1.0e-63
Match length
                   141
% identity
                   (AC004005) putative ribosomal protein L7 [Arabidopsis
```

Seq. ID

```
403727
  Seq. No.
                    LIB3433-011-Q6-K1-C4
  Seq. ID
 Method
                    BLASTX
  NCBI GI
                    g1705735
  BLAST score
                    403
                    3.0e-39
  E value
                    79
 Match length
                    96
  % identity
 NCBI Description
                    CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 11 (CDPK 11)
                    >gi 1362175 pir__S56651 probable calcium-dependent protein
                    kinase (clone OSCPK11) - rice >gi_587500_emb_CAA57156
                     (X81393) calcium-dependent protein kinase [Oryza sativa]
  Seq. No.
                    403728
  Seq. ID
                    LIB3433-011-Q6-K1-F2
  Method
                    BLASTX
  NCBI GI
                    q4731316
  BLAST score
                    187
- E value
                    2.0e-14
 Match length
                    49
                    76
  % identity
                    (AF120093) elongation factor 1-alpha [Nicotiana tabacum]
 NCBI Description
                    403729
  Seq. No.
  Seq. ID
                    LIB3433-012-Q6-K1-A11
 Method
                    BLASTN
 NCBI GI
                    q3282393
  BLAST score
                    313
                    1.0e-176
  E value
 Match length
                    395
                    95
  % identity
 NCBI Description Oryza sativa aie2 mRNA, partial cds
                    403730
  Seq. No.
                    LIB3433-012-Q6-K1-B3
  Seq. ID
 Method
                    BLASTX
- NCBI GI
                    g3914557
  BLAST score
                    176
  E value
                    9.0e-13
 Match length
                    36
                    100
  % identity
                    RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED
 NCBI Description
                    PROTEIN) >gi 1155265 (U40219) possible apospory-associated
                    protein [Pennisetum ciliare]
  Seq. No.
                    403731
                    LIB3433-013-Q6-K1-D11
  Seq. ID
 Method
                    BLASTN
  NCBI GI
                    g19052
  BLAST score
                    51
  E value
                    1.0e-19
 Match length
                    111
                    87
  % identity
  NCBI Description H.vulgare Mybl gene
 Seq. No.
                    403732
```

LIB3433-014-Q6-K1-A2

E value

1.0e-44

```
Method
                   BLASTX
NCBI GI
                   g2865175
BLAST score
                   268
                   4.0e-36
E value
Match length
                   114
                   68
% identity
NCBI Description
                   (AB010945) AtRerlA [Arabidopsis thaliana]
                   >gi 4914434_emb_CAB43637.1_ (AL050351) AtRer1A [Arabidopsis
                   thaliana]
                   403733
Seq. No.
Seq. ID
                   LIB3433-014-Q6-K1-H12
Method
                   BLASTX
NCBI GI
                   q1899025
BLAST score
                   186
                   5.0e-26
E value
Match length
                   91
                   66
% identity
NCBI Description
                   (U28215) hexokinase 2 [Arabidopsis thaliana] >gi 3687232
                   (AC005169) hexokinase [Arabidopsis thaliana]
Seq. No.
                   403734
                   LIB3433-015-Q6-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q388260
BLAST score
                   338
E value
                   9.0e-32
Match length
                   114
% identity
                   67
NCBI Description
                   (X62457) H1-1flk [Arabidopsis thaliana]
Seq. No.
                   403735
Seq. ID
                   LIB3433-015-Q6-K1-A9
Method
                   BLASTN
NCBI GI
                   q3821780
BLAST score
                   36
E value
                   8.0e-11
Match length
                   36
% identity
                   100
NCBI Description
                  Xenopus laevis cDNA clone 27A6-1
Seq. No.
                   403736
Seq. ID
                   LIB3433-015-Q6-K1-B4
Method
                   BLASTX
NCBI GI
                   q4512712
BLAST score
                   204
E value
                   2.0e-16
Match length
                   108
% identity
                   45
NCBI Description
                   (AC006569) unknown protein [Arabidopsis thaliana]
                   403737
Seq. No.
Seq. ID
                   LIB3433-015-Q6-K1-B6
Method
                   BLASTX
NCBI GI
                   q4097342
BLAST score
                   450
```

Seq. ID

```
Match length
                  84
                  49
% identity
NCBI Description (U57640) Bowman-Birk type trypsin inhibitor [Oryza sativa]
                  403738
Seq. No.
Seq. ID
                  LIB3433-015-Q6-K1-B7
Method
                  BLASTX
NCBI GI
                  g4406810
BLAST score
                  339
E value
                  6.0e-32
                  90
Match length
                  64
% identity
NCBI Description (AC006201) unknown protein [Arabidopsis thaliana]
                  403739
Seq. No.
Seq. ID
                  LIB3433-015-Q6-K1-B8
                  BLASTX
Method
NCBI GI
                  g2431769
                  217
BLAST score
E value
                  1.0e-17
Match length
                  60
                  73
% identity
NCBI Description (U62752) acidic ribosomal protein Pla [Zea mays]
Seq. No.
                  403740
                  LIB3433-015-Q6-K1-C10
Seq. ID
Method '
                  BLASTN
NCBI GI
                  g4097153
BLAST score
                  63
E value
                  7.0e-27
                  107
Match length
                  89
% identity
NCBI Description
                  Oryza sativa type 1 metallothionein-like (rgMT-1) gene,
                  complete cds
Seq. No.
                  403741
Seq. ID
                  LIB3433-015-Q6-K1-C3
Method
                  BLASTX
NCBI GI
                  q4850330
BLAST score
                  321
E value
                  1.0e-29
Match length
                  63
% identity
NCBI Description (AB027123) cytochrome c oxidase subunit 5c [Oryza sativa]
Seq. No.
                  403742
                  LIB3433-015-Q6-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q505136
BLAST score
                  159
E value
                  1.0e-12
Match length
                  54
% identity
NCBI Description
                  (D30794) ferredoxin [Oryza sativa]
Seq. No.
                  403743
```

LIB3433-015-Q6-K1-D3

E value

1.0e-79

```
Method
                   BLASTX
                   q2760839
NCBI GI
BLAST score
                   284
E value
                   2.0e-25
                   90
Match length
% identity
                   (AC003105) putative receptor kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403744
Seq. ID
                   LIB3433-015-Q6-K1-E4
Method
                   BLASTX
NCBI GI
                   q3257095
BLAST score
                   190
E value
                   3.0e-14
Match length
                   122
% identity
                   (AP000003) 840aa long hypothetical cell division control
NCBI Description
                   protein (transitional endoplasmic reticulum ATPase)
                   [Pyrococcus horikoshii]
                   403745
Seq. No.
Seq. ID
                   LIB3433-015-Q6-K1-E5
Method
                   BLASTX
NCBI GI
                   q2244940
BLAST score
                   260
E value
                   1.0e-22
Match length
                   124
% identity
                  (Z97339) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403746
                   LIB3433-015-Q6-K1-E6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4176421
BLAST score
                   36
E value
                   9.0e-11
Match length
                   44
% identity
                   Oryza sativa rpl12-1 gene for chloroplast ribosomal protein
NCBI Description
                   L12, complete cds
Seq. No.
                   403747
Seq. ID
                   LIB3433-015-Q6-K1-E7
Method
                   BLASTX
NCBI GI
                   q2407287
BLAST score
                   188
E value
                   4.0e-14
Match length
                  . 59
% identity
NCBI Description (AF017366) metallothionein-like protein [Oryza sativa]
Seq. No.
                   403748
Seq. ID
                   LIB3433-015-Q6-K6-A2
Method
                   BLASTX
NCBI GI
                   q2895866
BLAST score
                   749
```

Match length

```
Match length
                   169
% identity
                   89
NCBI Description
                   (AF045770) methylmalonate semi-aldehyde dehydrogenase
                   [Oryza sativa]
                   403749
Seq. No.
Seq. ID
                   LIB3433-015-Q6-K6-H2
Method
                   BLASTX
NCBI GI
                   g2995990
BLAST score
                   298
E value
                   9.0e-27
Match length
                   125
% identity
NCBI Description
                   (AF053746) dormancy-associated protein [Arabidopsis
                   thaliana] >gi 2995992 (AF053747) dormancy-associated
                  protein [Arabidopsis thaliana]
                   403750
Seq. No.
Seq. ID
                  LIB3433-015-Q6-K7-E3
Method
                  BLASTX
NCBI GI
                   q4512685
BLAST score
                   268
E value
                   2.0e-23
Match length
                  130
% identity
                  44
                   (AC006931) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087)
                  hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   403751
Seq. ID
                  LIB3433-015-Q6-K7-H11
Method
                  BLASTX
                   g2293480
NCBI GI
BLAST score
                   265
E value
                   6.0e-26
Match length
                   73
% identity
                   88
                   (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
                   403752
Seq. No.
Seq. ID
                  LIB3433-016-Q6-K6-C11
Method
                  BLASTN
NCBI GI
                   g2773153
BLAST score
                   272
                   1.0e-151
E value
                   369
Match length
% identity
                   93
NCBI Description
                  Oryza sativa abscisic acid- and stress-inducible protein
                   (Asr1) mRNA, complete cds
                   403753
Seq. No.
                  LIB3433-016-Q6-K6-C4
Seq. ID
Method
                  BLASTX
                  q4371292
NCBI GI
                   208
BLAST score
                   1.0e-16
E value
```

NCBI GI

```
% identity
                   (AC006260) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403754
Seq. ID
                   LIB3433-016-Q6-K6-C6
Method
                   BLASTX
NCBI GI
                   g231924
BLAST score
                   242
E value
                   2.0e-20
Match length
                   53
% identity
                   85
                  CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC18I)
NCBI Description
                   403755
Seq. No.
Seq. ID
                   LIB3433-016-Q6-K6-E10
Method
                   BLASTX
NCBI GI
                   q5679842
BLAST score
                   241
E value
                   2.0e-20
Match length
                   93
                   60
% identity
                   (AJ243961) 11332.6 [Oryza sativa]
NCBI Description
Seq. No.
                   403756
                   LIB3433-016-Q6-K6-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2662310
BLAST score
                   273
E value
                   2.0e-25
Match length
                   77
% identity
                   82
NCBI Description
                  (AB009307) bpw1 [Hordeum vulgare]
                   403757
Seq. No.
Seq. ID
                   LIB3433-017-Q6-K1-A2
Method
                   BLASTX
                   g2668744
NCBI GI
BLAST score
                   605
                   6.0e-63
E value
Match length
                   112
                   100
% identity
NCBI Description
                   (AF034946) ubiquitin conjugating enzyme [Zea mays]
                   403758
Seq. No.
Seq. ID
                   LIB3433-017-Q6-K1-G4
Method
                   BLASTN
NCBI GI
                   q6016845
BLAST score
                   121
E value
                   1.0e-61
Match length
                   141
                   96
% identity
NCBI Description
                  Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
                   403759
Seq. No.
Seq. ID
                   LIB3433-017-Q6-K1-H2
Method
                   BLASTX
```

g2388906

NCBI Description

```
BLAST score
                  211
E value
                  9.0e-17
Match length
                  112
% identity
                  38
NCBI Description (Z98974) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  403760
                  LIB3433-017-Q6-K1-H4
Seq. ID
Method
                  BLASTN .
NCBI GI
                  g6016845
BLAST score
                  60
E value
                  5.0e-25
Match length
                  83
                  93
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                  403761
                  LIB3433-017-Q6-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g121528
BLAST score
                  292
                  7.0e-28
E value
                  111
Match length
% identity
                  66
NCBI Description
                  GOS9 PROTEIN >gi 100683 pir S19115 GOS9 protein - rice
                  >gi 20242 emb CAA36189 (X51909) GOS9 [Oryza sativa]
Seq. No.
                  403762
Seq. ID
                  LIB3433-018-Q6-K6-D4
Method
                  BLASTX
NCBI GI
                  g2429292
BLAST score
                  197
E value
                  3.0e-15
Match length
                  117
% identity
                  45
NCBI Description (AF014470) peroxidase [Oryza sativa]
Seq. No.
                  403763
                  LIB3433-018-Q6-K6-E4
Seq. ID
Method
                  BLASTX
                  g2493147
NCBI GI
BLAST score
                  315
E value
                 4.0e-29
                  77
Match length
                  84
% identity
NCBI Description
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi 857574
                  (U27098) H+-ATPase [Oryza sativa]
                  403764
Seq. No.
                  LIB3433-019-P1-K1-A8
Seq. ID
Method
                  BLASTX
                  q1076732
NCBI GI
BLAST score
                  455
E value
                  2.0e-45
Match length
                  120
% identity
                  type-1 pathogenesis-related protein - barley
```

```
pathogenesis-related protein [Hordeum vulgare]
Seq. No.
Seq. ID
                   LIB3433-019-P1-K1-F4
                   BLASTX
Method
                   q6102610
NCBI GI
BLAST score
                   299
                   4.0e-27 □
E value
                   136
Match length
% identity
                   (AF187317) CAF protein [Arabidopsis thaliana]
NCBI Description
                   403766
Seq. No.
                   LIB3433-020-P1-K1-C3
Seq. ID
                   BLASTX
Method
                   g2497883
NCBI GI
BLAST score
                   226
                   2.0e-18.
E value
Match length
                   56
                   75
% identity
                   METALLOTHIONEIN-LIKE PROTEIN TYPE 1 >gi_1362174_pir__S57768
NCBI Description
                   metallothionein-like protein - rice >gi_687638 (U18404)
                   metallothionein-like protein [Oryza satīva] >gi 1815626
                   (U43529) metallothionein-like type 1 [Oryza satīva]
                   >gi_4097154_gb_AAD10376.1_ (U46159) type 1 rice
metallothionein-like gene; Method: conceptual translation
                   supplied by author. [Oryza sativa]
                   403767
Seq. No.
                   LIB3433-020-P1-K1-E1
Seq. ID
                   BLASTX
Method
                   g2497883
NCBI GI
                   153
BLAST score
                   5.0e-10
E value
                   62
Match length
                   56
% identity
                   METALLOTHIONEIN-LIKE PROTEIN TYPE 1 >gi_1362174_pir__S57768
NCBI Description
                   metallothionein-like protein - rice >gi_687638 (U18404)
                   metallothionein-like protein [Oryza sativa] >gi_1815626
                   (U43529) metallothionein-like type 1 [Oryza sativa]
                   >qi 4097154 gb AAD10376.1_ (U46159) type 1 rice
                   metallothionein-like gene; Method: conceptual translation
                   supplied by author. [Oryza sativa]
                   403768
Seq. No.
                   LIB3433-020-P1-K1-E12
Seq. ID
                   BLASTX
Method
                   q3482979
NCBI GI
                   205
BLAST score
                   2.0e-16
E value
                   76
Match length
                   46
% identity
                    (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                   >gi 4567258_gb_AAD23672.1_AC007070_21 (AC007070)
```

>gi_732807_emb_CAA88618 (Z48728) type-1

hypothetical protein [Arabidopsis thaliana]

```
403769
Seq. No.
Seq. ID
                   LIB3433-020-P1-K1-E2
Method
                   BLASTX
                   q4506745
NCBI GI
BLAST score
                   287
                   7.0e-26
E value
Match length
                   97
                   59
% identity
                   ribosomal protein S9 >gi 1173285 sp P46781 RS9 HUMAN 40S
NCBI Description
                   RIBOSOMAL PROTEIN S9 >gi 1362936 pir S55917 ribosomal
                   protein S9 - human >gi 5\overline{5}0023 (\overline{01}497\overline{1}) ribosomal protein S9
                   [Homo sapiens] >gi 1096943 prf 2113200F ribosomal protein
                   S9 [Homo sapiens]
                   403770
Seq. No.
                   LIB3433-020-P1-K1-E4
Seq. ID
Method
                   BLASTX
                   g4033424
NCBI GI
BLAST score
                   581
                   4.0e-60
·E value
                   125
Match length
                   92
% identity
                   SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE
NCBI Description
                   PHOSPHO-HYDROLASE) (PPASE) >gi 2668746 (AF034947) inorganic
                   pyrophosphatase [Zea mays]
                   403771
Seq. No.
                   LIB3433-020-P1-K1-E8
Seq. ID
Method
                   BLASTX
                   g3122599
NCBI GI
                   155
BLAST score
                   4.0e-10
E value
                   76
Match length
                   42
% identity
NCBI Description
                   PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP OXIDASE)
                   >qi 1653389 dbj BAA18303 (D90913) pyridoxamine 5-phosphate
                   oxidase [Synechocystis sp.]
Seq. No.
                   403772
Seq. ID
                   LIB3433-020-P1-K1-F4
Method
                   BLASTX
                   g2407287
NCBI GI
BLAST score
                   185
                   9.0e-14
E value
                   59
Match length
% identity
                   (AF017366) metallothionein-like protein [Oryza sativa]
NCBI Description
                   403773
Seq. No.
                   LIB3433-020-P1-K1-G10
Seq. ID
Method
                   BLASTX
                   q4678941
NCBI GI
BLAST score
                   327
E value
                   8.0e-31
Match length
                   133
% identity
NCBI 'Description
                   (AL049711) gamma response I protein [Arabidopsis thaliana]
```

Seq. ID

```
Seq. No.
                  403774
                  LIB3433-020-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4895197
BLAST score
                  145
                  6.0e-09
E value
Match length
                  44
% identity
                  (AC007661) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  403775
Seq. No.
Seq. ID
                  LIB3433-020-P1-K1-G4
                  BLASTX
Method
                  q129591
NCBI GI
                  620
BLAST score
E value
                  1.0e-64
                  135
Match length
% identity
                  93
                  PHENYLALANINE AMMONIA-LYASE >qi 295824 emb CAA34226
NCBI Description
                  (X16099) phenylalanine ammonia-lyase [Oryza sativa]
                  403776
Seq. No.
Seq. ID
                  LIB3433-020-P1-K1-G6
Method
                  BLASTX
                  g1888357
NCBI GI
                  325
BLAST score
                  5.0e-34
E value
Match length
                  148
                  55
% identity
                  (X98130) alpha-mannosidase [Arabidopsis thaliana]
NCBI Description
                  >gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
                  403777
Seq. No.
                  LIB3433-021-P1-K1-C2
Seq. ID
Method
                  BLASTX
                ູ,g3335375
NCBI GI
BLAST score
                  521
                  4.0e-53
E value
Match length
                  141
% identity
                  (AC003028) putative amidase [Arabidopsis thaliana]
NCBI Description
                  403778
Seq. No.
Seq. ID
                  LIB3433-021-P1-K1-C4
Method
                  BLASTX
                  g4099408
NCBI GI
                  478
BLAST score
                  4.0e-48
E value
Match length
                  116
% identity
                  (U86763) delta-type tonoplast intrinsic protein [Triticum
NCBI Description
                  aestivum]
                  403779
Seq. No.
```

LIB3433-021-P1-K1-G12

Match length

% identity

```
Method
                   BLASTX
                   g3935150
NCBI GI
BLAST score
                   429
E value
                   3.0e-42
Match length
                   107
                   72
 % identity
NCBI Description (AC005106) T25N20.14 [Arabidopsis thaliana]
                   403780
Seq. No.
Seq. ID
                   LIB3433-022-P1-K1-B7
Method
                   BLASTN
                   g5650779
NCBI GI
BLAST score
                   35
                   6.0e-10
E value
                   35
Match length
                   100
% identity
NCBI Description Gallus gallus RGS protein RGS-17 mRNA, complete cds
                   403781
Seq. No.
                   LIB3433-022-P1-K1-D10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4127456
                   276
BLAST score
                   2.0e-24
E value
                   100
Match length
                   60
% identity
NCBI Description
                   (AJ010818) Cpn21 protein [Arabidopsis thaliana]
Seq. No.
                   403782
                   LIB3433-022-P1-K1-D12
Seq. ID
Method
                   BLASTX
                   q5103825
NCBI GI
BLAST score
                   178
                   5.0e-13
E value
Match length
                   49.
% identity
                   (AC007591) ESTs gb_AA650895, gb_AA720043 and gb_R29777 come
NCBI Description
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   403783
                   LIB3433-022-P1-K1-D4
Seq. ID
                   BLASTX
Method
                   q2293566
NCBI GI
BLAST score
                   402
                   3.0e-39
E value
                   77
Match length
                   100
% identity
                   (AF012896) ADP-ribosylation factor 1 [Oryza sativa]
NCBI Description
Seq. No.
                   403784
                   LIB3433-022-P1-K1-E1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q5734616
BLAST score
                   283
E value
                   1.0e-158
```

Seq. ID

```
NCBI Description Oryza sativa genomic DNA, chromosome 6, clone:P0538C01
Seq. No.
                  403785
Seq. ID
                  LIB3433-023-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q1684851
BLAST score
                  189
                  3.0e-14
E value
Match length
                  61
                  61
% identity
NCBI Description
                  (U77935) DnaJ-like protein [Phaseolus vulgaris]
                  403786
Seq. No.
                  LIB3433-023-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2407287
BLAST score
                  327
E value
                  2.0e-30
Match length
                  68
% identity
                  (AF017366) metallothionein-like protein [Oryza sativa]
NCBI Description
Seq. No.
                  403787
                  LIB3433-023-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2773154
BLAST score
                  227
E value
                  6.0e-19
Match length
                  83
% identity
                  (AF039573) abscisic acid- and stress-inducible protein
NCBI Description
                  [Oryza sativa]
Seq. No.
                  403788
Seq. ID
                  LIB3433-023-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g1389835
BLAST score
                  147
E value
                  3.0e-09
Match length
                  73
% identity
                  47
                  (U59284) Linum usitatissimum peroxidase (FLXPER3) mRNA,
NCBI Description
                  complete cds. [Linum usitatissimum]
Seq. No.
                  403789
                  LIB3433-023-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3882356
BLAST score
                  333
E value
                  5.0e-31
Match length
                  136
% identity
NCBI Description
                  (U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis
                  thaliana]
Seq. No.
                  403790
```

LIB3433-023-P1-K1-E9

```
Method
                   BLASTX
 NCBI GI
                   q2760830
 BLAST score
                   272
                   2.0e-32
 E value
 Match length
                   120
 % identity
 NCBI Description
                    (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
                   thaliana]
 Seq. No.
                   403791
                   LIB3433-023-P1-K1-F1
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q459009
 BLAST score
                   332
                   6.0e-31
 E value
 Match length
                   110
 % identity
                   58
 NCBI Description
                   (U00037) similar to multifunctional aminoacyl-tRNA
                   synthetase, especially to the prolyl-tRNA synthetase region
                    [Caenorhabditis elegans]
                   403792
 Seq. No.
                   LIB3433-023-P1-K1-F5
 Seq. ID
 Method
                   BLASTX
NCBI GI
                   g2662341
 BLAST score
                   644
                   2.0e-67
 E value
                   143
 Match length
 % identity
 NCBI Description
                   (D63580) EF-1 alpha [Oryza sativa]
                   >gi 2662345 dbj BAA23659 (D63582) EF-1 alpha [Oryza
                   sativa] >gi 2662347 dbj BAA23660 (D63583) EF-1 alpha
                    [Oryza sativa]
 Seq. No.
                   403793
                   LIB3433-023-P1-K1-F7
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   q1710807
 BLAST score
                   347
 E value
                   5.0e-33
 Match length
                   125
 % identity
                   RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60
 NCBI Description
                   KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) >qi 1185390
                    (U21105) alphacpn60 [Pisum sativum]
 Seq. No.
                    403794
 Seq. ID
                   LIB3433-023-P1-K1-G7
                   BLASTX
 Method
 NCBI GI
                   q6091722
 BLAST score
                   430
                   2.0e-42
 E value
 Match length
                   106
 % identity
 NCBI Description
                   (AC010797) putative ribosomal protein L13 [Arabidopsis
```

thaliana]

```
Seq. No.
                  403795
                  LIB3433-023-P1-K1-H2
Seq. ID
Method
                  BLASTN
                  g5531935
NCBI GI
                  54
BLAST score
                  2.0e-21
E value
Match length
                  114
                  87
% identity
                  Zea mays putative transcription factor mRNA sequence
NCBI Description
                  403796
Seq. No.
                  LIB3433-024-P1-K1-A12
Seq. ID
Method
                  BLASTN
                  q5007079
NCBI GI
BLAST score
                  51
                   5.0e-20
E value
                  107
Match length
                  88
% identity
                  Oryza sativa poly(A)-binding protein gene, partial cds
NCBI Description
                   403797
Seq. No.
                  LIB3433-024-P1-K1-C8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g3914019
                   187
BLAST score
                   3.0e-14
E value
                   93
Match length
                   51
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_2305014
                   (AF004317) S-adenosyl-L-methionine synthetase homolog [Musa
                   acuminata]
                   403798
Seq. No.
                   LIB3433-024-P1-K1-D3
Seq. ID
                   BLASTX
Method
                   g5001734
NCBI GI
BLAST score
                   532
                                                                             1.0
                   2.0e-54
E value
Match length
                   140
                   69
% identity
                   (AF129511) very-long-chain fatty acid condensing enzyme
NCBI Description
                   CUT1 [Arabidopsis thaliana]
Seq. No.
                   403799
Seq. ID
                   LIB3433-024-P1-K1-F1
                   BLASTX
Method
NCBI GI
                   g2149640
BLAST score
                   497
                   3.0e-50
E value
Match length
                   119
% identity
                   (U91995) Argonaute protein [Arabidopsis thaliana]
NCBI Description
                   >gi 5733867_gb_AAD49755.1_AC007932_3 (AC007932) Identical
                   to gb_U91995 Argonaute protein from Arabidopsis thaliana.
                   ESTs gb H76075, gb_AA720232, gb_N65911 and gb_AA651494 come
```

from this gene

NCBI Description

```
403800
Seq. No.
                  LIB3433-024-P1-K1-F11
Seq. ID
                  BLASTX
Method
                  q398845
NCBI GI
BLAST score
                  550
                  5.0e-61
E value
                  128
Match length
                  87
% identity
                  (X74654) beta3 tubulin [Zea mays]
NCBI Description
Seq. No.
                  403801
                  LIB3433-024-P1-K1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q585551
BLAST score
                  499
                  1.0e-50
E value
Match length
                  112
                  86
% identity
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                  >gi 629798 pir S43330 nucleoside-diphosphate kinase (EC
                  2.7.4.6) - rice >gi 303849 dbj BAA03798 (D16292)
                  nucleoside diphosphate kinase [Oryza sativa]
Seq. No.
                  403802
                  LIB3433-024-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2119055
BLAST score
                  222
                  2.0e-18
E value
                  57
Match length
                  77
% identity
NCBI Description
                  signal recognition paticle 54K protein - tomato (cv.
                  Rentita)
Seq. No.
                  403803
                  LIB3433-025-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2529663
BLAST score
                  593
E value
                  1.0e-61
Match length
                  139
                  76
% identity
                   (AC002535) putative lysophospholipase [Arabidopsis
NCBI Description
                  thaliana] >qi 3738277 (AC005309) putative lysophospholipase
                   [Arabidopsis thaliana]
                  403804
Seq. No.
                  LIB3433-025-P1-K1-G8
Seq. ID
Method
                  BLASTX
                  g3298460
NCBI GI
                  379
BLAST score
E value
                  1.0e-36
                  98
Match length
                  73
% identity
```

(AB012268) SAMIPB [Aster tripolium]

NCBI GI

```
403805
Seq. No.
Seq. ID
                  LIB3433-025-P1-K1-H4
Method
                  BLASTX
                  q409007
NCBI GI
BLAST score
                  344
                  2.0e-32
E value
                  81
Match length
% identity
                  79
                  BBI-M=Bowman-Birk trypsin inhibitor-related protein [Zea
NCBI Description
                  mays=corn, Peptide, 102 aa] >gi 447268 prf 1914141A
                  trypsin inhibitor-related protein [Zea mays]
Seq. No.
                  403806
                  LIB3433-026-P1-K1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2801537
BLAST score
                  176
E value
                  3.0e-94
Match length
                  329
% identity
                  Oryza sativa harpin induced gene 1 homolog (Hin1) mRNA,
NCBI Description
                  complete cds
                  403807
Seq. No.
Seq. ID
                 : LIB3433-026-P1-K1-D12
                  BLASTX
Method
                  g5902928
NCBI GI
BLAST score
                  478
                  5.0e-48
E value
Match length
                  91
% identity
                  100
NCBI Description (AB029509) small GTP-binding protein OsRac2 [Oryza sativa]
                  403808
Seq. No.
Seq. ID
                  LIB3433-026-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q4531444
BLAST score
                  249
                  4.0e-21
E value
                  95
Match length
                  55
% identity
NCBI Description (AC006224) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  403809
                  LIB3433-027-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1658315
BLAST score
                  346
                  1.0e-32
E value
Match length
                  92
                  72
% identity
NCBI Description (Y08988) osr40g3 [Oryza sativa]
                  403810
Seq. No.
Seq. ID
                  LIB3433-028-P1-K1-C3
Method
                  BLASTX
```

g3860323

% identity

46

```
269
BLAST score
                   9.0e-24
E value
                   77
Match length
                   66
% identity
                   (AJ012688) hypothetical protein [Cicer arietinum]
NCBI Description
                   403811
Seq. No.
                   LIB3433-028-P1-K1-E1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g287297
BLAST score
                  41
E value
                   1.0e-13
                   105
Match length
                   86
% identity
                  Oryza sativa mRNA for aspartate aminotransferase, complete
NCBI Description
                   cds
Seq. No.
                   403812
                   LIB3433-030-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4455206
BLAST score
                   301
E value
                   4.0e-27
Match length
                   181
% identity
                   44
                   (AL035440) putative beta-1, 3-glucanase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   403813
Seq. ID
                   LIB3433-031-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   q100598
BLAST score
                   485
E value
                   7.0e-49
Match length
                   126
% identity
                  ubiquitin / ribosomal protein S27a-1 - barley >gi 167073
NCBI Description
                   (M60175) ubiquitin [Hordeum vulgare]
Seq. No.
                   403814
Seq. ID
                   LIB3433-031-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   q4006868
BLAST score
                   350
E value
                   4.0e-33
Match length
                   119
% identity
                   (Z99707) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403815
Seq. ID
                   LIB3433-031-P1-K1-H7
Method
                  BLASTX
NCBI GI
                   g2465151
BLAST score
                   227
E value
                   1.0e-18
Match length
                   115
```

ř,

Method

BLASTX

```
NCBI Description (Z99753) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  403816
                  LIB3433-032-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5263319
BLAST score
                  167
                  3.0e-12
E value
Match length
                  67
                  49
% identity
                  (AC007727) ESTs gb N96028, gb F14286, gb_T20680, gb_F14443,
NCBI Description
                  gb AA657300 and gb N65244 come from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  403817
Seq. ID
                  LIB3433-032-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q2462834
BLAST score
                  207
                  3.0e-16
E value
Match length
                  95
% identity
                  44
                  (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  403818
Seq. No.
                  LIB3433-032-P1-K1-G2
Seq. ID
                  BLASTX
Method
                  q459895
NCBI GI
BLAST score
                  292
E value
                  1.0e-33
                  86
Match length
% identity
                  (L29418) sus1 gene product [Zea mays]
NCBI Description
Seq. No.
                  403819
                  LIB3433-033-P1-K1-D5
Seq. ID
                  BLASTN
Method
                  g1808687
NCBI GI
BLAST score
                  90
E value
                  1.0e-42
                  246
Match length
% identity
                  89
                  S.stapfianus pSD.13 mRNA
NCBI Description
                  403820
Seq. No.
Seq. ID
                  LIB3433-033-P1-K1-E5
                  BLASTX
Method
NCBI GI
                  q1332579
BLAST score
                  490
                  3.0e-64
E value
Match length
                  180
% identity
                  (X98063) polyubiquitin [Pinus sylvestris]
NCBI Description
Seq. No.
                  403821
                  LIB3433-033-P1-K1-E8
Seq. ID
```

BLAST score

```
q1729971
NCBI GI
BLAST score
                   668
                   4.0e-70
E value
Match length
                  149
% identity
                  87
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                  rice >gi 473997 dbj BAA05017 (D25534) gamma-Tip [Oryza
                  sativa]
                   403822
Seq. No.
Seq. ID
                  LIB3433-033-P1-K1-F10
Method
                  BLASTX
                  q3935141
NCBI GI
                   342
BLAST score
                   6.0e-32
E value
Match length
                  109
                   53
% identity
                  (AC005106) T25N20.5 [Arabidopsis thaliana]
NCBI Description
                   403823
Seq. No.
                  LIB3433-033-P1-K1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2662310
BLAST score
                   521
                   7.0e-53
E value
                   106
Match length
% identity
                  (AB009307) bpwl [Hordeum vulgare]
NCBI Description
Seq. No.
                   403824
Seq. ID
                  LIB3433-033-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   q283008
BLAST score
                   922
                   1.0e-100
E value
Match length
                   185
% identity
                   sucrose synthase (EC 2.4.1.13) - rice
NCBI Description
                   >gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza
                   sativa]
                   403825
Seq. No.
                   LIB3433-033-P1-K1-H10
Seq. ID
                   BLASTX
Method
NCBI GI
                   a629858
                   580
BLAST score
E value
                   8.0e-60
                   129
Match length
% identity
NCBI Description protein kinase C inhibitor - maize
                   403826
Seq. No.
Seq. ID
                   LIB3433-034-P1-K1-F7
Method
                   BLASTX
                   q2118425
NCBI GI
```

```
E value
                  2.0e-20
                  60
Match length
% identity
                  80
                  subtilisin/chymotrypsin inhibitor - maize
NCBI Description
                  >gi 475253 emb_CAA55588_ (X78988) proteinase inhibitor [Zea
                  mays] >gi 475922 emb CAA49593 (X69972) proteinase
                  inhibitor [Zea mays] > gi_559538_emb_CAA57677_ (X82187)
                  substilin /chymotrypsin-like inhibitor [Zea mays]
                  403827
Seq. No.
                  LIB3433-034-P1-K1-F9
Seq. ID
Method
                  BLASTX
                  g2811122
NCBI GI
BLAST score
                  205
                  5.0e-16
E value
Match length
                  107
% identity
                  38
                   (U87318) NaDC-2 [Xenopus laevis]
NCBI Description
                  403828
Seq. No.
                  LIB3433-035-P1-K1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2335198
BLAST score
                  66
                  1.0e-28
E value
                  122
Match length
                  88
% identity
                  Oryza sativa clone RGCH8 chitinase gene, complete cds
NCBI Description
Seq. No.
                   403829
                  LIB3433-037-P1-K1-H7
Seq. ID
                  BLASTN
Method
                  q1212995
NCBI GI
BLAST score
                   48
E value
                   5.0e-18
Match length
                  147
                  85
% identity
                  H.vulgare mRNA for UDP-glucose pyrophosphorylase
NCBI Description
Seq. No.
                   403830
                  LIB3433-038-P1-K1-A7
Seq. ID
Method
                  BLASTX
                   q295355
NCBI GI
BLAST score
                   154
                   1.0e-10
E value
Match length
                   62
                   50
% identity
                   (L13653) peroxidase [Lycopersicon esculentum]
NCBI Description
                   403831
Seq. No.
                   LIB3433-038-P1-K1-C6
Seq. ID
                   BLASTX
Method
                   q1888357
NCBI GI
BLAST score
                   243
E value
                   2.0e-20
                   97
Match length
% identity
                   56
```

```
NCBI Description (X98130) alpha-mannosidase [Arabidopsis thaliana]
                  >gi 1890154 emb CAA72432 (Y11767) alpha-mannosidase
                  precursor [Arabidopsis thaliana]
                  403832
Seq. No.
                  LIB3433-038-P1-K1-G6
Seq. ID
Method
                  BLASTX
                  g170031
NCBI GI
BLAST score
                  214
                  3.0e-17
E value
Match length
                  73
% identity
                  59
NCBI Description (M10594) nodulin 35 [Glycine max]
Seq. No.
                  403833
Seq. ID
                  LIB3433-038-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q2832672
BLAST score
                  247
                  5.0e-21
E value
Match length
                  51
% identity
NCBI Description (AL021712) nifU-like protein [Arabidopsis thaliana]
Seq. No.
                  403834
Seq. ID
                  LIB3433-039-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  q5410347
BLAST score
                  92
E value
                  5.0e-44
Match length
                  383
                  87
% identity
NCBI Description Sorghum bicolor BAC clone 110K5, partial sequence
Seq. No.
                  403835
Seq. ID
                  LIB3433-040-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  g2331130
BLAST score
                  62
E value
                  4.0e-26
Match length
                  94
% identity
NCBI Description
                  Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
                  cds
Seq. No.
                  403836
Seq. ID
                  LIB3433-040-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q401138
BLAST score
                  187
E value
                  6.0e-14
Match length
                  105
                  46
% identity
NCBI Description SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1)
                  >gi 418758 pir__S29242 sucrose synthase (EC 2.4.1.13) Ss1 -
                  barley >gi_19106_emb_CAA46701_ (X65871) sucrose synthase
```

[Hordeum vulgare]

```
403837
Seq. No.
Seq. ID
                  LIB3433-040-P1-K1-H12
Method
                  BLASTX
                  q462195
NCBI GI
                  437
BLAST score
E value
                  3.0e-43
                  98
Match length
                  87
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN)
NCBI Description
                  >gi 100682 pir__S21636 GOS2 protein - rice
                  >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa]
                  >gi_3789950 (AF094774) translation initiation factor [Oryza
                  sativa]
Seq. No.
                  403838
Seq. ID
                  LIB3433-042-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  q2773153
BLAST score
                  158
E value
                  9.0e-84
Match length
                  193
                  96
% identity
                  Oryza sativa abscisic acid- and stress-inducible protein
NCBI Description
                  (Asrl) mRNA, complete cds
                  403839
Seq. No.
                  LIB3433-042-P1-K1-H11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q786129
BLAST score
                  40
                  4.0e-13
E value
                  48
Match length
% identity
                  Oryza sativa root-specific RCc2 mRNA, complete cds
NCBI Description
                  403840
Seq. No.
                  LIB3433-045-P1-K1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2130067
BLAST score
                  717
E value
                  5.0e-76
Match length
                  139
                  99
% identity
                  aspartate transaminase (EC 2.6.1.1), mitochondrial - rice
NCBI Description
                  >gi 2696240 dbj BAA23815.1 (D67043) aspartate
                  aminotransferase [Oryza sativa]
                  403841
Seq. No.
                  LIB3433-045-P1-K1-B1
Seq. ID
Method
                  BLASTX
                  q2117620
NCBI GI
BLAST score
                  177
E value
                  1.0e-12
Match length
                  160
% identity
NCBI Description peroxidase (EC 1.11.1.7) 1A - alfalfa
```

% identity

```
>gi 971558 emb CAA62225_ (X90692) peroxidase1A [Medicago
                  satīva]
                  403842
Seq. No.
Seq. ID
                  LIB3433-045-P1-K1-H6
Method
                  BLASTX
                  g1076740
NCBI GI
                  537
BLAST score
                  9.0e-60
E value
Match length
                  143
                  78
% identity
                  chitinase (EC 3.2.1.14) - rice >gi 407472_emb_CAA40107.
NCBI Description
                   (X56787) chitinase [Oryza sativa] >gi 500616_dbj_BAA03750_
                   (D16222) endochitinase [Oryza sativa]
                  >gi_742301_prf__2009354A chitinase [Oryza sativa]
Seq. No.
                  403843
Seq. ID
                  LIB3433-048-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  q2062705
                                          371
                  32
BLAST score
                  4.0e-09
E value
Match length
                  32
                  100
% identity
                  Human butyrophilin (BTF5) mRNA, complete cds
NCBI Description
                  403844
Seq. No.
Seq. ID
                  LIB3433-048-P1-K1-D6
Method
                  BLASTX
                  g3273243
NCBI GI
BLAST score
                  377
                  1.0e-36
E value
                  78
Match length
% identity
                   (AB004660) NLS receptor [Oryza sativa]
NCBI Description
                  >gi 3273245 dbj BAA31166 (AB004814) NLS receptor [Oryza
                  sativa]
Seq. No.
                  403845
Seq. ID
                  LIB3433-048-P1-K1-E2
Method
                  BLASTN
                  q1196834
NCBI GI
                  42
BLAST score
                  1.0e-14
E value
Match length
                  42
                  100
% identity
                  Oryza sativa (clone 14b) osmotin protein (14b) gene, 3'
NCBI Description
                  complete cds
Seq. No.
                  403846
                  LIB3433-048-P1-K1-F6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q5777612
BLAST score
                  97
                  4.0e-47
E value
Match length
                  228
```

Method

BLASTX

```
Oryza sativa chromosome 4 BAC q3037-207F1 complete genome
NCBI Description
Seq. No.
                   403847
                  LIB3433-048-P1-K1-G3
Seq. ID
Method
                  BLASTX
                  g5921933
NCBI GI
BLAST score
                   287
                   1.0e-25
E value
Match length
                  81
                   59
% identity
                  CYTOCHROME P450 85 (DWARF PROTEIN) >gi 1421741 (U54770)
NCBI Description
                   cytochrome P450 homolog [Lycopersicon esculentum]
Seq. No.
                   403848
Seq. ID
                  LIB3433-049-P1-K1-A7
Method
                  BLASTX
NCBI GI
                   q4586676
BLAST score
                   259
                   2.0e-22
E value
Match length
                   78
% identity
                   (AB025047) sterol 14-demethylase [Oryza sativa]
NCBI Description
Seq. No.
                   403849
                   LIB3433-049-P1-K1-C9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2244998
BLAST score
                   397
E value
                   2.0e-38
Match length
                   121
                   70
% identity
                   (Z97341) transcriptional adaptor like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   403850
                   LIB3433-050-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3033396.
BLAST score
                   314
E value
                   8.0e-29
Match length
                   113
% identity
                   (AC004238) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403851
                   LIB3433-052-P1-K1-A5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4582434
BLAST score
                   426
E value
                   6.0e-42
Match length
                   93
% identity
NCBI Description
                   (AC007196) unknown protein [Arabidopsis thaliana]
Seq. No.
                   403852
Seq. ID
                   LIB3433-052-P1-K1-B8
```

Method

NCBI GI

BLASTX

q730463

```
g2130073
NCBI GI
                  406
BLAST score
                  1.0e-39
E value
Match length
                  131
                  67
% identity
                  fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1,
NCBI Description
                  cytosolic - rice >qi 786178 dbj BAA08845 (D50307) aldolase
                  C-1 [Oryza sativa] >gi 790970_dbj_BAA08830_ (D50301)
                  aldolase C-1 [Oryza sativa]
                  403853
Seq. No.
                  LIB3433-052-P1-K1-C4
Seq. ID
                  BLASTX
Method
                  q1362010
NCBI GI
BLAST score
                  155
E value
                  2.0e-10
                  47
Match length
% identity
                  35
                  ubiquitin-like protein 9 - Arabidopsis thaliana
NCBI Description
Seq. No.
                  403854
                  LIB3433-052-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4455210
BLAST score
                  456
E value
                  3.0e-51
Match length
                  139
% identity
                  (AL035440) putative aspartate-tRNA ligase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  403855
                  LIB3433-053-P1-K1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2293567
BLAST score
                  78
                  7.0e-36
E value
Match length
                  92
                  98
% identity
NCBI Description
                  Oryza sativa HvB12D homolog mRNA, complete cds
Seq. No.
                  403856
                  LIB3433-054-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1173218
BLAST score
                  505
E value
                  3.0e-51
Match length
                  110
                  91
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S15A >gi 440824 (L27461) ribosomal
                  protein S15 [Arabidopsis thaliana] >gi 2150130 (AF001412)
                  cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
Seq. No.
                  403857
                  LIB3433-055-P1-K1-A3
Seq. ID
```

Match length

```
BLAST score
                   301
 E value
                   2.0e-27
 Match length
                   102
 % identity
                   56
                   60S RIBOSOMAL PROTEIN L33-B (L37B) (YL37) (RP47)
 NCBI Description
                   >gi 630323 pir S44069 ribosomal protein L35a.e.c15 - yeast
                   (Saccharomyces cerevisiae) >qi 484241 (L23923) ribosomal
                   protein L37 [Saccharomyces cerevisiae]
                   >gi 1420537 emb CAA99454 (Z75142) ORF YOR234c
                   [Saccharomyces cerevisiae]
                   403858
 Seq. No.
 Seq. ID
                   LIB3433-055-P1-K1-F4
                   BLASTX
 Method
                   q6009909
 NCBI GI
                   212
 BLAST score
 E value
                   6.0e-17
                   43
 Match length
 % identity
                   (AB018242) histone H2A-like protein [Solanum melongena]
 NCBI Description
                   403859
 Seq. No.
                   LIB3433-056-P1-K1-A11
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g4506745
 BLAST score
                   267
                   2.0e-23
 E value
                   102
 Match length
                   51
 % identity
 NCBI Description
                   ribosomal protein S9 >qi 1173285 sp P46781 RS9 HUMAN 40S
                   RIBOSOMAL PROTEIN S9 >qi 1362936 pir S55917 ribosomal
                   protein S9 - human >gi 550023 (U14971) ribosomal protein S9
                   [Homo sapiens] >gi 1096943 prf 2113200F ribosomal protein
                   S9 [Homo sapiens]
 Seq. No.
                   403860
 Seq. ID
                   LIB3433-056-P1-K1-A3
. Method .
                   BLASTX
                   g1172042
 NCBI GI
 BLAST score
                   189
 E value
                   3.0e-14
 Match length
                   63
 % identity
                   PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (ACETYLGLUCOSAMINE
 NCBI Description
                   PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE)
                   >qi 2130266 pir S59642 hypothetical protein SPAC13C5.05c -
                   fission yeast (Schizosaccharomyces pombe)
                   >qi 908894 emb CAA90456 (Z50112) phosphomannomutase
                   phosphoserine [Schizosaccharomyces pombe]
                   403861
 Seq. No.
                   LIB3433-056-P1-K1-B4
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g3608154
 BLAST score
                   187
                   5.0e-14
 E value
```

```
% identity
NCBI Description (AC005314) unknown protein [Arabidopsis thaliana]
Seq. No.
                  403862
Seq. ID
                  LIB3433-056-P1-K1-C2
                  BLASTN
Method
                  q433216
NCBI GI
BLAST score
                  76
                  2.0e-34
E value
Match length
                  154
                  88
% identity
NCBI Description
                  Rice mRNA for ascorbate peroxidase (gene name SS622),
                  partial cds
                  403863
Seq. No.
                  LIB3433-056-P1-K1-D6
Seq. ID
Method
                  BLASTN
                  q429016
NCBI GI
BLAST score
                  37
                  1.0e-11
E value
                  69
Match length
% identity
                  Rice mRNA for Wilm's tumor suppressor (gene name SS501),
NCBI Description
                  partial cds
                  403864
Seq. No.
                  LIB3433-056-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5669871
BLAST score
                  680
                  1.0e-71
E value
                  139
Match length
% identity
                  (AF135014) dihydrolipoamide S-acetyltransferase [Zea mays]
NCBI Description
                  403865
Seq. No.
                  LIB3433-056-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2293480
BLAST score
                  276
E value
                  7.0e-25
Match length
                  74
% identity
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
Seq. No.
                  403866
                  LIB3433-056-P1-K1-G2
Seq. ID
Method
                  BLASTX
                  g547712
NCBI GI
BLAST score
                  259
                  7.0e-23
E value
Match length
                  76
% identity
                  72
                  EUKARYOTIC INITIATION FACTOR 4A (EIF-4A)
NCBI Description
                  >gi_542153_pir__S38358 translation initiation factor eIF-4A
                  - rice >gi 303844 dbj BAA02152 (D12627) eukaryotic
```

initiation factor 4A [Oryza sativa]

```
403867
Seq. No.
Seq. ID
                  LIB3433-056-P1-K1-G3
                  BLASTX
Method
NCBI GI
                  g1076732
BLAST score
                   328
                  1.0e-30
E value
                  85
Match length
                   68
% identity
                  type-1 pathogenesis-related protein - barley
NCBI Description
                  >gi 732807_emb_CAA88618_ (Z48728) type-1
                  pathogenesis-related protein [Hordeum vulgare]
                   403868
Seq. No.
                  LIB3433-057-P1-K1-A2
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1184112
BLAST score
                   216
                   5.0e-31
E value
Match length
                   97
                   76
% identity
                   (U46138) Zn-induced protein [Oryza sativa]
NCBI Description
                   403869
Seq. No.
                   LIB3433-057-P1-K1-H6
Seq. ID
Method
                   BLASTX
                   g3123244
NCBI GI
BLAST score
                   188
                   3.0e-15
E value
                   132
Match length
                   41
% identity
                  ALPHA-MANNOSIDASE IIX (MANNOSYL-OLIGOSACCHARIDE
NCBI Description
                   1,3-1,6-ALPHA-MANNOSIDASE) (MAN IIX)
                   >gi_1132479_dbj_BAA09510_ (D55649) alpha mannosidase II
                   isozyme [Homo sapiens]
                   403870
Seq. No.
Seq. ID
                   LIB3433-058-P1-K1-B9
                   BLASTN
Method
NCBI GI
                   g809513
BLAST score
                   79
E value
                   2.0e-36
                   154
Match length
% identity
                  Rice mRNA for ferredoxin-nitrite reductase, complete cds
NCBI Description
                   403871
Seq. No.
                  LIB3433-058-P1-K1-C1
Seq. ID
                  BLASTX
Method
                   g2341025
NCBI GI
                   221
BLAST score
                   7.0e-18
E value
                   63
Match length
% identity
                   (AC000104) F19P19.2 [Arabidopsis thaliana]
NCBI Description
```

403872

Seq. No.

BLAST score

```
LIB3433-058-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076289
BLAST score
                  254
                  2.0e-22
E value
Match length
                  69
                  57
% identity
                  amino acid permease AAP5 - Arabidopsis thaliana
NCBI Description
                  >gi_608673_emb_CAA54632_ (X77501) amino acid permease
                  [Arabidopsis thaliana]
                  403873
Seq. No.
Seq. ID
                  LIB3433-061-P1-K1-A7
                  BLASTX
Method
                  q4884530
NCBI GI
                  542
BLAST score
                  1.0e-55
E value
                  107
Match length
% identity
                  98
                  (AB027430) beta-1,3-glucanase [Oryza sativa]
NCBI Description
                  403874
Seq. No.
                  LIB3433-061-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3695061
                  232
BLAST score
E value
                  8.0e-20
                  56
Match length
                  80
% identity
NCBI Description
                  (AF064788) rac GTPase activating protein 2 [Lotus
                  japonicus]
                  403875
Seq. No.
                  LIB3433-061-P1-K1-G5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g21693
                  305
BLAST score
                  3.0e-28
E value
Match length
                  60
                  83
% identity
                  (X66012) cathepsin B [Triticum aestivum]
NCBI Description
Seq. No.
                  403876
                  LIB3433-061-P1-K1-H1
Seq. ID
                  BLASTX
Method
                  g2293480
NCBI GI
BLAST score
                  332
                  3.0e-31
E value
Match length
                  69
                  91
% identity
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
                  403877
Seq. No.
Seq. ID
                  LIB3433-061-P1-K1-H12
                  BLASTX
Method
NCBI GI
                  g4388726
```

Match length

356

3~0

```
E value
                  9'.0e-50
Match length
                  136
                  71
% identity
                   (AC006413) putative 12-oxophytodienoate-10,11-reductase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  403878
                  LIB3433-061-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2995990
BLAST score
                  157
E value
                   9.0e-11
Match length
                   64
% identity
NCBI Description
                   (AF053746) dormancy-associated protein [Arabidopsis
                  thaliana] >qi 2995992 (AF053747) dormancy-associated
                  protein [Arabidopsis thaliana]
Seq. No.
                  403879
Seq. ID
                  LIB3434-001-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g551288
BLAST score
                  150
E value
                  8.0e-10
                  102
Match length
% identity
NCBI Description
                   (Z33611) phosphoglycerate mutase [Zea mays]
Seq. No.
                  403880
Seq. ID
                  LIB3434-001-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  a5917726
BLAST score
                  192
                  4.0e-18
E value
Match length
                  74
% identity
                   (AF178530) serine/threonine protein phosphatase 1; PP1
NCBI Description
                   [Malus domestica]
Seq. No.
                  403881
                  LIB3434-002-P1-K1-E10
Seq. ID
Method
                  BLASTN
                  g2244603
NCBI GI
BLAST score
                  47
                  1.0e-17
E value
Match length
                  95
                  88
% identity
                  Oryza sativa gene for betaine aldehyde dehydrogenase,
NCBI Description
                  complete cds
Seq. No.
                  403882
                  LIB3434-002-P1-K1-E7
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4850329
BLAST score
                  88
                  1.0e-41
E value
```

NCBI Description

```
% identity
                  81
                  Oryza sativa COX5c mRNA for cytochrome c oxidase subunit
NCBI Description
                  5c, complete cds
Seq. No.
                  403883
                  LIB3434-003-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3979986
BLAST score
                  253
                  3.0e-22
E value
                  52
Match length
                  96
% identity
                  (298866) predicted using Genefinder; similar to Core
NCBI Description
                  histone H2A/H2B/H3/H4; cDNA EST EMBL: D71193 comes from this
                  gene; cDNA EST yk477a9.3 comes from this gene; cDNA EST
                  CEESG32RD comes from this gene; cDNA EST yk201g11.3 come
                  403884
Seq. No.
Seq. ID
                  LIB3434-003-P1-K1-C2
                  BLASTX
Method
                  q5360230
NCBI GI
                  578
BLAST score
                  7.0e-60
E value
Match length
                  106
                  99
% identity
                  (AB015287) Ran [Oryza sativa]
NCBI Description
                  403885
Seq. No.
Seq. ID
                  LIB3434-004-P1-K1-A2
Method
                  BLASTX
                  q2293480
NCBI GI
BLAST score
                  360
                  7.0e-36
E value
                  85
Match length
% identity
                  95
                  (AF011331) glycine-rich protein [Oryza sativa]
NCBI Description
                  403886
Seq. No.
                  LIB3434-004-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4567319
BLAST score
                  735
                  5.0e-78
E value
Match length
                  178
                  78
% identity
                  (AC005956) putative copper amine oxidase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  403887
Seq. ID
                  LIB3434-004-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  q6016845
BLAST score
                  77
E value
                  4.0e-35
Match length
                  93
% identity
```

Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Match length

```
403888
Seq. No.
                  LIB3434-004-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4249382
BLAST score
                  253
                  7.0e-22
E value
                  77
Match length
                  62
% identity
                   (AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                  putative permease from Arabidopsis thaliana BAC
                  gb AC004481. [Arabidopsis thaliana]
                  403889
Seq. No.
Seq. ID
                  LIB3434-005-P1-K1-A2
Method
                  BLASTN
                  q4097153
NCBI GI
BLAST score
                  104
                  1.0e-51
E value
Match length
                  158
% identity
                  100
                  Oryza sativa type 1 metallothionein-like (rgMT-1) gene,
NCBI Description
                  complete cds
Seq. No.
                  403890
                  LIB3434-005-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3334456
BLAST score
                  149
E value
                  1.0e-09
Match length
                  74
% identity
                  ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE
NCBI Description
                  SUBUNIT) (A1 140 KD SUBUNIT) (RF-C 140 KD SUBUNIT)
                  (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA)
                  >gi_422807_pir__JN0599 DNA-binding protein PO-GA - human
                  >gi 296908 emb CAA80355 (Z22642) PO-GA [Homo sapiens]
                  >qi 307338 (L14922) DNA-binding protein [Homo sapiens]
                  >gi 2827257 (AF040250) DNA binding protein [Homo sapiens]
Seq. No.
                  403891
                  LIB3434-005-P1-K1-H12
Seq. ID
Method .
                  BLASTX
NCBI GI
                  q4091008
BLAST score
                  305
E value
                  4.0e-28
Match length
                  86
% identity
                  (AF040700) methionyl-tRNA synthetase [Oryza sativa]
NCBI Description
Seq. No.
                  403892
                  LIB3434-007-P1-K1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3789949
BLAST score
                  266
E value
                  1.0e-148
```

NCBI Description

```
% identity
                  99
                  Oryza sativa translation initiation factor (GOS2) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  403893
                  LIB3434-007-P1-K1-B1
Seq. ID
Method
                  BLASTX
                  g1346780
NCBI GI
BLAST score
                  152
                  9.0e-10
E value
                  38
Match length
% identity
                  76
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP-X ISOZYME 2
NCBI Description
                  >gi 629550 pir S42559 phosphoprotein phosphatase (EC
                  3.1.3.16) X-2 (clone EP128) - Arabidopsis thaliana
                  >gi_397590_emb_CAA80312 (Z22596) protein phosphatase
                  [Arabidopsis thaliana]
Seq. No.
                  403894
                  LIB3434-007-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4586602
BLAST score
                  494
E value
                  4.0e-50
Match length
                  103
% identity
NCBI Description
                  (AB025005) pyruvate kinase [Cicer arietinum]
Seq. No.
                  403895
                  LIB3434-007-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4063821
BLAST score
                  402
E value
                  2.0e-39
Match length
                  75
% identity
NCBI Description
                  (AB015204) plastidic ATP sulfurylase [Oryza sativa]
Seq. No.
                  403896
Seq. ID
                  LIB3434-007-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1944573
BLAST score
                  659
E value
                  3.0e-69
Match length
                  162
% identity
                  (Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]
NCBI Description
Seq. No.
                  403897
Seq. ID
                  LIB3434-007-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g3513727
BLAST score
                  259
                  7.0e-23
E value
Match length
                  87
% identity
```

(AF080118) contains similarity to TPR domains (Pfam:

BLAST score

E value Match length 466 8.0e-47

106

```
thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative
                  protein [Arabidopsis Thaliana]
                  403898
Seq. No.
                  LIB3434-007-P1-K1-G11
Seq. ID
Method
                  BLASTX
                  q2493147
NCBI GI
BLAST score
                   471
                   3.0e-47
E value
Match length
                  94
                   100
% identity
                  VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_857574
NCBI Description
                   (U27098) H+-ATPase [Oryza sativa]
Seq. No.
                   403899
                   LIB3434-007-P1-K1-G2
Seq. ID
Method
                  BLASTX
                   q1729971
NCBI GI
BLAST score
                   235
                   7.0e-20
E value
                   47
Match length
% identity
                   TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                   (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein -
                   rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza
                   sativa]
Seq. No.
                   403900
                   LIB3434-007-P1-K1-H5
Seq. ID
                   BLASTX
Method
                   q2662310
NCBI GI
                   391
BLAST score
E value
                   3.0e-41
                   97
Match length
% identity
                   (AB009307) bpw1 [Hordeum vulgare]
NCBI Description
                   403901
Seq. No.
                   LIB3434-008-P1-K1-A1
Seq. ID
Method
                   BLASTN
                   q2331130
NCBI GI
BLAST score
                   39
                   1.0e-12
E value
Match length
                   75
                   89
% identity
                   Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete
NCBI Description
Seq. No.
                   403902
                   LIB3434-008-P1-K1-B1
Seq. ID
                   BLASTX
Method
NCBI GI
                   q2498077
```

TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis

BLAST score

```
% identity
                  80
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                  (PP18) >gi 1777930 (U55019) nucleoside diphosphate kinase
                  [Saccharum officinarum]
                  403903
Seq. No.
Seq. ID
                  LIB3434-008-P1-K1-E2
Method
                  BLASTX
                                                        g6041853
NCBI GI
BLAST score
                  351
E value
                  3.0e-33
Match length
                  128
% identity
                  52
NCBI Description
                 (AC009853) hypothetical protein [Arabidopsis thaliana]
                  403904
Seq. No.
Seq. ID
                  LIB3434-008-P1-K1-E6
Method
                  BLASTX
                  g3880399
NCBI GI
BLAST score
                  161
                  9.0e-11
E value
                  71
Match length
% identity
                  (Z71267) predicted using Genefinder; cDNA EST yk275h2.3
NCBI Description
                  comes from this gene; cDNA EST yk309g11.3 comes from this
                  gene; cDNA EST yk309g11.5 comes from this gene; cDNA EST
                  yk275h2.5 comes from this gene [Caenorhabditis elegans]
Seq. No.
                  403905
Seq. ID
                  LIB3434-008-P1-K1-G4
Method
                  BLASTX
                  q3790569
NCBI GI
BLAST score
                 164
                  1.0e-11
E value
Match length
                  58
% identity
                  (AF078822) RING-H2 finger protein RHA2a [Arabidopsis
NCBI Description
                  thaliana] >gi_5103808_gb_AAD39638.1_AC007591_3 (AC007591)
                  Identical to gb_AF078822 RING-H2 finger RHA2a protein from
                  Arabidopsis thaliana. ESTs gb N37587, gb T04684,
                  gb AA394318, gb Z35014 and gb AA713343 come from this gene
Seq. No.
                  403906
                  LIB3434-008-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4204761
                  249
BLAST score
E value
                  1.0e-21
Match length
                  84
% identity
NCBI Description
                  (U51192) peroxidase precursor [Glycine max]
                  403907
Seq. No.
Seq. ID
                  LIB3434-009-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q1632831
```

```
E value
                   5.0e-32
Match length
                   79
                   81
% identity
                   (Z49698) orf [Ricinus communis]
NCBI Description
                   403908
Seq. No.
                   LIB3434-009-P1-K1-H6
Seq. ID
                   BLASTX
Method
                   g6015742
NCBI GI
BLAST score
                   198
                   2.0e-15
E value
Match length
                   76
                   51
% identity
                   (Y18930) ribonuclease PH [Sulfolobus solfataricus]
NCBI Description
Seq. No.
                   403909
                   LIB3434-010-P1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1805654
BLAST score
                   556
E value
                   4.0e-57
Match length
                   165
% identity
                   62
                   (X99972) calmodulin-stimulated calcium-ATPase [Brassica
NCBI Description
                   oleracea]
Seq. No.
                   403910
Seq. ID
                   LIB3434-010-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   q2935529
BLAST score
                   663
E value
                   1.0e-69
Match length
                   150
% identity
NCBI Description
                   (AF049069) No definition line found [Pinus radiata]
Seq. No.
                   403911
Seq. ID
                   LIB3434-010-P1-K1-D1
Method
                   BLASTN
NCBI GI
                   q303858
BLAST score
                   209
E value
                   1.0e-114
Match length
                   217
% identity
                   99
                  Rice mRNA for brain specific protein (S94 gene), complete
NCBI Description
                   cds
Seq. No.
                   403912
Seq. ID
                   LIB3434-010-P1-K1-D8
Method
                  BLASTN
NCBI GI
                   q5688948
BLAST score
                   115
E value
                   5.0e-58
Match length
                   183
% identity
                   91
NCBI Description
                  Oryza sativa gene for mitochondrial ribosomal portein S14,
```

13.

succinate dehydrogenase iron-protein subunit (SDHB)

NCBI GI

```
403913
Seq. No.
                   LIB3434-010-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3869088
                   603
BLAST score
                   8.0e-63
E value
Match length
                   117
% identity
                   (ABO19427) elongation factor-1 alpha [Nicotiana paniculata]
NCBI Description
                   403914
Seq. No.
Seq. ID
                   LIB3434-011-P1-K1-A2
Method
                   BLASTX
                   g3859116
NCBI GI
                   337
BLAST score
                   1.0e-31
E value
Match length
                   106
% identity
                   72
                  (AF031609) unknown [Oryza sativa]
NCBI Description
                   403915
Seq. No.
                  LIB3434-011-P1-K1-C4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g6056413
BLAST score
                   217
                   1.0e-17
E value
                   55
Match length
                   82
% identity
                  (AC009525) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   403916
Seq. No.
Seq. ID
                   LIB3434-011-P1-K1-G6
                   BLASTN
Method
NCBI GI
                   q5929929
BLAST score
                   44
                   1.0e-15
E value
                   80
Match length
                   90
% identity
NCBI Description
                  Zea mays voltage-dependent anion channel protein 1b
                  (vdac1b) mRNA, complete cds; nuclear gene for mitochondrial
                  product
                   403917
Seq. No.
Seq. ID
                  LIB3434-012-P1-K1-A3
                   BLASTN
Method
NCBI GI
                   g5922603
                   201
BLAST score
                   1.0e-109
E value
Match length
                   220
                   99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0705D01
                   403918
Seq. No.
Seq. ID
                   LIB3434-012-P1-K1-E3
Method
                   BLASTN
```

g2662344

% identity

```
BLAST score
                  79
E value
                  9.0e-37
                  108
Match length
                  95
% identity
                  Oryza sativa mRNA for EF-1 alpha, complete cds
NCBI Description
Seq. No.
                  403919
                  LIB3434-012-P1-K1-G5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1136122
BLAST score
                  284
                  6.0e-26
E value
                  57
Match length
                  93
% identity
NCBI Description
                  (X91807) alfa-tubulin [Oryza sativa]
                  403920
Seq. No.
                  LIB3434-014-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2351580
BLAST score
                  684
                  4.0e-76
E value
Match length
                  155
% identity
                  (U82433). thymidine diphospho-glucose 4-6-dehydratase
NCBI Description
                  homolog [Prunús armeniaca]
Seq. No.
                  403921
Seq. ID
                  LIB3434-014-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q4538897
BLAST score
                  402
                  4.0e-39
E value
Match length
                  138
% identity
                  54
                  (AL049482) AX110P-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  403922
Seq. ID
                  LIB3434-014-P1-K1-E5
Method
                  BLASTX
NCBI, GI
                  q464981
BLAST score
                  554
E value
                  3.0e-57
Match length
                  107
% identity
                  93
                  UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 388207 (L23762)
                  ubiquitin carrier protein [Lycopersicon esculentum]
Seq. No.
                  403923
Seq. ID
                  LIB3434-015-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g2983642
BLAST score
                  336
E value
                  3.0e - 31
Match length
                  174
```

Seq. ID

```
NCBI Description (AE000728) diaminopimelate decarboxylase [Aquifex aeolicus]
Seq. No.
                   403924
                  LIB3434-015-P1-K1-A2
Seq. ID
Method
                  BLASTX
                   q5103812
NCBI GI
BLAST score
                   596
                   9.0e-62
E value
                  168
Match length
% identity
                   67
                   (ACO07591) Similar to gb AJ005073 Alix (ALG-2-interacting
NCBI Description
                  protein X) from Mus musculus. ESTs gb R90133, gb Z17944 and
                   gb AA605465 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   403925
Seq. ID
                  LIB3434-015-P1-K1-A4
Method
                  BLASTX
NCBI GI
                   q4056568
.BLAST score
                   605
                   7.0e-63
E value
Match length
                  163
% identity
NCBI Description
                  (U90944) PDI-like protein [Zea mays]
Seq. No.
                   403926
                  LIB3434-015-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4467095
BLAST score
                   193
E value
                   2.0e-14
Match length
                  45
% identity
                  (AL035538) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403927
                  LIB3434-015-P1-K1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q6016845
BLAST score
                  171
E value
                   3.0e-91
Match length
                  271
                 · 99
% identity
NCBI Description Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
Seq. No.
                   403928
                  LIB3434-015-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g100598
BLAST score
                   382
E value
                  1.0e-36
                  108
Match length
% identity
NCBI Description
                  ubiquitin / ribosomal protein S27a-1 - barley >gi 167073
                   (M60175) ubiquitin [Hordeum vulgare]
Seq. No.
                   403929
```

LIB3434-015-P1-K1-B7

Match length

```
BLASTX
Method
                   g5081779
NCBI GI
BLAST score
                   473
                   1.0e-47
E value
                   92
Match length
% identity
                   93
                   (AF150630) cellulose synthase [Gossypium hirsutum]
NCBI Description
                   403930
Seq. No.
                   LIB3434-015-P1-K1-C1
Seq. ID
Method
                   BLASTN
                   g6016845
NCBI GI
                   191
BLAST score
                   1.0e-103
E value
Match length
                   251
% identity
                   94
                   Oryza sativa genomic DNA, chromosome 1, clone:P0711E10
NCBI Description
                   403931
Seq. No.
                   LIB3434-015-P1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1184774
BLAST score
                   692
                   5.0e-73
E value
Match length
                   157
% identity
                   (U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase
NCBI Description
                   GAPC3 [Zea mays]
Seq. No.
                   403932
Seq. ID
                   LIB3434-015-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   q4544390
BLAST score
                   450
E value
                   1.0e-44
Match length
                   127
                   65
% identity
                   (AC007047) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   403933
Seq. ID
                   LIB3434-015-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   q5007084
BLAST score
                   908
E value
                   2.0e-98
Match length
                   172
                   98
% identity
                   (AF155333) NADP-specific isocitrate dehydrogenase [Oryza
NCBI Description
                   sativa]
Seq. No.
                   403934
Seq. ID
                   LIB3434-015-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   q2914706
BLAST score
                   707
E value
                   9.0e-75
```

Match length

```
% identity
                  83
                  (AC003974) putative homeobox protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  403935
                  LIB3434-015-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454472
BLAST score
                  157
                  3.0e-10
E value
Match length
                  53
% identity
                  62
NCBI Description
                  (AC006234) unknown protein [Arabidopsis thaliana]
                  403936
Seq. No.
Seq. ID
                  LIB3434-015-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q121332
BLAST score
                  869
E value
                  9.0e-94
Match length
                  168
                  98
% identity
                  GLUTAMINE SYNTHETASE ROOT ISOZYME (GLUTAMATE--AMMONIA
NCBI Description
                  LIGASE) (CLONE LAMBDA-GS8) >gi 68590 pir AJRZQB
                  glutamate--ammonia ligase (EC 6.3.1.2) beta, cytosolic -
                  rice >gi 20358 emb CAA32460 (X14244) cytosolic glutamine
                  syntethase (AA 1-357) [Oryza sativa]
                  403937
Seq. No.
Seq. ID
                  LIB3434-015-P1-K1-H1
Method
                  BLASTX
                  q283008
NCBI GI
                  813
BLAST score
                  3.0e-87
E value
                  158
Match length
                  99
% identity
NCBI Description
                  sucrose synthase (EC 2.4.1.13) - rice
                  >gi 20366 emb CAA46017 (X64770) sucrose synthase [Oryza
                  sativa]
                 403938
Seq. No.
                  LIB3434-015-P1-K1-H10
Seq. ID
Method
                  BLASTX
                  q6056418
NCBI GI
                  419
BLAST score
                  4.0e-41
E value
Match length
                  153
% identity
                  50
                  (AC009525) Similar to beta-glucosidases [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  403939
                  LIB3434-015-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2245012
BLAST score
                  195
                  1.0e-14
E value
```

```
% identity
                  72
                  (Z97341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  403940
                  LIB3434-016-P1-K1-A11
Seq. ID
Method
                  BLASTN
                  g538427
NCBI GI
                  274
BLAST score
                  1.0e-152
E value
Match length
                  285
                  99
% identity
NCBI Description
                  Oryza sativa ribosomal protein S16 mRNA, complete cds
Seq. No.
                  403941
                  LIB3434-016-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q445613
BLAST score
                  353
E value
                  2.0e-33
Match length
                  97
                  70
% identity
                  ribosomal protein L7 [Solanum tuberosum]
NCBI Description
Seq. No.
                  403942
                  LIB3434-016-P1-K1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g167043
BLAST score
                  41
E value
                  1.0e-13
Match length
                  53
                  94
% identity
                  Barley glyceraldehyde-3-phosphate dehydrogenase mRNA, 3'
NCBI Description
Seq. No.
                  403943
                  LIB3434-016-P1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1174162
BLAST score
                  406
E value
                  1.0e-39
Match length
                  88
% identity
                  (U44976) ubiquitin-conjugating enzyme [Arabidopsis
NCBI Description
                  thaliana] >gi 3746915 (AF091106) E2
                  ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
                  403944
Seq. No.
                  LIB3434-016-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1705434
BLAST score
                  291
                  3.0e-26
E value
Match length
                  103
% identity
NCBI Description
                  BIBENZYL SYNTHASE >gi 758243 emb CAA56276 (X79903)
```

bibenzyl synthase [Phalaenopsis sp.]

```
Seq. No.
                  403945
Seq. ID
                  LIB3434-016-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g1710424
BLAST score
                  265
                  6.0e-28
E value
Match length
                  103
% identity
                  67
                  50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21)
NCBI Description
                  >gi 2129718 pir S71282 ribosomal protein L21 - Arabidopsis
                  thaliana >gi 11\overline{49}573_emb_CAA89887_ (Z49787) chloroplast
                  ribosomal large subunit protein L21 [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3434-016-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  q2351580
BLAST score
                  596
E value
                  8.0e-62
                  134
Match length
% identity
                  (U82433) thymidine diphospho-glucose 4-6-dehydratase
NCBI Description
                  homolog [Prunus armeniaca]
                  403947
Seq. No.
                  LIB3434-016-P1-K1-H5
Seq. ID
Method
                  BLASTX
                  g1519249
NCBI GI
BLAST score
                  440
E value
                  5.0e-44
                  89
Match length
                  100
% identity
                  (U65956) GF14-b protein [Oryza sativa]
NCBI Description
Seq. No.
                  403948
                  LIB3434-016-P1-K1-H6
Seq. ID
Method
                  BLASTX
                              e. E.
NCBI GI
                  g133867
                  438
BLAST score
E value
                  9.0e-48
Match length
                  114
% identity
                  40S RIBOSOMAL PROTEIN S11 >gi 82722 pir S16577 ribosomal
NCBI Description
                  protein S11 - maize >gi 22470 emb CAA39438 (X55967)
                  ribosomal protein S11 [Zea mays]
                  403949
Seq. No.
                  LIB3434-017-P1-K1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4835773
BLAST score
                  36
E value
                  1.0e-10
Match length
                  68
% identity
                  Arabidopsis thaliana chromosome 1 BAC T16B5 sequence,
NCBI Description
```

complete sequence

Seq. No.

403955

```
Seq. No.
                   403950
                  LIB3434-017-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1305525
BLAST score
                  585
                  1.0e-60
E value
Match length
                  116
                  97
% identity
                  (U55212) Wilms' tumor-related protein QM [Oryza sativa]
NCBI Description
                   403951
Seq. No.
                  LIB3434-021-P1-K1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1163180
BLAST score
                  86
                  2.0e-40
E value
Match length
                  102
% identity
                  96
                  Glycine max arginine decarboxylase mRNA, complete cds
NCBI Description
                   403952
Seq. No.
                  LIB3434-021-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1001532
BLAST score
                  312
                   5.0e-29
E value
                  87
Match length
% identity
NCBI Description
                   (D64000) hypothetical protein [Synechocystis sp.]
                   403953
Seq. No.
                  LIB3434-021-P1-K1-H5
Seq. ID
                  BLASTX
Method
                  q401140
NCBI GI
BLAST score
                   684
                   3.0e-72
E value
                  126
Match length
% identity
                  SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2)
NCBI Description
                  >gi 20095_emb_CAA41774_ (X59046) sucrose-UDP
                  glucosyltransferase (isoenzyme 2) [Oryza sativa]
                  >qi 1587662 prf 2207194A sucrose synthase:ISOTYPE=2 [Oryza
                  sativa]
                   403954
Seq. No.
Seq. ID
                  LIB3434-023-P1-K1-B11
Method
                  BLASTX
                  g2498077
NCBI GI
                   570
BLAST score
                  8.0e-59
E value
Match length
                  125
% identity
                  84
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                   (PP18) >gi 1777930 (U55019) nucleoside diphosphate kinase
                   [Saccharum officinarum]
```

Method

BLASTX

```
LIB3434-023-P1-K1-C10
Seq. ID
Method
                  BLASTX
                  g129591
NCBI GI
BLAST score
                  231
                   7.0e-25
E value
                  85
Match length
                   74
% identity
                  PHENYLALANINE AMMONIA-LYASE >gi_295824_emb_CAA34226_
NCBI Description
                   (X16099) phenylalanine ammonia-lyase [Oryza sativa]
Seq. No.
                   403956
                  LIB3434-023-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4803960
BLAST score
                   150
                   3.0e-10
E value
Match length
                  50
% identity
                   (AC006202) putative carbonic anhydrase [Arabidopsis
NCBI Description
                   thaliana]
                   403957
Seq. No.
Seq. ID
                  LIB3434-024-P1-K1-C12
Method
                  BLASTX
NCBI GI
                   g3201541
BLAST score
                   641
E value
                   3.0e-67
Match length
                   136
% identity
                   86
                   (AJ005077) TCTR2 protein [Lycopersicon esculentum]
NCBI Description
Seq. No.
                   403958
                   LIB3434-024-P1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1174162
BLAST score
                   686
                   2.0e-72
E value
Match length
                   137
% identity
                   88
NCBI Description
                   (U44976) ubiquitin-conjugating enzyme [Arabidopsis
                   thaliana] >gi 3746915 (AF091106) E2
                   ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
Seq. No.
                   403959
Seq. ID
                   LIB3434-024-P1-K1-H4
Method
                  BLASTX
NCBI GI
                   g3790743
BLAST score
                  189
E value
                   5.0e-14
Match length
                   64
% identity
                   53
NCBI Description
                   (AF099919) contains similarity to cytochrome C oxidase
                   assembly protein COX17 homologues [Caenorhabditis elegans]
Seq. No.
                   403960
Seq. ID
                   LIB3434-025-P1-K1-A2
```

NCBI GI

E value

BLAST score

Match length

% identity

q2583108

3.0e - 32

343

123

```
NCBI GI
                  q1706958
BLAST score
                  541
E value
                  2.0e-55
                  137
Match length
                  77
% identity
                  (U58284) cellulose synthase [Gossypium hirsutum]
NCBI Description
                  403961
Seq. No.
                  LIB3434-025-P1-K1-B9
Seq. ID
                  BLASTX
Method
                  q1477428
NCBI GI
BLAST score
                  199
                  3.0e-15
E value
                  50
Match length
% identity
                  80
NCBI Description
                  (X99623) alpha-tubulin 1 [Hordeum vulgare]
Seq. No.
                  403962
                  LIB3434-025-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q5091616
BLAST score
                  352
E value
                  3.0e-33
Match length
                  179
                  44
% identity
                  (AC007454) F23M19.3 [Arabidopsis thaliana]
NCBI Description
                  403963
Seq. No.
Seq. ID
                  LIB3434-025-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q3290022
BLAST score
                  373
                   6.0e-36
E value
Match length
                  95
% identity
                  75
                   (AF044173) cysteine synthase; CS-B; O-acetylserine (thiol)
NCBI Description
                  lyase; plastidic isoform [Solanum tuberosum]
Seq. No.
                   403964
Seq. ID
                  LIB3434-025-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q5901954
BLAST score
                  160
                  1.0e-10
E value
Match length
                  96
% identity
                  FGFR1 oncogene partner >gi 4454263 emb CAA77020 (Y18046)
NCBI Description
                  FGFR1 oncogene partner (FOP) [Homo sapiens]
                  403965
Seq. No.
Seq. ID
                  LIB3434-026-P1-K1-A2
                  BLASTX
Method
```



```
NCBI Description (AC002387) putative surface protein [Arabidopsis thaliana]
Seq. No.
                  403966
                  LIB3434-026-P1-K1-H1
Seq. ID
Method
                  BLASTN
                  g4761585
NCBI GI
BLAST score
                  34
                  5.0e-10
E value
                  58
Match length
                  90
% identity
NCBI Description
                  Malus domestica GD4-2 profilin mRNA, complete cds
                  403967
Seq. No.
Seq. ID
                  LIB3434-027-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q2501064
BLAST score
                  229
                  2.0e-19
E value
Match length
                  65
                  68
% identity
                  PROBABLE THREONYL-TRNA SYNTHETASE, CYTOPLASMIC
NCBI Description
                   (THREONINE--TRNA LIGASE) (THRRS) >gi 2191162 (AF007270)
                  Similar to threonyl-tRNA synthetase; coded for by A.
                  thaliana cDNA R65376 [Arabidopsis thaliana]
                  403968
Seq. No.
                  LIB3434-027-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3643610
BLAST score
                  515
                  2.0e-52
E value
Match length
                  110
% identity
                  87
NCBI Description
                   (AC005395) putative serine/threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                  403969
                  LIB3434-027-P1-K1-G6
Seq. ID
Method
                  BLASTX
                  g1777312
NCBI GI
BLAST score
                  273
E value
                  5.0e-24
                  87
Match length
% identity
NCBI Description
                   (D30622) novel serine/threonine protein kinase [Arabidopsis
                  thaliana]
                  403970
Seq. No.
                  LIB3434-028-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4874301
BLAST score
                  171
E value
                  2.0e-12
Match length
                  40
% identity
                  82
NCBI Description
                   (AC006053) proton-ATPase-like protein [Arabidopsis
```

thaliana]

NCBI GI

E value

BLAST score

Match length

g3786009

3.0e-41

419

115

```
Seq. No.
                   403971
Seq. ID
                  LIB3434-028-P1-K1-F6
Method
                  BLASTX
                   q120668
NCBI GI
BLAST score
                  183
                   6.0e-14
E value
                  49
Match length
                   67
% identity
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi 82399 pir A24159 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment)
                  >gi 167044 (M36650) glyceraldehyde-3-phosphate
                   dehydrogenase [Hordeum vulgare] >gi 225347 prf 1301218A
                   dehydrogenase, glyceraldehydephosphate [Hordeum vulgare var.
                   distichum]
Seq. No.
                  403972
                  LIB3434-029-P1-K1-A2
Seq. ID
Method:
                  BLASTX
NCBI GI
                  g2914710
BLAST score
                  579
E value
                   1.0e-59
Match length
                  181
                  57
% identity
NCBI Description
                  (AC003974) putative beta-D-galactosidase [Arabidopsis
                  thaliana]
Seq. No.
                   403973
Seq. ID
                  LIB3434-029-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q4249382
BLAST score
                  599
E value
                   4.0e-62
Match length
                  168
% identity
NCBI Description
                   (AC005966) Strong similarity to gi 3337350 F13P17.3
                  putative permease from Arabidopsis thaliana BAC
                  gb AC004481. [Arabidopsis thaliana]
Seq. No.
                  403974
Seq. ID
                  LIB3434-030-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q2078350
BLAST score
                  587
E value
                  7.0e-61
Match length
                  135
% identity
NCBI Description
                  (U95923) transaldolase [Solanum tuberosum]
Seq. No.
                   403975
Seq. ID
                  LIB3434-031-P1-K1-A7
Method
                  BLASTX
```